>lcl|NZ\_FO834906.1\_prot\_1 [gene=dnaA] [locus\_tag=BN49\_RS01145] [protein=chromosomal replication initiator protein DnaA] [pseudo=true] [partial=5'] [location=<694..1935] [gbkey=CDS]

YLNNINGLLNDFCGADAPQLRFEVGAKPASSLQKGAVSPAAAAIPAAQVQTARAAPTIVRPGWDNVPAPA

EPTYRSNVNVKHTFDNFVEGKSNQLARAAARQVADNPGGAYNPLFLYGGTGLGKTHLLHAVGNGIVARKP

NAKVVYMHSERFVQDMVKALQNNAIEEFKRYYRSVDALLIDDIQFFANKERSQEEFFHTFNALLEGNQQI

ILTSDRYPKEINGVEDRLKSRFGWGLTVAIEPPELETRVAILMKKADENDIRLPGEVAFFIAKRLRSNVR

ELEGALNRVIANANFTGRAITIDFVREALRDLLALQEKLVTIDNIQKTVAEYYKIKVADLLSKRRSRSVA

RPRQMAMALAKELTNHSLPEIGDAFGGRDHTTVLHACRKIEQLREESHDIKEDFSNLIRTLSS

>lcl|NZ\_FO834906.1\_prot\_WP\_004145090.1\_2 [gene=dnaN] [locus\_tag=BN49\_RS01150] [protein=DNA polymerase III subunit beta] [protein\_id=WP\_004145090.1] [location=1940..3040] [gbkey=CDS]

MKFTVEREHLLKPLQQVSGPLGGRPTLPILGNLLLQVADGALSLTGTDLEMEMVARVALVQPHEAGATTV

PARKFFDICRGLPEGAEIAVQLEGDRMLVRSGRSRFSLSTLPAADFPNLDDWQSEVEFTLPQATMKRLIE

ATQFSMAHQDVRYYLNGMLFETEGSELRTVATDGHRLAVCSMPLEASLPNHSVIVPRKGVIELMRMLDGG

DTPLRVQIGSNNIRAHVGDFIFTSKLVDGRFPDYRRVLPKNPDKHLEAGCDILKQAFARAAILSNEKFRG

VRLYVSENQLKITANNPEQEEAEEILDVTYAGTEMEIGFNVSYVLDVLNALKCENVRILLTDSVSSVQIE

DAASQSAAYVVMPMRL

>lcl|NZ\_FO834906.1\_prot\_WP\_004150293.1\_3 [gene=recF] [locus\_tag=BN49\_RS01155] [protein=DNA replication/repair protein RecF] [protein\_id=WP\_004150293.1] [location=3248..4321] [gbkey=CDS]

MSLSRLLIKDFRNIEHADLALSPGFNFLVGANGSGKTSVLEAIYTLGHGRAFRSLQIGRVIRHEQDAFVL

HGRLQGEERETAIGLTKDKQGDSKVRIDGTDGHKVAELAHLMPMQLITPEGFTLLNGGPKYRRAFLDWGC

FHNEAGFFTAWSNLKRLVKQRNAALRQVSRYAQLRPWDLELIPLAEQISRWRAEYSAAIVEDMADTCQQF

LPEFTLTFSFQRGWEKETDYAEVLERNFERDRMLTYTAHGPHKADFRIRADGAPVEDTLSRGQLKLLMCA

LRLAQGEFLTRVSGRRCLYLIDDFASELDDARRGLLSSRLKATQSQVFVSAISAEHVMDMSDKNSKMFRV

EKGKITD

>lcl|NZ\_FO834906.1\_prot\_WP\_004173845.1\_4 [gene=gyrB] [locus\_tag=BN49\_RS01160] [protein=DNA topoisomerase (ATP-hydrolyzing) subunit B] [protein\_id=WP\_004173845.1] [location=4350..6764] [gbkey=CDS]

MSNSYDSSSIKVLKGLDAVRKRPGMYIGDTDDGTGLHHMVFEVVDNAIDEALAGYCKDIVVTIHSDNSVS

VQDDGRGIPTGIHPEEGVSAAEVIMTVLHAGGKFDDNSYKVSGGLHGVGVSVVNALSQKLELVIQRDNKV

HKQMYEHGVPQAPLAVTGETDKTGTMVRFWPSLETFTNVTEFEYDILAKRLRELSFLNSGVSIRLRDKRD

GKEDHFHYEGGIKAFVEYLNKNKTPIHPNIFYFSTEKDGIGVEVALQWNDGFQENIYCFTNNIPQRDGGT

HLAGFRAAMTRTLNAYMDKEGYSKKAKVSATGDDAREGLIAVVSVKVPDPKFSSQTKDKLVSSEVKSAVE

QQMNELLSEYLLENPSDAKIVVGKIIDAARAREAARRAREMTRRKGALDLAGLPGKLADCQERDPALSEL

YLVEGDSAGGSAKQGRNRKNQAILPLKGKILNVEKARFDKMLSSQEVATLITALGCGIGRDEYNPDKLRY

HSIIIMTDADVDGSHIRTLLLTFFYRQMPEIVERGHVYIAQPPLYKVKKGKQEQYIKDDEAMDQYQISIA

LDGATLHTNANAPALAGEPLEKLVAEFNATQKMIGRMERRFPKALLKELIYQPTLTEADLADEQKVTRWV

NTLVSELNEKEQHGSQWKFDLHENKELQHFEPVIRVRTHGVDTDYPLDNEFIMGPEYRRICALGEKLRGL

MEEDAYIERGERRQPVASFEQALDWLVKESRRGLSIQRYKGLGEMNPDQLWETTMDPDSRRMLRVTVKDA

IAADQLFTTLMGDAVEPRRAFIEENALKAANIDI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151530.1\_5 [gene=yidA] [locus\_tag=BN49\_RS01165] [protein=sugar-phosphatase] [protein\_id=WP\_004151530.1] [location=6966..7778] [gbkey=CDS]

MAIKLIAIDMDGTLLLPDHTISPAVKAAIAAARERGVNVVLTTGRPYAGVHSYLKELHMEQPGDYCITYN

GALVQKAGDGSTVAQTALSYDDYRFLEQLSREVGSHFHALDRNTLYTANRDISYYTVHESYVATIPLVFC

EAEKMDPEIQLLKVMMIDEPAILDQAIARIPAEVKEKYTVLKSAPYFLEILDKRVNKGTGVKSLADALGI

KPEEIMAIGDQENDIAMIEFAGVGVAMDNAIPAVKEAANFITKSNLEDGVAFAIEKYVLA

>lcl|NZ\_FO834906.1\_prot\_WP\_075209882.1\_6 [locus\_tag=BN49\_RS01170] [protein=hypothetical protein] [protein\_id=WP\_075209882.1] [location=7928..9010] [gbkey=CDS]

MNIYHRLMLVTLPFASVQICAAAEPTAPLEPAYAYHGAEPADLSAPESRQPAAAASSSLLPLLGDEARKR

GYVLPLPFGVSINYMDMRQNINVDSINFTGLSLDGRNIDCGKDPVCKHAVNNIFANGPVSLDNAFQIGVG

HTRESSKTETLKLDAWLLPFMNVYGLVGHTEGHSISQIAVGLKGPNGKVVPLPGMQDLDFRLDFKGTTYG

MGTTLVGGVGNWFTVLDANYTQTRFDILDGSIDALTFSPRVGYRFSTPSVDALHLPAGKLNLWVGSMYQD

VQQEFKGSLSDLSMPSPMLQNMVNLANQDNNGRFDVKQHLQSPWNVLVGAQYELTQNFNITTEFGFAERN

SFFIAGEYRF

>lcl|NZ\_FO834906.1\_prot\_WP\_016528946.1\_7 [locus\_tag=BN49\_RS01175] [protein=BamA/TamA family outer membrane protein] [protein\_id=WP\_016528946.1] [location=9007..10140] [gbkey=CDS]

MSRLFITFLLLMVCPTGSQAEALSREKIDGWLQHLGASDKFDASKGIDWGVMPGPFYTPELGLGIGTAVV

GLYRPDPQDTTSQNSTLTLSGYASSTGAFGLSVKNYTFFDRDLWRVFVDGSIANTPTYYWGQGFHAGDKD

NEKEKYTAQVLTLRPTLYRQLIDHVYLGAGWSLAAQNADEMDHDDRPKIENTPQGPSVFSSGASIDINWD

DRDFVPNPRRGQYANLRYTHYAPGLGSDTRFEEFQLHYSHYHALSEKSVLAWEVDGAFTQGEVPWSMMPL

LGSDERMRGYYQGRYRDKNVVSGQLEYRRQLTWRHGIVAWAGAGTMGPSLSSLNNGRWLPSAGVGYRFEF

KPRVNVRLDYGIGNGSSGFYFQVGEAF

>lcl|NZ\_FO834906.1\_prot\_WP\_004145084.1\_8 [gene=dgoR] [locus\_tag=BN49\_RS01180] [protein=D-galactonate utilization transcriptional regulator DgoR] [protein\_id=WP\_004145084.1] [location=10370..11059] [gbkey=CDS]

MTLNKTDRIVISLGKQIVSGKYVPGSALPAEAELCEEFETSRNIIREVFRSLMAKRLIEMKRYRGAFVAP

RNQWNYLDTEVLQWVLENDYDPRLISAMSEVRNLVEPAIARWAAERATSSDLAEIESALNDMIANNQNRD

AFNEADIRYHEAVLQSVHNPVLQQLSVAISSLQRAVFERTWMGDEGNMPKTLQEHKALFDAIRHQDSDAA

EQAALTMIASSTRRLKEIT

>lcl|NZ\_FO834906.1\_prot\_WP\_004145083.1\_9 [locus\_tag=BN49\_RS01185] [protein=2-dehydro-3-deoxygalactonokinase] [protein\_id=WP\_004145083.1] [location=11056..11934] [gbkey=CDS]

MTARYIAIDWGSTNLRAWLYQGEECLESRQSEAGVTRLNGRSPAAVLAEITQHWRDGATPVVMAGMVGSN

VGWKIAPYLPLPAAFSDIGQQLTAVGDNIWIIPGLCVSRDDNHNVMRGEETQLLGARALAPSSVYVMPGT

HCKWVLADRRQIHDFRTVLTGELHHLLLQHSLVGAGLPPQETSAAAFAAGLQRGINNPAVLPQLFEVRAS

HVLGALPREQVSEFLSGLLIGAEVATLSDTFAGQQAISLVAGSSLTSRYQQAFAAIGREVSAVAGDTAFQ

TGIRSIAYAVAN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530020.1\_10 [locus\_tag=BN49\_RS01190] [protein=2-dehydro-3-deoxy-6-phosphogalactonate aldolase] [protein\_id=WP\_016530020.1] [location=11918..12535] [gbkey=CDS]

MQWQTNLPLIAILRGITPDEALAHVGAVIDAGFDAVEIPLNSPQWEKSIPQVVDAYGEQALIGAGTVLQP

EQVDRLAAMGCRLIVTPNIQPEVIRRAVGYGMTVCPGCATASEAFSTLDAGAQALKIFPSSAFGPDYIKA

LKAVLPPEVPVFAVGGVTPENLAQWINAGCVGAGLGSDLYRAGQSVERTAQQAAAFVKAYREAVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530021.1\_11 [gene=dgoD] [locus\_tag=BN49\_RS01195] [protein=galactonate dehydratase] [protein\_id=WP\_016530021.1] [location=12532..13680] [gbkey=CDS]

MKITNITTYRLPPRWMFLKIETDEGIVGWGELVIEGRARTVEAAVHEFGDYLIGQDPARINDLWQVMYRG

GFYRGGPIMMSAIAGIDQALWDIKGKVLNAPVWQLMGGLVRDKIKAYSWVGGDRPAEVIDGIKKLRGIGF

DTFKLNGCEEMGIIDNSRAVDAAVNTVAQIREAFGNEIEFGLDFHGRVSAPMAKVLIKELEPYRPLFIEE

PVLAEQAEYYPRLAAQTHIPIAAGERMFSRFEFKRVLEAGGVAILQPDLSHAGGITECYKIAGMAEAYDV

GLAPHCPLGPIALAACLHVDFVSHNAVFQEQSMGIHYNKGAELLDFVKNKEDFNMEGGFFKPLMKPGLGV

EIDEARVIELSKNAPDWRNPLWRYEDGSVAEW

>lcl|NZ\_FO834906.1\_prot\_WP\_046042092.1\_12 [locus\_tag=BN49\_RS01200] [protein=MFS transporter] [protein\_id=WP\_046042092.1] [location=13858..15186] [gbkey=CDS]

MVSGFAMPKIWRQIAMDISVTAVKTGRRRYLTLIMIFITVVICYVDRANLAVASAHIQEEFGISKAEMGY

VFSAFAWLYTLCQIPGGWFLDRVGSRLTYFIAIFGWSVATLLQGFATGLMSLIGLRAITGIFEAPAFPTN

NRMVTSWFPEHERASAVGFYTSGQFVGLAFLTPLLIWIQELLSWHWVFIVTGGIGIIWSLIWFKVYQPPR

LTKSISKAELDYIRDGGGLVDGDAPLKKEARQPLSKADWKLVFHRKLVGVYLGQFAVTSTLWFFLTWFPN

YLTQEKGITALKAGFMTTVPFLAAFFGVLLSGWLADKLVKKGYSLGVARKTPIICGLLISTCIMGANYTN

DPIWIMALMALAFFGNGFASITWSLVSSLAPMRLIGGVFNFVGGLGGITVPLVIGYLAQDYGFGPALVYI

SVVALIGALSYILLVGDVKRVG

>lcl|NZ\_FO834906.1\_prot\_WP\_004150284.1\_13 [locus\_tag=BN49\_RS01205] [protein=DUF3748 domain-containing protein] [protein\_id=WP\_004150284.1] [location=15238..16464] [gbkey=CDS]

MKQVTFAPRHHQLTNINTWTPDSQWLVFDVRPSGASFTGETIERVNVNSGTVETIYRATQGAHVGVVTVH

PTQERYVFIHGPERPDAQWQYDFHHRRGVVAFQGAVENLDAMDITPPYTPGALRGGSHVHVYSPNGQFVS

FTYNDHVLHERDPALDLRNVGVAAPYGPVTPQGQHPREYGGSHWCVLVSRTTPAPAPGSDEINRAYEEGW

VGNHTLAFIGDTLAENGDKVPELFIVDLPQDEAGWKQPGGAPLAGTATTMPAPPAGVSQRRLTFTHHRRY

PGLVNVPRHWVRANPQATAIAFLMRDDAGVVQLWLISPQGGEPRQLTHHASGIQSAFNWHPSGEWLGFAL

EDRIACCHAGTGDITFLTDTHAHAPSADAIVFSPDGKQIAWMEEVDGYRQLWVTQTGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151524.1\_14 [locus\_tag=BN49\_RS01210] [protein=YceK/YidQ family lipoprotein] [protein\_id=WP\_004151524.1] [location=complement(16466..16798)] [gbkey=CDS]

MKSRRLLKLVLFSGIISLSGCSSVMSHTGGKEGTYPGTRSSAQTLGDSDTNWGVKSLVALDMPFTAVMDT

LLLPWDMFRTDSSIKSRVEKSEKATLATNSVIPPAPMPAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004151523.1\_15 [gene=ibpA] [locus\_tag=BN49\_RS01215] [protein=heat shock chaperone IbpA] [protein\_id=WP\_004151523.1] [location=17113..17526] [gbkey=CDS]

MRNFDLSPLYRSAIGFDRLFNLLENNQSQSNGGYPPYNVELVDENHYRIAIAVAGFAESELEITAQDNLL

IVKGAHAAEQKERTYLYQGIAERNFERKFQLAENIHVRGANLVNGLLYIDLERVIPEANKPRRIEIN

>lcl|NZ\_FO834906.1\_prot\_WP\_004145074.1\_16 [gene=ibpB] [locus\_tag=BN49\_RS01220] [protein=heat shock chaperone IbpB] [protein\_id=WP\_004145074.1] [location=17643..18071] [gbkey=CDS]

MRNYDLSPLLRQWIGFDKLASALQTAGESQSFPPYNIEKSDDNHYRITLALAGFRQEDLDIQLEGTRLVV

KGTPQQPEKETTWLHQGLVSQAFSLSFTLADNMEVSGATFTNGLLHIDLTRNEPEQIAPQRIAISERPAL

NS

>lcl|NZ\_FO834906.1\_prot\_17 [gene=dinD] [locus\_tag=BN49\_RS30170] [protein=DNA damage-inducible protein D] [pseudo=true] [location=18208..19032] [gbkey=CDS]

MNEQQPFEAIRKSDEAGREYWSARNLGPLLDYKEWRNFYKVIAKAIISCEASGHPSADHFVETNKMVELG

SGASRNLEDFHLSRYACYLVVQNGDPSKPVIAAGQTYFALQTRRQELQDDQIFKSLREDEK\*LFLHNELK

EHNKHLVETAQRAGVETTLDFAVFQNHGYKGLYGGLDQKAIHERKGLKKSQKILDYMGSTELAANLFRAT

QTEEKLRRDAVDSKQLANKTHYDVGQKVRQTIKDLGGTMPEALPSPEKSIQQLTIAAKNKNAPE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042103.1\_18 [locus\_tag=BN49\_RS01230] [protein=putative transporter] [protein\_id=WP\_046042103.1] [location=19134..20795] [gbkey=CDS]

MSEIALTVSVLALVAVVGLWIGNVKIRGVGFGIGGVLFGGIIVGHFVDQAGVALSSPMLHFIQEFGLILF

VYTIGIQVGPGFFASLRVSGLRLNLFAILIVILGGMVTAVLHKLFNIPLPVVLGIFSGAVTNTPALGAGQ

QILRDLGVPFEVVDQMGMSYAMAYPFGICGILLTMWLVRLFFRINVEKEAQRFEESSGNGHAHLHTINVR

VENPNLNQMAIQDVPMLNNDNIVCSRLKRGELLMVPAPGTLIQAGDLLHLVGRPEDLHNAQLVIGQEVAT

SLSTRGTDLKVERVVVTNEKVLGKKIRDLHVKQRYDVVISRLNRAGVELVASSSASLQFGDILNLVGRPE

AIDAVAAELGNAQQKLQQVQMLPVFIGIGLGVLLGSIPLFIPGFPAALKLGLAGGPLIMALILGRIGSIG

KLYWFMPPSANLALRELGIVLFLAVVGLKSGGDFVATLTQGDGLSWIAYGIFITAIPLLTVGILARMLAK

MNYLTLCGMLAGSMTDPPALAFANNLHATSGAAALSYATVYPLVMFLRIITPQLLAVLFWGLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151520.1\_19 [locus\_tag=BN49\_RS01235] [protein=GntR family transcriptional regulator] [protein\_id=WP\_004151520.1] [location=complement(20787..21509)] [gbkey=CDS]

MIYKSIADRLRLRLNSADFAIGSPLPGEKKLAEEFGVARMTIRKAIDLLVDWGLVVRRHGSGTYVARKDV

HHETSNLTGLAEVLRKQGKEVVSQVLAFEVMPAPPAIASLLRIKIDERIYFSRRVRYVDGKPLMLEDSYM

PVKLFRNLSLSHLEGSKFDYIEKECGIIISGNYETLTPVLADKQLARSMNVPEQTPLLRITSLSYSDSGE

FLNYSVMFRNASEYQVDYHLRRVQAQSPLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002923307.1\_20 [locus\_tag=BN49\_RS01240] [protein=alpha-glucoside-specific PTS transporter subunit IIBC] [protein\_id=WP\_002923307.1] [location=21808..23430] [gbkey=CDS]

MLSQIQRFGGAMFTPVLLFPFAGIVVGIAIMLRNPMFVGEALTAPDSLFAQIVHIIEEGGWTVFRNMPLI

FAVGLPIGLAKQAQGRACLAVLVSFLTWNYFINAMGMTWGHFFGVDFSAEPTAGSGLTMIAGIKTLDTSI

IGAIVISGLVTALHNRYFDKPLPVFLGIFQGSSFVVIVAFLAMIPCAWLTLLGWPKVQLGIESLQAFLRS

AGALGVWVYIFLERILIPTGLHHFVYGPFIFGPAVVEGGLQVYWAEHLQAFSQSTEPLKTLFPEGGFALH

GNSKVFGSVGIALALYFTAAPENRVKVAGLLIPATLTAMLVGITEPLEFTFLFISPLLFAVHAVLAATMA

TVMYICGVVGNFGGGLLDQFLPQNWIPMFHHHASMMFIQIGIGLCFTALYFVVFRTLILRLNLKTPGREE

SEIKLYSKADYQAARGKTTAAAAPETRLGQAAGFLQALGGADNIESINNCATRLRIALVDMAKTQSDDVF

KALGAHGVVRRGNGIQVIVGLHVPQVRDQLENLMKDSLSTEHTTMTEAVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002923306.1\_21 [locus\_tag=BN49\_RS01245] [protein=6-phospho-alpha-glucosidase] [protein\_id=WP\_002923306.1] [location=23427..24749] [gbkey=CDS]

MKKFSVVIAGGGSTFTPGIVLMLLANQDRFPLRSLKFYDNDGARQETIAEACKVILKEQAPEIEFSYTTD

PQAAFTDVDFVMAHIRVGKYPMREQDEKIPLRHGVLGQETCGPGGIAYGMRSIGGVLELVDYMEKYSPNA

WMLNYSNPAAIVAEATRRLRPNAKILNICDMPIGIEGRMAQIVGLKDRKQMRVRYYGLNHFGWWTSIEDL

DGNDLMPKLREYVAKYGYVPPSNDPHTEASWNDTFAKAKDVQALDPQTMPNTYLKYYLFPDYVVAHSNPE

RTRANEVMDHREKNVFSACRAIIAAGKSTAGDLEIDEHASYIVDLATAIAFNTQERMLLIVPNNGAIHNF

DADAMVEIPCLVGHNGPEPLTVGDIPHFQKGLMSQQVAVEKLVVDAWEQRSYHKLWQAITLSKTVPSASV

AKAILDDLIAANKDYWPELH

>lcl|NZ\_FO834906.1\_prot\_WP\_002923305.1\_22 [locus\_tag=BN49\_RS01250] [protein=DUF202 domain-containing protein] [protein\_id=WP\_002923305.1] [location=24851..25198] [gbkey=CDS]

MKISRLGEAPDYRFSLANERTFLAWIRTALGFLAAGVGLDQLAPDFATPLIREILALLLCLFAGGMAIYG

YLRWLNNEKAMRLKQDLPYTRTLLVISILLLAVVAAVMLLVVYGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002923304.1\_23 [locus\_tag=BN49\_RS01255] [protein=DUF202 domain-containing protein] [protein\_id=WP\_002923304.1] [location=25188..25550] [gbkey=CDS]

MADKRRARRESDPGLQPERTSLAWFRTLLGYGALMALAIKHSWHRAGLPFWLSIGVLAIVAVILWGYTRR

RHLMDVDDSDFLQPRAVRDKFLIALAVLSLAFLFAVTHLQPIVLFIRDMS

>lcl|NZ\_FO834906.1\_prot\_WP\_004889115.1\_24 [locus\_tag=BN49\_RS01260] [protein=hypothetical protein] [protein\_id=WP\_004889115.1] [location=25625..26047] [gbkey=CDS]

MEAHHCHQPQAFYAQLRQQGLTAIHFIPQLAAGDAALWGEFLCAVFHRWVREDIGRINILLFSETLSAWC

GETLTQPGAPAANSACYGCPWLRLCRCGEQEDPLCAGYRQFYDFSGPYMRVMRDLRRQQRPPEALMPLLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530744.1\_25 [gene=dsdA] [locus\_tag=BN49\_RS01265] [protein=D-serine ammonia-lyase] [protein\_id=WP\_016530744.1] [location=complement(26051..27379)] [gbkey=CDS]

MKNADLTTLTATFPLVQDLIALKETTWFNPATTTLAEGLPYVGLTADDVQDAHARLQRFAPYLAAAFPET

AASGGIIESEVVAIPAMKRSLEQKFGQPISGELLLKKDSHLPISGSIKARGGIYEVLTHAEKLALEAGLL

TTADDYRKLLTPEFKQFFSQFSIAVGSTGNLGMSIGIMSARIGFQVTVHMSADARAWKKAKLRSHGVTVV

EYEEDYGVAVEQGRKAAESDPNCFFIDDENSRTLFLGYAVAGERLKAQFAQAGRVVDADHPLFVYLPCGV

GGGPGGVAFGLKLAFGDHVHCLFAEPTHSPCMLLGVYTGLHDQIAVQDLGIDNLTAADGLAVGRASGFVG

RAMERLLDGFYTLDDQTMYDMLGWLAKAENIRLEPSALAGMAGPQRVCASQAYHQLQGLGEQQLQQSTHL

VWATGGGMVPEEEMAQYLAKGR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530745.1\_26 [gene=dsdX] [locus\_tag=BN49\_RS01270] [protein=D-serine transporter DsdX] [protein\_id=WP\_016530745.1] [location=complement(27396..28733)] [gbkey=CDS]

MESQIWVVSTLLISIVLIVLTIVKLKFHPFLALLLASFFVGAMMGMGPLEMVNAIESGIGGTLGFLAAVI

GLDTILGKMMEVSGAAERIGLTLQRCRWLSADVIMVLVGLICGITLFVEVGVVLLIPLAFSIAKKTNTSL

LKLAIPLCTALMAVHCVVPPHPAALFVANKLGADIGTVIVYGLLVGLIASLVGGPLFLRLLGNRLPFKPV

PAEFSNLDVREESTLPSLGATLFTVLLPIGLMLVKTVAELNMAKGGTLYTVLEFIGNPITAMFIAVFVAY

YMLGIRRQMGMGVLLTHTENGFGSIANILLIIGAGGAFNAILKSSGLADSLAVILSNLDMHPILLAWLVA

LILHAAVGSATVAMMGATAIVAPMLPLYPGVSPEIIAIAIGSGAIGCTIVTDSLFWLVKQYCGASLSETF

KYYTTATFIASLLALAATFLLSFII

>lcl|NZ\_FO834906.1\_prot\_WP\_040146642.1\_27 [locus\_tag=BN49\_RS30805] [protein=hypothetical protein] [protein\_id=WP\_040146642.1] [location=28855..28959] [gbkey=CDS]

MTSKYAMGQINSSFSGSSGIIFLSSRLPIIARSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150274.1\_28 [gene=dsdC] [locus\_tag=BN49\_RS01275] [protein=DNA-binding transcriptional regulator DsdC] [protein\_id=WP\_004150274.1] [location=28959..29882] [gbkey=CDS]

MDVLKTLGTRLLNGWQLSRLSTFEVAARHESFALAADELALTPSAVSHRINQLEEELGIQLFVRSHRKVE

LTREGKRVYWALKASLDGLNQEILDIKNQELSGSLTVYSRPSIAQCWLVPALGDFSRRYPAISLTVLTGN

DNVNLQRAGIDLAIYFDDAPSSQLSHHFLMDEAIVPVCTPYYARQLQLTSNPASLRHCTLLHDRQAWSND

SGTDEWFSWAQQFGIELPQSSGIGFDRSDLAVIAAMNHVGVAMGRKRLVQKRLESGELIAPFGDMTLKCH

QHYYVTTLPGRQWPKIDAFIEWLHSLT

>lcl|NZ\_FO834906.1\_prot\_WP\_004181587.1\_29 [gene=emrD] [locus\_tag=BN49\_RS01280] [protein=multidrug efflux MFS transporter EmrD] [protein\_id=WP\_004181587.1] [location=complement(30042..31226)] [gbkey=CDS]

MKRHKNFNLLLMLVLLVAVGQMAQTIYIPAIADMAVALNVREGAVQSVMAAYLLTYGISQLFYGPLSDRV

GRRPVILVGMSIFMLATLVAITTHSLPVLIAASAMQGMGTGVGGVMARTLPRDLYEGAQLRHANSLLNMG

ILVSPLIAPLLGGILDTLWSWRACYAFLLVLCAGVTFSMAKWMPETRPEGAPRTKLLASYKTLFGTGAFN

CYLLMLIGGLAGIAVFEACSGVLMGAVLGLSSMAVSILFILPIPAAFFGAWFAGRPNKRFPTLMWQSVIC

CLLAGLMMWIPGLLGIMTVWTLLVPAALFFFGAGMLFPLATSGAMEPFPFLAGTAGALVGGLQNIGSGVL

AWLSAMMPQTGQGSLGLLMMLMGLLILLCWLPLASRFTHHQQPV

>lcl|NZ\_FO834906.1\_prot\_WP\_002923296.1\_30 [locus\_tag=BN49\_RS01285] [protein=DMT family transporter] [protein\_id=WP\_002923296.1] [location=complement(31402..32235)] [gbkey=CDS]

MTLTVFCILLFAALLHASWNAIVKASGDKMYAAIGVSGSAALIALVMLPFAPQPALVSAPYLLASCALQV

VYTVLVAKTYQVSDMSQTYPLMRGTAPLLVAAISVLFLGDRLSPLAWLGIGVICLAILAMAFNGRASSRK

GIVLALINACFIAGYTLVDGTGVRLAGSALGYTLWTFFMNGFCLLCWAMVARRREASRYLRQHWKKGILG

GIGTMGSYGLALWAMTQAPLAVVAALRETSILFGALIAFIVLKEQLMPLRIVAACGIAAGAILLRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002923294.1\_31 [locus\_tag=BN49\_RS01290] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002923294.1] [location=complement(32304..32750)] [gbkey=CDS]

MPPLLIAATTPDAPGFAALRIESLEQHFNMLRRLAENWQSGKNRFNAPGETLLGAFVNHQLVGVCGINSD

PFSPQPRAGRIRHLYISERYRRRGIGQQLLVSVITHSSAWFDFLNTHAPAQAWPFYERLGFRPVYDEPRV

THRLFCSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004145059.1\_32 [gene=tisB] [locus\_tag=BN49\_RS01295] [protein=type I toxin-antitoxin system toxin TisB] [protein\_id=WP\_004145059.1] [location=complement(32841..32960)] [gbkey=CDS]

MCSLTTGDARMGGMDIIILILKLMVAVLQLLDAVLKQFR

>lcl|NZ\_FO834906.1\_prot\_WP\_014343455.1\_33 [locus\_tag=BN49\_RS30810] [protein=hypothetical protein] [protein\_id=WP\_014343455.1] [location=complement(33164..33331)] [gbkey=CDS]

MSKNKLNLYKHRFYVFTMDLFSSTKICAKDHSSAQKGRKQKTPPERGFYQHGYRW

>lcl|NZ\_FO834906.1\_prot\_WP\_002923286.1\_34 [gene=ivbL] [locus\_tag=BN49\_RS28505] [protein=ilvB operon leader peptide IvbL] [protein\_id=WP\_002923286.1] [location=33344..33439] [gbkey=CDS]

MNATLIASTLLKTAPAAVVVVSVVVVVGNAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004173858.1\_35 [gene=ilvB] [locus\_tag=BN49\_RS01300] [protein=acetolactate synthase large subunit] [protein\_id=WP\_004173858.1] [location=33544..35232] [gbkey=CDS]

MASSGTTSNTMRFTGAQLVVHLLERQGITMVSGIPGGSILPIYDALSQSTQIRHILARHEQGAGFIAQGM

ARTEGKPAVCMACSGPGATNLVTAIADARLDSIPLVCITGQVPASMIGTDAFQEVDTYGISIPITKHNYL

VRDIAELPQVISDAFRIAQSGRPGPVWIDIPKDVQSATIELEALPEPGERAPAPAFAPESVREAAAMINA

AKRPVLYLGGGVINAPQAIRELAEKANLPTTMTLMALGMLPKAHPLSLGMLGMHGARSTNFILQEADLLI

VLGARFDDRAIGKTEQFCPNAKIIHVDIDRAELGKIKQPHVAIQGDVAEVLAQLNPQIEAQPREEWRQLV

ADLQREFPCAIPQESDPLSHYGLINAVAACVDDEAIITTDVGQHQMWTAQAYPLNRPRQWLTSGGLGTMG

FGLPAAIGAALANPQRKVICFSGDGSLMMNIQEMATAAENQLDVKIILLNNEALGLVHQQQSLFYQQGVF

AATYPGMINFMQIAAGFGLQTCDLNNEVDPQAALQAIIDRPGPALIHVRIDAQQKVYPMVPPGAANTEMV

GE

>lcl|NZ\_FO834906.1\_prot\_WP\_002923283.1\_36 [gene=ilvN] [locus\_tag=BN49\_RS01305] [protein=acetolactate synthase small subunit] [protein\_id=WP\_002923283.1] [location=35236..35523] [gbkey=CDS]

MQKQCDNVILELTVRNHPGVMTHVCGLFARRAFNVEGILCLPIQGSEHSRIWLLVNDDQRLGQMISQIEK

LEDVTKVARNQSDPTMFNKIAVFFE

>lcl|NZ\_FO834906.1\_prot\_WP\_002923282.1\_37 [gene=uhpA] [locus\_tag=BN49\_RS01310] [protein=transcriptional regulator UhpA] [protein\_id=WP\_002923282.1] [location=35674..36267] [gbkey=CDS]

MTTIALIDDHLIVRSGFAQLLGLEADFQVVAEFGSGREALTGLPGRGVQVCICDISMPDISGLELLSQLP

KGMATIMLSVHDSPALIEQALNAGARGFLSKRCSPDELIAAVRTVAAGGCYLTPDIAMKLAAGRQDPLTK

RERQVAEKLAQGMAVKEIAAELGLSPKTVHVHRANLLEKLGVSNDVELARRMFDSWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004151519.1\_38 [gene=uhpB] [locus\_tag=BN49\_RS01315] [protein=signal transduction histidine-protein kinase/phosphatase UhpB] [protein\_id=WP\_004151519.1] [location=36285..37766] [gbkey=CDS]

MLSVIGCAFIFAAAWFCLWSISLHLVERADLAVLLFPFGLRLGLMLQCPRGYWPVLLGTEWLLILWLAQE

VALAHPIILMTGSLLTLLPVALISRYRQQRDWLTLLRQGGALMAAALLQSLPWLAEGDEGLNALLLTLTG

GLTLAPTCLVFWHYLTSTVWRPLGPALVAQPVNWRGRHLIWYLLLFTISLWLQLGLPAELSRFTPFCLAL

PIIALAWHYGWQGALIATLMNAIALIASQTWHDHPVDLLLSLLAQSLTGLLLGAGIQRLRELNQSLQSEL

ARNRRLAERLLETEESVRRDVARELHDDIGQTITAIRTQAGIVQRLAPDNASVRQSGQLIEQLSLGVYDS

VRRLLGRLRPRQLDDLPLEQAVRSLMREMELEDRGIVSHLDWRINEAGLSENQRVTLFRVCQEGLNNIVK

HASASAVTLQGWQQDERLMLVLEDDGCGLPPGSNLQGFGLTGMRERVTALGGTLTISCTHGTRVCVNLPL

RYA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145056.1\_39 [locus\_tag=BN49\_RS01320] [protein=MFS transporter] [protein\_id=WP\_004145056.1] [location=37778..39106] [gbkey=CDS]

MFAFLKAPPDAAPISDKRELDARYRYWRRHILLTIWLGYALFYFTRKSFNAAVPEILASNVLTRSDIGLL

ATLFYITYGLSKFFSGIVSDRSDARYFMGLGLIATGVVNILFGFSSSLWAFALLWALNAFFQGWGSPVCA

RLLTAWYSRTERGGWWALWNTAHNVGGALIPMVVGAAALHYGWRAGMTIAGCLAILAGLYLCWRLRDRPQ

AVGLPAVGDWRHDALEIAQQQEGAGMSRKAILTRYVLANPYIWLLSLCYVLVYVVRAAINDWGNLYMSET

LGVDLVTANSAVTMFELGGFIGALVAGWGSDKLFNGNRGPMNLIFAAGILLSVGGLWLMPFASYVMQAAC

FFTTGFFVFGPQMLIGMAAAECSHKEAAGAATGFVGLFAYLGASLSGWPLAQVMDIWHWTGFFVVIAIAA

GISALLLLPFLNAQAPRTASEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002923280.1\_40 [gene=uhpT] [locus\_tag=BN49\_RS01325] [protein=hexose-6-phosphate:phosphate antiporter] [protein\_id=WP\_002923280.1] [location=39252..40643] [gbkey=CDS]

MLAFLNQVRKPTLDLPLDVRRKMWFKPFMQSYLVVFIGYLTMYLIRKNFNIAQNDMISTYGLSMTQLGMI

GLGFSITYGVGKTLVSYYADGKNTKQFLPFMLILSAICMLGFSASMGAGSTSLFLMIAFYALSGFFQSTG

GSCSYSTITKWTPRRKRGTFLGFWNISHNLGGAGAAGVALFGANYLFDGHVIGMFIFPSIIALIVGFIGL

RYGSDSPESYGLGTAEELFGEAISEEDKETEENAMTKWQIFVEYVLKNKVIWLLCFSNIFLYVVRIGIDQ

WSTVYAFQELKLSKEVAIQGFTLFEVGALVGTLLWGWLSDLANGRRALVACIALALIIATLGVYQHASNQ

YVYLASLFALGFLVFGPQLLIGVAAVGFVPKKAIGAADGIKGTFAYLIGDSFAKLGLGMIADGTPVFGLT

GWAGTFAALDAAAVGCICLMAIVAIFEERKIRREKKNRILQTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181583.1\_41 [locus\_tag=BN49\_RS01330] [protein=DUF1198 domain-containing protein] [protein\_id=WP\_004181583.1] [location=40780..41232] [gbkey=CDS]

MIWIGLATLVVVFVVGFRVLTSDSRRAIRRLSERLGITPVPLESMIDQLGKTAGNEYLRYLERPNEAHLQ

NAAQVLLIWQVAIVDASEKNLHYWYRLMQKARLAAPITEAQIRLAQGFLRELDPDMSDLHNLQQRYNDLF

LPEDGVHWLH

>lcl|NZ\_FO834906.1\_prot\_WP\_004173862.1\_42 [locus\_tag=BN49\_RS01335] [protein=DNA-binding transcriptional regulator] [protein\_id=WP\_004173862.1] [location=complement(41362..41685)] [gbkey=CDS]

MTAKNKYKSPAFEAIHSAASGLFSVGAIPQETMRHFDESCLGSVAALQPIEIKALREQLNVSQPVFARYL

NTSVSTVQKWETGAKRPSGMSLKLLSVVQKHGLKILL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151518.1\_43 [locus\_tag=BN49\_RS01340] [protein=type II toxin-antitoxin system RelE/ParE family toxin] [protein\_id=WP\_004151518.1] [location=complement(41669..42028)] [gbkey=CDS]

MRIFKTKWFAREASSHGISDDELYQAIQSALQGKVVDLGGGVYKKRLNKNRDRAIILTKSAEYWFYTFLY

AKQDMANINHRELMGFRELAKHYANLSEEKTTVLVKSKELVEICDDSKK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532491.1\_44 [gene=nepI] [locus\_tag=BN49\_RS01345] [protein=purine ribonucleoside efflux pump NepI] [protein\_id=WP\_016532491.1] [location=42240..43433] [gbkey=CDS]

MSHSNEAKPHARDLARPNWSAVFAVAFCVACLITVEFLPVSLLTPMALDLGISEGMAGQSVTTTAFVAMF

SSLFITTVIGKTDRRYVVILFSLLLTLSCLLVSFADSFTLLLLGRACLGLALGGFWAMSASLTMRLVPMR

VVPKALSIIFGAVSIALVIAAPLGSFLGGLIGWRNVFNGAAVMGVLCTLWVLKALPSLPGESASQQQNMF

GLLKRPGVMAGMCAIFMAFAGQFAFFTYIRPVYMTLAGFDVDGLTLVLLSFGIASFIGTSLSSVLLKRSV

KAALAIAPLVLTACAVALVLWGESKIIASTVAIIWGFAFALIPVGWSTWITRSLSDQAEKAGSIQVAVIQ

LANTCGAAVGGIALDHLGLLSPLVLSGILMLFTGLLVAAKVKVNSPA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532492.1\_45 [locus\_tag=BN49\_RS01350] [protein=phosphonoacetaldehyde hydrolase] [protein\_id=WP\_016532492.1] [location=complement(43430..44239)] [gbkey=CDS]

MNRISALILDWAGTTVDFGSFAPTQIFVEAFRQAFDIEITLEEARVPMGLGKWQHIEALGKLPAVDSRWQ

AKFGRAMTAADIDAIYAAFMPLQIAKVVDFSAPIAGVVDTIATFRAEGLKIGSCSGYPRPVMEKLVPAAA

AQGYAPDHWVATDDLAAGGRPGPWMALQNVITLGIDDVAHCVKVDDAAPGISEGLHAGMWSVGLAVSGNE

FGATWEEYQAMSKAEIATRRERAAGKLYAAGAHYVVDTLADLPEVIADINARLAKGERP

>lcl|NZ\_FO834906.1\_prot\_WP\_046042128.1\_46 [gene=phnW] [locus\_tag=BN49\_RS01355] [protein=2-aminoethylphosphonate--pyruvate transaminase] [protein\_id=WP\_046042128.1] [location=complement(44249..45352)] [gbkey=CDS]

MTSRNYLLLTPGPLTTSRKVKEAMLFDSCTWDDDYNLGVVQTIRQQLVQLATPADGYTAVLLQGSGSYAV

EAVLGSVIGEQGKVLIVSNGAYGARMIEMAQLMGIACHPYDCGEVSRPDAAAIEQILQNDPAITHIAMVH

SETTTGMLNPIEEVAELAKRYDKRYIVDAMSSFGGIPLDIAALNIDYLISSANKCIQGVPGFAFVIAREA

ELAACKGRSRSLSLDLYAQWRCMEDNHGKWRFTSPTHTVLAFAQALKELAQEGGVSARHQRYRNNQRRLV

AGMRALGFRPLLDDSLHSPIITAFYSPDAPQYRFHTFYQKLKDQGFVIYPGKVSQSDCFRIGNIGEVYDA

DITALLAAIDNAMYWKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004145049.1\_47 [gene=phnR] [locus\_tag=BN49\_RS01360] [protein=phosphonate utilization transcriptional regulator PhnR] [protein\_id=WP\_004145049.1] [location=45494..46213] [gbkey=CDS]

MKSPSGEMPQYLMIKAQLQARIQNGALKSGDKLPSERELCALFNTTRITVRESLAQLEASGVIYRADRRG

WFVTPERLWLDPTQNTNFHKLCLEQGREPKTVLLDGRLAAVPLDVMAPLALQPFDQVYLLTRLRYADGRP

VCYCENHCLPARVPELLRHDLNGSLTEIYQTHYDLIYTSMHLSFYPTSMPPQAAEALGVMEGRPALLLRR

LNYDQHGRILDYDIEYWRHDSLRIEVDTH

>lcl|NZ\_FO834906.1\_prot\_WP\_004173867.1\_48 [gene=phnS] [locus\_tag=BN49\_RS01365] [protein=2-aminoethylphosphonate ABC transporter substrate-binding protein] [protein\_id=WP\_004173867.1] [location=46392..47405] [gbkey=CDS]

MKLSRLALLSLFALTSSPVWADGVVTVYSADGLHDGDNSWYQSQFAAFTKATGIKVQYVEGGSGAIVERL

AKERTNPQADVLVTVPPFIQRAAKEQLLATFTPQGSAQIPGANDRYAPLVNNYLTFIYNSQLLKSAPASW

QDLLDSRYKNKLQYSTPGQAGDGTAVMLQAFHSLGGKDAGFAYLGKLQANNVGPSASTGKLTALVNKGEL

YVANGDLQMNLSQMARNPNVKIFWPADDKGERSALALPYTIGLVQNGPNSENGKKLINFLLDKPAQSSVS

ARSWGLPVRSDVAPDDANFKAAKAALDGVKSWEPNWDDVAVSLSADIARWHKVTDSE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150258.1\_49 [gene=phnT] [locus\_tag=BN49\_RS01370] [protein=2-aminoethylphosphonate ABC transport system ATP-binding subunit PhnT] [protein\_id=WP\_004150258.1] [location=47411..48523] [gbkey=CDS]

MLMKTTVTSSPSLAGTSGITLDSLRVSYHGNVVLKPLSLTIEPGEVLALIGPSGSGKTTVLRAIAGFVQP

AGGRILIGDTDVTQLPPYKRGLAMVVQNYALFPHMKVEDNVAFGLRAQKQPRGLIAERVTEALKIVGMAD

YATRYPHQLSGGQQQRVAIARAIAVRPRVLLLDEPLSALDAQIRHNMVEEIARLHRELPELTILYVTHDQ

TEALTLADKIGIMKDGSLIAHGETHELYHYPPNRFSAEFLGRANILQATALKDSPEPGLVSVSCGGGLIN

AFSRGGLHGNNKLLCIRPQHMSLAPRSATSNRLNATLTSVHWQGDLTHLLCDVAGEAVRIVMTHVNPLPR

AGDKLALYFEPGDAVLIEVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042131.1\_50 [gene=phnU] [locus\_tag=BN49\_RS01375] [protein=2-aminoethylphosphonate ABC transporter permease subunit] [protein\_id=WP\_046042131.1] [location=48523..49383] [gbkey=CDS]

MAQTLTLARPARNLRPYLWLALPLLVLATLFFYPLLLIAEQALRDASGNLSLETFWQVIDSKRFIGALLN

TLQIAVFATLGCLVLGSVLALILVFIPFPGSQLVGRVIDTFIALPTFLITLAFTFIYGSAGLLNGTLMAL

FAFELPPVDFLYSINGVILAEITVFTPLVMRPLMAGLRQIDKSQLEAASILGAHPLRVITHVIFPAALPA

LMAGGSLCLLLTTNEFGIVLFIGAKGVNTLPMMVYSKAILESDYSVACMIALINILLSLGLFMLYRLAAA

RTGVRS

>lcl|NZ\_FO834906.1\_prot\_WP\_004145044.1\_51 [gene=phnV] [locus\_tag=BN49\_RS01380] [protein=2-aminoethylphosphonate ABC transport system, membrane component PhnV] [protein\_id=WP\_004145044.1] [location=49386..50183] [gbkey=CDS]

MLIWSRKGRAAAGALAVTLFAGVFLLPLAVILLSSLSKQWNGLLPTGFTFAHFVNAFRGAAWDSLFSSLM

VGFCASLLALLCGMWAALALRQYGATLQKYLGLAFYLPSAIPSVSVGLGILVAFSQGPLQMNGTFFIVLA

AHFVLISAFTFSNVTTGLARISADIENVASSLGASPWYRLRHVTLPLMTPWMISALALSLSLSMGELGAT

VMIYPPGWTTLPVTIFSLTDRGNIADGSALTIVLVGVTLLLMMKLERIARRLSQR

>lcl|NZ\_FO834906.1\_prot\_WP\_022615681.1\_52 [locus\_tag=BN49\_RS01385] [protein=carbohydrate porin] [protein\_id=WP\_022615681.1] [location=complement(50383..51762)] [gbkey=CDS]

MNTVKKLPLAMAVVAALCPISVMAQEFTQEQIDAIVAKAVDKALADRQAKIDAAANKKVDVITNPETTAA

SPDMAIPFGLKFSGYARYGAHFQTGDQKYVGVDGSYNGASAIGRLGNESNGGEFQISKAFKSAQGAIWDL

NVMFDHWSDEVNLKKAYVGVTNVLESNPNAYIWAGRDFHQRPQQGINDYFWMNHDGQGAGVKNFDIGGVQ

FDVAAVSQVKSCSPEVMADETNPSRITCTGSSDTGDNGHYALTTKTHNIKAGPIDVEVYANYGFDSKAVD

SDARLEAWQGGLVLSHTNDSGVNKVILRYSDNSDNSVYNKTDDLTTVYASFEGSHKFTQQAQVEYLLAFH

DYDNGKDNADNRKNYGAIVRPMYFWNDVHSTWLEAGYQRVDYDQGGDNHGWKLTLSQNIAIGMGPEFRPM

LRFYVTGGQVDNEHTAKVNNTKDQQLDSLNVGGMFEAWF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530292.1\_53 [locus\_tag=BN49\_RS01390] [protein=PTS lactose/cellobiose transporter subunit IIA] [protein\_id=WP\_016530292.1] [location=complement(51907..52209)] [gbkey=CDS]

MMELEDAVMEIIVNAGQSRSLCFEALHAARTGNIDEARLLLNEADGYARRAHQMQTQLIGQDAGEARQPM

TLIMVHAQDHLMNSLLAREFSEELIHLYQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002923156.1\_54 [locus\_tag=BN49\_RS01395] [protein=PTS cellobiose transporter subunit IIC] [protein\_id=WP\_002923156.1] [location=complement(52307..53629)] [gbkey=CDS]

MSSLYQSMIAVIEQSITPLAGRLGQQKYVIAIRDGFTAALPFMIIGSFMLVFIFPPFSPDTTNGFARGWL

DFSQHYREQLMLPFNLSMGVMTFFISVGIGASLGRQFQLDPVMSGLLAFMAFLLVAAPYADGKISTQYLS

GQGIFTALITAIYSTRVYAWLKQNNITIRLPKEVPTGVARSFEILIPVLVVIATLHPLNLFIEAQTGMIL

PQAIMHLLEPLVSASDSLPAILLSVLMCQIFWFAGIHGSLIVTGIMNPFWMANLSANQAALAAGTVLPHV

YLQGFWDHYLLIGGVGSTLPLAFLLLRSRATHLRTIGKMGIVPSFFNINEPILFGAPIIMNPMMFIPFVC

VPMVNAVLAYGATRLGWLSQVVSLTPWTTPAPIGASWAANWTLSPVVMCLICMVMSAVIYLPFLRAYERS

LMKTEVEKAKNSVPVAETVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004145041.1\_55 [locus\_tag=BN49\_RS01400] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_004145041.1] [location=complement(53641..53955)] [gbkey=CDS]

MYKIMLCCSAGMSTSLLVRKMVEAANERDLPVQIDAYGVSEFDMQFPQYQVVLLGPQVKYMLKTLSDKAA

SLNIPVQPIDTMDYGMQRGDNVLNYALSLIPAAH

>lcl|NZ\_FO834906.1\_prot\_WP\_002923154.1\_56 [locus\_tag=BN49\_RS01405] [protein=LacI family transcriptional regulator] [protein\_id=WP\_002923154.1] [location=54249..55190] [gbkey=CDS]

MSTINDVSRLAGVSKATVSRVLSGSRGVKEASRQAVLQAAEALNYRPNMIAQSLLSQSTGCIGVICAQDN

INQTTSYLYALEKQLSQHQKHLLLRFANTSHGVMNSLEELTCGLCDNVLIIGARFPLNINRPDVVLVDCL

DSEGDNSIQFDHAFAAETACHYLISQGRRQIALIHPQSSGFADQVLLGYKHALEKNFLPFNRNLVFLDNT

SPSVAVQELVNNATTLNFNALLVSDEQQAQRVVPQLQAFNRAVPQNVMVFSLAGSLQLPGIPTIPAIEYS

MDAMASRIVNWLTEKTDNPGGSPLRGDLIIPKH

>lcl|NZ\_FO834906.1\_prot\_WP\_002923153.1\_57 [locus\_tag=BN49\_RS01410] [protein=aromatic acid/H+ symport family MFS transporter] [protein\_id=WP\_002923153.1] [location=55402..56772] [gbkey=CDS]

MNHTNVVDVKAWIDTRPVSRFQWNVLLLCFIIIMLDGYDAAVMGFVAPALIEDWGISRAEMGPILGAAMF

GVAIGALVAGPLSDRYGRKRILLWSVALFALFSLAGAVAQSPTQLALMRFLTGLGLGAVMPNCVTLVAEY

MPERRKGVMITLMYSGFNVGSGLGGFIAAGLLSHYSWHSALVFGGVLPLVVLPFMIVMLPESAMNMVARR

LPGEQIARALNRLGGQFTAETVFQLNAPPITRSSKVAQLFRHGYARGTIALWLTYFMGLFVIYLLNGWLP

TILRSGGLSLQQAAMMTGLFQLGGPLGGILVGMLMDRASAKAVIAATYFLGCLCLLSQGVMDFGSAALSV

LIFISGMCINGAQNGLQAYSPAYYQTEIRATGVSWMHGIGRTGAILSSTLGGMLMLAVPGHSSIFLVLAL

PACLAGICILLHRMNHAKPRLTEAELDALSSPLEHR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530403.1\_58 [locus\_tag=BN49\_RS01415] [protein=gallate dioxygenase] [protein\_id=WP\_016530403.1] [location=56786..58048] [gbkey=CDS]

MANILGGIAVSHTPTIGFAVDHHKQQDPAWAPIFQSFEPLQRWLEEKKPDALVYIFNDHVTAFFFDHYST

FTLGIDSQYDVADEGGGPRCLPPVQGNAALSRHIGASLMADEFDMSFFMDKKLDHGLFSPLSALLPWDET

QGWPTAVIPLQIGVLQFPVPSARRCYKLGQALRRAIESFPEDINVAIVATGGLSHQVHGERCGFNNPDWD

AQFVDMLVNDPEKLTEMTLGEYAELGGMEGSEVIMWLVMRGALSANVTETWRDYYLPSMTGIATLILENN

ARLPPVDTLTRHRQHMAQQLAGVEKLPGTYPFTHERSLNGLRLNRFLHRLIEPAWRERFLQSPQSLYAEA

GLSEEEQQLLNARDWRGLIQYGASFFLLEKMGAVVGVSNLHIYAAMRGQTLEAFQQTRNQQVTYSVAGKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002923147.1\_59 [locus\_tag=BN49\_RS01420] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002923147.1] [location=complement(58045..59271)] [gbkey=CDS]

MLKRKHDKIINIMQLRFFCQVALRGSVSRAADDLFRTQSAITRAIRDLEAALNVTLFERHYSGMVPTEYG

KCILPRARRAIDDLQAIPALLQKHHTRSSGPLADAGWLFNTRRLAIFIQLYHVNHTQTVAQQLGITQPAV

SAALKVLEKGADSALFRRTPEGVRPTPAAELLYPPVSRALNELENIWSDLAARRGVLEGTVRIGALPLSR

TRLLPSAIAAFLAQHPGITLMTNESPYESLVADMRAGNIDFIIGALRQDEDLPDLCSEALFEEDMLILLR

NNHPLLRHPDPRSQLATAQWVLPRANAPARNLLDKAFVTLGLPLPQPTVETGDAAMVRGLLQGSDMLAAV

SASQMRFETDNGLLSVLPVPLPDTTRRIGLTFRAGSLPSPATQALLRFIYQQVQDGAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004211137.1\_60 [gene=galB] [locus\_tag=BN49\_RS01425] [protein=4-oxalmesaconate hydratase] [protein\_id=WP\_004211137.1] [location=59399..60139] [gbkey=CDS]

MSHPVSEKSALVVSAHSADFVWRAGGAIALHALQGYQVHVVCLSFGERGESAKLWRKGNMTEEAVKQVRR

EEAQAAAAILGASVEFFDIGDYPLRADKETLFRLADVYRRIQPHFVLTHSLHDPYNYDHPLASHLAQEAR

IIAQAEGYRPGEKIVSAPPVYCFEPHQPEQCNWKPDVLLDITAVWEKKYQAIQCMQGQEHLWEYYTRVAL

QRGVQAKRNIGITAARDIVHGEAFQSIFPRVTENLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145036.1\_61 [locus\_tag=BN49\_RS01430] [protein=4-carboxy-4-hydroxy-2-oxoadipate aldolase/oxaloacetate decarboxylase] [protein\_id=WP\_004145036.1] [location=60136..60849] [gbkey=CDS]

MNLLNKKGLVIRHLPRHDEAVLRRCEAAGVATLHEAWDRQGLMGPAIRPIQQGVSRAGNAVTVLVTPGDN

WMFHVAVEQCRAGDILVVAPTSPCGDGFFGDLLATSLQSRGVVGLVGDIGIRDSQTLREMGFAVWSRQVY

AQGTVKESLGSVNVPVICAGQLVQPGDVVVADDDGVVVLPHARVRDVLHKAEARMSNELAKRERMRNGEL

GLDIYAMRPRLAEKGLRYYDRADEVEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530402.1\_62 [locus\_tag=BN49\_RS01435] [protein=4-oxalomesaconate tautomerase] [protein\_id=WP\_016530402.1] [location=60850..61935] [gbkey=CDS]

MAQRGIPCLWMRGGTSKAACFLADDLPADPVRRDAVLLAVMGSPDPRQIDGIGGADPLTSKVAIIRRSAR

PDADVDYLFAQVNVAAATVDYGQNCGNILAAVGPFAIERGLVRYDAPLTRVRIFMENTGQLAVAEIPCDA

DGVNYVGESRIDGVPGSASPILLHFLDVAGSSCGALLPTGRVRDRFDGIEVTCIDNGMPVILLRACDLGC

TGYETREQLDNDDALKRRLESIRLQAGPLMQLGDVSQRTVPKMTLIAEPRHGGAISSRTFIPHRCHASIG

VFGAVSVASACLLPGSVAQGLAQVAPGDTPLLSVEHPTGEFSVTLQLDADGALAGCGLLRTARLLFAGEV

FIPARVWPREE

>lcl|NZ\_FO834906.1\_prot\_WP\_023279339.1\_63 [locus\_tag=BN49\_RS01440] [protein=NAD(P)-dependent oxidoreductase] [protein\_id=WP\_023279339.1] [location=61938..62801] [gbkey=CDS]

MTIAFIGFGEAGGILAADLAREHAVTMWDCKLNGPEREAMGKKARDSRVQVGNSLAQALEGATLVFSTVT

AGEALKVAQQAAALLQPGQYFLDLNSVAPETKRQAAEHFLPGAYIDVAVMAPVPPARLQTPLLIGGPQAE

AIAPRLQRLGLNARYGASTVGQVSAIKMCRSVMIKGLEALTTECLFAAREYGVEEEVLSSLHHSFPSLGW

TGAFPDYLISRVAEHGIRRSEEMEEVVKTLRDVGSAGIMSEAIAKSQRQLPEQMAARSLSYRQLTPFDWK

TLVARLK

>lcl|NZ\_FO834906.1\_prot\_WP\_171819489.1\_64 [locus\_tag=BN49\_RS01445] [protein=hypothetical protein] [protein\_id=WP\_171819489.1] [location=complement(62805..63080)] [gbkey=CDS]

MVCLVTALSATSAWAESPLQRLQFEQQKQQVLKAVKEKCAPASHLSDNDFANKVLATDGNKNAVREATLA

KERNNQKSYQAAIDKIVCPAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004234160.1\_65 [locus\_tag=BN49\_RS01450] [protein=DMT family transporter] [protein\_id=WP\_004234160.1] [location=complement(63202..64140)] [gbkey=CDS]

MIPLCHISLEEKMGSSKKGMLNVLIAAVLWGSSGVCAQFIMQESQMSSPFLTMTRLLFAGLILLMLGFVH

GDRIFRVLQNRRDALSLLFFSLFGALTVQFTFLMTIEKSNAATATVLQFLSPTIIVAWFALARKARPTPL

VLGAICTSLAGTFLLVTHGNPTTLSISPAALFWGIASAFAAAFYTTYPSTLIARYGTLPIVGWSMLFGGA

MLLPFYGGQGTDFVVNGSLLLAFFYLVVIGTSLTFSLYLNGAQKIGGAKAGILSCAEPLSSALLSLLLLG

ITFTLPDWLGTLLILASVVLIAIDSRRRVRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042135.1\_66 [gene=murP] [locus\_tag=BN49\_RS01455] [protein=PTS N-acetylmuramic acid transporter subunit IIBC] [protein\_id=WP\_046042135.1] [location=complement(64256..65689)] [gbkey=CDS]

MAKITKEMIARILAHVGGAANVAQAGNCMTRLRLTLRDESLADSAAIRQIDGVMGVIVSDEQFQVVLGPG

KAQTAAEMMNGLLEAAPAAAPTLADVAAEKKQALKGKQTSAVQKFLAKFATIFTPLIPGFIAVGLLLGFA

TLAEQVFVLENAHPNASLVALIGYMKVFSKGMFTFLSILIGYNAQKAFGGSGVNGAIIASLFVLGYNPEA

TSGFYAGISTFFGHGIDPRGNIIGVLIAAILGAWVERQVRRVMPANLDMILTSAVTLLIMGAVTFTVIMP

IGGWLFTGMSWLFLHLNGNPFGSAVLAGLFLLAVMFGVHQGFVPVYFAQVDAQGFNSLFPILAMAGAGQV

GAALALFWRAKRDSLLRTQIKGAIIPGFLGIGEPLIYGVTLPRMKPFVTACLGGACGGFFVGLIAWLGLP

VGLNTVFGPSGLVALPLMTSGSGIYAGMAVYAGGLAVSYLCGFVLTWLFGSKNVDLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002923109.1\_67 [gene=murQ] [locus\_tag=BN49\_RS01460] [protein=N-acetylmuramic acid 6-phosphate etherase] [protein\_id=WP\_002923109.1] [location=complement(65714..66616)] [gbkey=CDS]

MSIDLSKLLTERRNANSANIDTLSTLEMLTVINQEDQQVAQAITPYLPQIAEVVDKVAAALQAGGRLIYI

GAGTSGRLGILDASECPPTFGTRPEQVVGIIAGGHKAILSAVENVEDNKAQGAMDLQNLNFSNRDVLVGL

AASGRTPYVIGAMEYAHSQNAFVAIVSCNPHGEMAQLADVAITPVVGPEVVTGSTRLKAGTAQKLVLNMI

STGAMIRVGKVYSNLMVDVEATNAKLIERQVSIVMEATDCDRATAQKALEACGRHCKTAIVMVLADLSAA

EAQSLLAKNNGYIRKALSNT

>lcl|NZ\_FO834906.1\_prot\_WP\_016531448.1\_68 [locus\_tag=BN49\_RS01465] [protein=multidrug effflux MFS transporter] [protein\_id=WP\_016531448.1] [location=complement(66779..67942)] [gbkey=CDS]

MARVSLSWALILGLLSGIGPLCTDFYLPALPEITQQLQATSTQTQLSLTAALIGLGLGQLFFGPLSDRIG

RLKPLALSLLLFIFSSAMCALTRDINMLIVWRFLQGFAGAGGSVLSRSIARDKYQGTLLTQFFALLMTVN

GIAPVLSPVLGGYVITAFDWRILFWTMAAIGGVLLVMSLAILRETRPATAAHASRQRPGQPVLKNRRFLR

FCLIQAFMMAGLFSYIGSSSFVMQSEYGMSAMQFSLLFGLNGIGLIIAAMIFSRLARRFSAESLLRGGLT

LAVSCAAIMLLFAWLHLPVLAMVGLFFTVSLMSGISTVAGAEAMSAVDAAQSGTASALMGTLMFVFGGIA

APLAGLGGETMLKMSLAMAICYLLALLLGLSKPRDAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004186228.1\_69 [gene=eefC] [locus\_tag=BN49\_RS01470] [protein=multidrug efflux RND transporter outer membrane subunit EefC] [protein\_id=WP\_004186228.1] [location=complement(67988..69352)] [gbkey=CDS]

MFRLSFMFIALLTAGCVSLDPHYDRPAAPVPATLPGAHGESTAVVGDWQKVVNDARLKKVVSIALNSNRD

VQKALADIEAARAQYGETRASLFPTVDAELSHTRSKTVASGLSSASQADGAVSSFELDLFGKNQSLSRAA

RETWLASEFTAQNTRLTMIADLTTAWVTLATDNSNLALAQQTMDSAANSRNIVARQMAVGTASAGDLSSA

ESVYQQARASVASYRTLVAQDKNAINLLAGETVPESLLPGTLESLGDNSIALVPAGVSSSVLLRRPDIQE

AEHNLKSANADIGAARANFFPSISLTASAGVGSDSLSSLFSHGMQVWSFAPSISLPLFTGGSNLAQLRYA

EAEKKGLIATYEKSIQSAFKDVADALARRETLSEELDAQRQYVAAEQTSLDIAMKSYQAGVGDYLSVLTA

QRTLWSAKTTLLSLQQTDLNNRITLWQSLGGGAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151514.1\_70 [gene=eefB] [locus\_tag=BN49\_RS01475] [protein=multidrug efflux RND transporter permease subunit EefB] [protein\_id=WP\_004151514.1] [location=complement(69356..72463)] [gbkey=CDS]

MFSRFFVRRPVFAWVIAILIMLAGVLAIRTLPVGQYPDVAPPAVKISATYTGASAETLENSVTQVIEQQL

TGLDHLLYFSSTSSSDGSVSITVTFEQGTDPDTAQVQVQNKVQQAESRLPSEVQQSGVTVEKSQSSFLLI

LAVYDKTNRATSSDISDWLVSNMQDPLARVEGVGSLQVFGAEYAMRVWMDPTKLASYSLMPSDVQSAIEA

QNVQVSAGKIGALPSSNAQQLTATVRAQSRLQTPDQFKAIIVKSQADGSVVRLSDVARVEMGSEDYTATA

NLNGHPAAGIAVMMAPGANALDTATLVKSKIAEFQRQMPQGYDIAYPKDSTEFIKISVEDVIQTLFEAII

LVVCVMYLFLQNFRATLIPAVAVPVVLLGTFGVLALFGYSINTLTLFAMVLAIGLLVDDAIVVVENVERI

MRDEGLPAREATEKSMGEISGALVAIALVLSAVFLPMAFFGGSTGVIYRQFSVTIISAMMLSVVVALTLT

PALCGALLSHSKPHTKGFFGAFNRLWGRTEAGYQRRVLGGLRRGAVMMGAYALICGAMALAMWKLPGSFL

PVEDQGEIMVQYTLPAGATAVRTAEVRRQVTDWFLTKEKANTDVIFTVDGFSFSGSGQNAGMAFVSLKNW

SQRKGDDNTAQAIALRATKELGTIRDATLFAMTPPSVDGLGQSNGFTFELMASGGTDRDSLMKLRSQLLA

AANQSSELQSVRANDLPQMPQLQVDIDNNKAVSLGLSLSDVTDTLSSAWGGTYVNDFIDRGRVKKVYIQG

ESDARAVPSDLGKWFVRGSDNSMTPFSAFATTHWQYGPESLVRYNGSAAFEIQGENAAGFSSGAAMDKME

KLADSLPAGSTWAWSGISLQEKLASGQAMSLYAISILVVFLCLAALYESWSVPFSVIMVIPLGLLGAALA

ATLRGLSNDVYFQVALLTTIGLSSKNAILIVEFAESAVDEGYSLSRAAIRAAQTRLRPIVMTSLAFIAGV

LPLAIATGAGANSRVAIGTGIIGGTLTATLLAVFFVPLFFVLVKRLFTRQRPSQE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529678.1\_71 [gene=eefA] [locus\_tag=BN49\_RS01480] [protein=multidrug efflux RND transporter periplasmic adaptor subunit EefA] [protein\_id=WP\_016529678.1] [location=complement(72463..73587)] [gbkey=CDS]

MKYIIAPIATALFLLSGCDNAQTSAPQQPTPEVGVVTLQSQPVPVVSQLTGRTTASLSAEVRPQVGGIIQ

KRLFTEGDMVKAGQALYQIDPSSYRATWNEAAAALKQAQALVVSDCQKAQRYASLVRDNGVSRQDADDAA

STCAQDKASVESKKAALESARINLNWTTVTAPIAGRIGISSVTPGALVSADQDTALATIRGLDTMYVDLT

RSSVDLLRLRKQSLASNSDTLSVTLTLEDGSTYQEKGRLALTEVAVDESTGSVTLRAIFPNPQHVLLPGM

FVRARIDEGIMNDAILAPQQGITRDAKGDATALVVDAANKVEQRTVETGDTYGDKWLVLSGLKAGDKLIV

EGTGKVAPGQTVKAVAVNNNGGNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150240.1\_72 [locus\_tag=BN49\_RS30815] [protein=hypothetical protein] [protein\_id=WP\_004150240.1] [location=73794..73916] [gbkey=CDS]

MIILIFPHYTIRRDNGKVFLLTFRTQKIKANNHGENKNIL

>lcl|NZ\_FO834906.1\_prot\_WP\_014343452.1\_73 [locus\_tag=BN49\_RS30820] [protein=hypothetical protein] [protein\_id=WP\_014343452.1] [location=complement(73876..73992)] [gbkey=CDS]

MLFVMISVINYLQYRAAEWLFSLSTFTKYSYFLHDYLP

>lcl|NZ\_FO834906.1\_prot\_WP\_004173879.1\_74 [locus\_tag=BN49\_RS01500] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004173879.1] [location=73967..74383] [gbkey=CDS]

MTLIITKSINPDDQQELFAGLRQYNQQYLDAAQFGDLGIYSRDAQGVMQGGLIAKRKGNWLCIEYLWVSE

TTRGRGLGSELMQEAEQQAQAQGCSHLLVDTFSFQALPFYQKLGYQLQMSLPDFPHAGMQRHYLSKAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529677.1\_75 [locus\_tag=BN49\_RS01505] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_016529677.1] [location=complement(74605..75252)] [gbkey=CDS]

MTAQKDQDTPRRPGRPRGKKPGTANREQLMDIALTLFARDGAGRASLNAIAKEAGVTPAMLHYYFSSRDA

LVTQLIEERFMPLRNHISRIFVDHPQDPVLALTMMVETLGHMAEKNAWFAPLWMQEIIGEMPILRQHMDA

RFGEERFQVMLGTVRRWQQEGKINPALAPELLFTTVISLVLVPFSRIHSDPRLQAVNRQTIVSHALALMG

HGVGG

>lcl|NZ\_FO834906.1\_prot\_WP\_017880064.1\_76 [locus\_tag=BN49\_RS01510] [protein=MFS transporter] [protein\_id=WP\_017880064.1] [location=75333..76826] [gbkey=CDS]

MTTQVANPPVQSIRLLFSALLLVMLLSALDQTIVSTALPTIVGELGGLDKLSWVVTAYILSSTIAVPLYG

KFGDLFGRKIVLQVAIGLFLVGSALCGLAQNMTQLVLMRGLQGLGGGGLMVISMAAVADVIPPANRGRYQ

GLFGGVFGLATVIGPLIGGFLVQHASWRWIFYINLPLGLFALLVIGAVFHSSNKRSQHQIDWLGAIYLSM

ALLCIILFTSEGGSVHAWNDPQLWCILAFGIVGIIGFIYEERMAAEPIIPLALFRNRSFLLCSLIGFVIG

MSLFGSVTFLPLYLQVVKEATPTEAGLQLIPLMGGLLLTSIISGRIISRTGKYRLFPILGTLLGVTGMVL

LTRITIHSPLWQLYLFTGVLGAGLGLVMQVLVLAVQNAMPAQMYGVATSGVTLFRSIGGSIGVALFGAVF

THVLQSNLQQLLPEGAVLPPGMNPVAVQHLPADIRLDYLDAFGAAIHAAFLMAAGIMAVAFVLSWLLKEA

PLKTATH

>lcl|NZ\_FO834906.1\_prot\_WP\_072200162.1\_77 [locus\_tag=BN49\_RS01515] [protein=LysR family transcriptional regulator] [protein\_id=WP\_072200162.1] [location=complement(76823..77794)] [gbkey=CDS]

MKNDNTGKVAIIFPQNGRIMDRLNAMALLVKVTELGSMSAAARALNMPLTTVSRHIGELESALGVRLLAR

TTRKLTLTDAGVDYVAAARRILEEVENAERQATGEYQEPKGELVISAPTMFGRQHVLPVISEFIARYPLI

RVRLLLSDRNADLVSDHVDLAVRIGDLADSSMVATRLGTMRIVACAHPALLAKYGEPQRPRDLAALPIIR

IESPMPYRGWRFRAAEREDQLINLPPVLSVTTPESAADAARLGVGVARLLHYQALDGLRHGELRLLLENV

EPDPAPVHLLYTARDLAPLKLRKFIDFAAPALRQALLRIAGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002923018.1\_78 [locus\_tag=BN49\_RS01520] [protein=pyridoxamine 5'-phosphate oxidase family protein] [protein\_id=WP\_002923018.1] [location=77833..78459] [gbkey=CDS]

MAATFLDIAITPDVMDVQHEMGSDSLWQTPRSRRQADRFGDSEAGMIATRDSFYLATVSQSGWPYIQHRG

GPPGFLHLLDDTTLAMADFGGNRQYITTGNLRGSDRACLFLMDYPRRARLKIYATVEVLAAEDHPQLLAQ

VAPANYRARIERLFLFHLQAFDWNCPQHITPRYSAQQVAEYSQNLQQRIHDLEQENQRLQQQLARRGE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529674.1\_79 [locus\_tag=BN49\_RS01525] [protein=nuclear transport factor 2 family protein] [protein\_id=WP\_016529674.1] [location=78462..78932] [gbkey=CDS]

MTEQRPPLPPFTRDSAIQKVRAAEDGWNSRDAEKVALAYTVDSEWRNRSEFVHGRGQIVEFLQRKWRKEQ

QYRLIKELWAWQENRIAVRFAYEWCDDSGNWFRSYGNENWEFDKHGLMQTRYACINDLPISESERLFHWP

QGRRPDDHPGLSELGL

>lcl|NZ\_FO834906.1\_prot\_WP\_004145017.1\_80 [locus\_tag=BN49\_RS01530] [protein=peroxidase-related enzyme] [protein\_id=WP\_004145017.1] [location=complement(78953..79489)] [gbkey=CDS]

MSRLADIREQDATGKAADIFAGIKKAMGKVPNAYLTIGGHSPAALQQALAHNAMLHKGSLSAQQLEAINL

SVSEATGCDYCLAAHTLMAKKAGFSSEQIHALRRGEYAEEAQLDALVKFAQTLVTTTGTLPEADVAALRN

AGFSDQQVIEIISAISAILFTNMVNRVNDTVVDFPKAD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529673.1\_81 [locus\_tag=BN49\_RS01535] [protein=AraC family transcriptional regulator] [protein\_id=WP\_016529673.1] [location=79606..80511] [gbkey=CDS]

MDSLSHLLALLAPRCEVNLHCRFGGRWQAGHQQMRSGVVPWHVVLRGEGRLNVGGQTHHLRAGDVVLLPH

GSPHLMESLVEWGQVLPVAHRFNGTVTEMRAGPAERALEMLCGEFYFGPHVSWLFSEASTLIHLHTDARE

DCPELDALLNILVRESLAQRPGGSAIVRSLGDTLLVLLLRMLLGEQQPPGGLLRLMSDERLMPAVLAVMA

TPEQPWTLESMAARAFLSRATFARHFARVYHLTPQAWLSQLRMALAARLLRLERQTNLEVIAERCGFQSL

ASFSKRFKMRYGVTPGEWRRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002922973.1\_82 [gene=nlpA] [locus\_tag=BN49\_RS01540] [protein=lipoprotein NlpA] [protein\_id=WP\_002922973.1] [location=80639..81448] [gbkey=CDS]

MRLRLQAAAAVMLAGLALVGCDQKGNEAKHIKVGVINGAEQDVAEVAKKVAKEKYGLEVELVGFSGSLLP

NESTNAGDLDANVFQHRPFLEQDNKAHNYHLVAVGNTFVFPMAGYSRKIKSVAELKDGATIAIPNDPTNL

GRALLLLQKEKLITLKAGTGLLPTAVDITDNPRNLKIMELEGAQLPRVLDDPKVDVAIISTTYLQQTGLS

PVRDGIFIEDKNSPYVNIIVTREDNKDAQNVKEFMQSYQSPEVAKAAETIFNGGAVPGW

>lcl|NZ\_FO834906.1\_prot\_WP\_002922972.1\_83 [locus\_tag=BN49\_RS01545] [protein=DMT family transporter] [protein\_id=WP\_002922972.1] [location=81473..82327] [gbkey=CDS]

MVRQRQADLLLIAATVIAACGWIFSREAIAGMPVFAFLGLRFFFAALLLLPFCRGFRPQKQHWPKLIISG

LWFALNLCLWIYSVSTTASLGEGAFIMSLSMMFVPLTAWVMMKVRPPRAWWECLPIAVVGLGLLSLHMPI

AFHPSQGWFLLTALVQSIWFCYTSRCAREVPLIPLTTVQLAITGIVGLTISAAVERWDQPMTLPTLGWLV

ASIVIATSLRFGLQMKGQKYAAVASAAIIMVLEPLLTVIAAALWYGEQLPLQKIIGGVLILVAQLWFRWR

MLKP

>lcl|NZ\_FO834906.1\_prot\_WP\_004186204.1\_84 [locus\_tag=BN49\_RS01550] [protein=NUDIX hydrolase] [protein\_id=WP\_004186204.1] [location=complement(82317..82877)] [gbkey=CDS]

MKKKLTAADMHDPQVIAETPWFSMRKVGIDVAPGERRDFYSIHYPRPAVGIVAIQDEKVLLIRHYRYLID

KVVWAIPSGGVDEEEDPAVAALRELREETGWQAQRVEEIIRFNPSYGSSDQLFITWLATGLRWVGMDADQ

DEVMETGWFTFDEINQLIARGEMPDGLSLVPLLQLMAQRRSGPLTA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529670.1\_85 [locus\_tag=BN49\_RS01555] [protein=MBL fold metallo-hydrolase] [protein\_id=WP\_016529670.1] [location=83044..83823] [gbkey=CDS]

MNITHIRNATQIIHYAGKRFLIDPMLADKGAWPGFPGTARSELRNPLVELPFSRDKIVDVDAVIVTHTHD

DHWDAAAIAAIPKTLPVFVQHEADAALLRSQGFQDLRLLSADSEFAGVRLLKTTSGQHGSDRTYAVPAMA

ERLGEACGVVFRHPQEKTLWLVGDTIWRDDIAADLLKLRPDVVVLNAGYAHVIGFGPIIMGKEDLLNVHF

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>lcl|NZ\_FO834906.1\_prot\_WP\_004145010.1\_86 [locus\_tag=BN49\_RS01560] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004145010.1] [location=83845..84798] [gbkey=CDS]

MKLTDVAIVAVEGFSPFHYAVPCMLFGDSVSEIKRFNLHICAERPGLLRARDGFALYATGDYAALEQADI

VVVPYWGEVDRRPPQALLDSLVRARDNGAEIVGLCLGAFVLGYAGLLDGRRAATHWEFEQDFQRRFPQVQ

LDINALYVDDQRIITSAGTAAALDCCLYIIRQRFGSLAANQIARRMIVSPHREGGQAQFIAQPVPKNTRD

ARINCLLDYLQQHIAEPHSLDSLARVVAMSRRTLTRHFARATGMSITDWLTAERLRRSQTLLEAGDLPVE

QVAEAVGYLSAVTWRQQFKARFGVSPTEWRRTFRRGA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530861.1\_87 [locus\_tag=BN49\_RS01565] [protein=NAD(P)-dependent alcohol dehydrogenase] [protein\_id=WP\_016530861.1] [location=complement(84795..85844)] [gbkey=CDS]

MLINAIGTYSASQPLESMAITRRDPGPQDVQIAIAYCGVCHSDLHQARSEWAGTLYPCVPGHEIVGRVTA

VGNAVSRYAVGDLVGVGCMVDSCQQCEECAEGLENYCDHMVLTYNGPTQDAPGHTLGGYSQQIVVNERYV

LRITHPEAQLAAVAPLLCAGITTYSPLRHWHVGPGKKVGVVGIGGLGHMGIKLAHAMGAHVVAFTTSESK

RNAARALGADDVVVSRNDDEMAAHVKSFDFILNTVAAPHNLDAFTTLLKRDGTMTLVGAPATPHPSPEVF

NLIFRRRSIAGSMIGGIPETQEMLDFCAEHGIVADIELIRSDEINEAWERMVKGDVKYRFVIDSATLAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151507.1\_88 [locus\_tag=BN49\_RS01570] [protein=winged helix-turn-helix transcriptional regulator] [protein\_id=WP\_004151507.1] [location=86217..86915] [gbkey=CDS]

MSIPAASLSTDQALPSFYYGRQTKPLFAVESLLSAFLPASSPFALPRSTYYRFPPTQAESGLILLEEGIA

SLCHAENNMVISTIFAPSLLGLIDGYGVFNGIPEKHHCSLFAETDLRGRWIGHQAAVEILNAQNLWQEMA

HVLAQRLMVLSMRSQEMVGVDSYPMVRTLLTELADYPEEYRRQINALSFIQRRTNLSRSRVMSILAELRK

GGYITVHRGVLEKITRTLPAHF

>lcl|NZ\_FO834906.1\_prot\_WP\_002922965.1\_89 [locus\_tag=BN49\_RS01575] [protein=antibiotic biosynthesis monooxygenase] [protein\_id=WP\_002922965.1] [location=complement(86966..87256)] [gbkey=CDS]

MISLIAVLKAKPGQTDALRQALQALLLPTRQEPGNLDYALFQLRDAPDTFYMREAWQGQDALDAHVAMPY

FQAFMTQMESLLAEPLRLDFLTPVEP

>lcl|NZ\_FO834906.1\_prot\_WP\_004181552.1\_90 [locus\_tag=BN49\_RS01580] [protein=zinc-binding alcohol dehydrogenase family protein] [protein\_id=WP\_004181552.1] [location=complement(87258..88265)] [gbkey=CDS]

MKAIAITQAAADGNNIPSLTEIDLPIPTAHGRDLLVAVKAISVNPVDTKVRAGFQGDTPRVLGWDAVGVV

QSVGEEVTLFAPGDEVWYAGALGRAGSNSEYQLVDERLVAHKPRTLDNASAAALPLTAITAWELLFHRLG

VEEGGNAGDTLLIVGAAGGVGSILTQLASKLTAMTVIGTASRPESQQWVREAGAHHVIDHSKPLADELAR

IGITSVTHVASLTNTEQHFNALINALAPQGKLALIDDPETLDVVPLKAKSLSLHWEFMFTRSMFETDDMI

AQHQLLTRVAALIDNHTIKTTLGEHYGAITAANLQKAHRQLETGRAVGKIVLEGF

>lcl|NZ\_FO834906.1\_prot\_WP\_002922963.1\_91 [locus\_tag=BN49\_RS01585] [protein=DUF3237 domain-containing protein] [protein\_id=WP\_002922963.1] [location=complement(88378..88845)] [gbkey=CDS]

MTPELRHCFSITIQVDKPIIVSRSPQTGKRQLIPIVGGSVSGQLRGHVLPGGVDSQIIEPDGTCRLSARY

ALQVAEGTVYVENNGIRRVPAQYHDQLFADDMRFFSDIPPEAIYFRTVPTFEVDAPALSWLTTSLFICAG

GRTQDGVMLDFYQVG

>lcl|NZ\_FO834906.1\_prot\_92 [locus\_tag=BN49\_RS01595] [protein=glycoside-pentoside-hexuronide family transporter] [pseudo=true] [location=89398..90790] [gbkey=CDS]

MKDHILSVKEKIGYGMGDAASHIIFDNVMLYMMFFYTDIFGIPAGFVGTMFLLARAGRDFRPVYGSACRP

YPQPLG\*VPPMDPLRRYPVRPRLRAGLQLAGFKPQRQADLRRRDLHAADPALHRGEYPLLRAGRRDHRQP

DAAHFAAVLALRAGDGGGHALHRADDAAGQLYRRRRQSARLPGGHRGAVGDCLPDAGLLLLYHQRACRSA

AEQYLDA\*RPARYLAQ\*PVAGGRRAHHPQYPRGLRSRRRDDVLHHLDHGLGGAVHRLPHDLLRRQPDWLG

AGETADRLEMQSQRLLVDQRPPGGAQRGDVLRTDGRRNHHVRLYLHHWRTAPAGDANPVGNDVRHRRLRR

MV\*RQTPDRHQLRRHPVCAQAGAGAGRRADRLDAGRRRL\*CRR\*NPEQRHPHHHYRLVHPRSGGVLPAER

GDRQTLLHAENAVPEKNDGRAGRGRASQRTRFHRRPDRQRMAKL

>lcl|NZ\_FO834906.1\_prot\_WP\_046042158.1\_93 [gene=yicI] [locus\_tag=BN49\_RS01600] [protein=alpha-xylosidase] [protein\_id=WP\_046042158.1] [location=90803..93121] [gbkey=CDS]

MKISDGNWLIQPGLNLIQPVQVYEVEQQGNEMVVYAAPRDVRERAWQLDTPLFTLRFFSPQEGIIGVRME

HFQGALDNGPHYPLNVQKDIHVEIENTAGFAELKSGSLSVRVTKGEFWGLDFLRDGVRITGSQLKNNGYV

QDSKTQRNYMFERLDLGVGETVYGLGERFTALVRNGQTVETWNEDGGTSTEQSYKNIPFYLTNRGYGVLV

NHPQRVSFEVGSEKVSKVQFSVEGEYLEYFVIDGPTPKAVLNRYTQFTGRPALPPAWSFGLWLTTSFTTN

YDEATVNSFIDGMAERHLPLHVFHFDCFWMKAFQWCDFEWDPQTFPDPEGMIKRLKAKGLKVCVWINPYI

GQRSPVFKELKEKGYLLKRPDGSLWQWDKWQPGLAIYDFTNPEARQWYADKLKGLVAMGVDCFKTDFGER

IPTDVQWFDGSDPQKMHNHYAFIYNELVWKVLKETVGEQEAVLFARSASVGAQQFPVHWGGDCYANYESM

AESLRGGLSIGMSGFGFWSHDIGGFENTAPAHVYKRWCAFGLLSSHSRLHGSKSYRVPWAYDDESCDVVR

HFTQLKCRMMPYLYRQAALANECGTPMLRAMLLEFPDDPACDYLDRQYMLGDSVLVAPVFSEAGEVQFYL

PEGHWTHLWHNDELPGSRWHKQHHDALSLPVYVRDNTLLALGNNDQKPDYAWHEGTAFQLFHLEDGREAR

CDVPAADGSTIFTLKARRQGNAIAVSGEGEARGWTLCLRNIPQVAGVQGGTQTGSELGVVVSAEGNTLTI

TL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530457.1\_94 [locus\_tag=BN49\_RS01605] [protein=SIS domain-containing protein] [protein\_id=WP\_016530457.1] [location=93277..93999] [gbkey=CDS]

MDVENIFRDVKLSKTEMTVLRFIQNDPEQCIRQGVRAVAEQCYSNPSSLVRLAKKLKFSGWLELVYFIKF

NITMPKLDVTNDIDYMSVQPEEALTPLLASLKQQRTLIHGSGFSQLIAQYIYNKFLVTGVNASLALWPDY

EILEQKNAACFDSIWIISKSGRSSSALNWVKALEGKEINLVCFTGDYQSPLAQAADTAFIIHDPQKFDDD

IYWSNPFFGYCILGFERLLKMWFTSLRSNS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530456.1\_95 [locus\_tag=BN49\_RS01610] [protein=maltose-6'-phosphate glucosidase] [protein\_id=WP\_016530456.1] [location=complement(94046..95254)] [gbkey=CDS]

MKLTVLGGGGVRSAFLAKSLAYNAHRIGLTEVVFLDNSADNLAIFGEIARYVFNTIRPDIQFSTTTDPVA

ALQDANYIITTLRVGGDESRIRDERIALEHNTLGQETTGAGGFAMAMRSIPAILGCEERDLSVECYGLNH

FSWFTHFTVRGEEVTERLIASPELYQKTAMQYFSPELVRLCDNQLLNEYLYYYYYRDEALKAIQGAGETR

GEQIARINQEMREALRTVDARTQPEAAFTIWMQHYLRRENSYMQNESRQEKFHTREPLTLRQFIEEPDTG

GYAGVALDILEAVNSTTTKRIVVSIQNNGTLDFLRPDDVIEISCDLSRDGLRPVTPVKVPTAQKNMIACV

KEYERLAVAAILQQDKSLAVRALMAHPLIGSYSLAKTLVEAYLDDEQFAAWR

>lcl|NZ\_FO834906.1\_prot\_WP\_002922953.1\_96 [locus\_tag=BN49\_RS01615] [protein=PTS transporter subunit EIIC] [protein\_id=WP\_002922953.1] [location=complement(95267..96826)] [gbkey=CDS]

MPEIRQRILENMQKFSRAMIGAVLFLPVIGLILALSSVLTNPTLIAETSFLHQLGQMLGDTFWPLFGNLG

LLFCVGISYGLAKDKKTEVALVSVMCFIMFLGANHSWLEHTHGLAEKINGEYYGTGQTQLLGFVVVDMGV

FLGIILGCTIAWVHNKVSAIELPGALSMYGGAKLTLVAMTPVVIFYAIAFTWIWPFMTHGISALTGFMKN

AGVAGVFVYGFFEKFLIPTGLHHFVWSPFQLTQIGGTLNVDGQVVSGTQAIFLAYMRHPDLTPVMNDALR

FSQQGMTTIFGLAGASLAFYHTAKPEKKAMAKAILLPAIITSMLTGITEPIEFTFLFVSPLLWVIHATLT

AASQAICDIFTVRPWGASGLIEFLIYNLPLPVSLTRWPGYVLIGIGQFAVYYVIFRTLVVKLNLKTPGRE

DDENVKLYSKAEYRQKVAQPQSVTDDIIRGLGGKENILSVDNCFTRLRVAVRDMARVDDTQLKNTGANGV

VRNRNEVQVIYGVKVGQVRSRVDNWLAEN

>lcl|NZ\_FO834906.1\_prot\_WP\_004186173.1\_97 [locus\_tag=BN49\_RS01620] [protein=AsmA family protein] [protein\_id=WP\_004186173.1] [location=complement(97072..98787)] [gbkey=CDS]

MKFLGKLILWLLVALLLVIIGAWFLLQTHWGARQASAWLSNGTGWQVSFDEMEHDFSSPLHVQLRNVTFG

REGKPATLVAKTVDIGFSTRQFSDPLHADEIVLNDGTLNLSPHSADLPFAADRLMLRNMAFNSPETGWAL

SAQRVTGGVSPWTPEAGNVLGKTAQIQMSAGSMTLNGVEASNVLIQGKIDQGEVTLSTLGADVARGTLTG

NAKRSADGSWRVDNLQLNEIRLQSPASLAEFFAPLTTVPSLQIGRLDITDARLQGPDWAVTDLDLSLRNL

TLSHGGWQSEDGTLSMNASEFIYGSLHLFDPILNAEFSPQGIALRQFSSRWEGGMVRTSGNWLRAGNALV

LDDTAFAGLEYTLPANWKQLWMTPLPAWLQSLTLKKFSASRNLIIDVDPAFPWQITALDGYGGELQLVKN

GSWGVWNGSATLNAAAATFNRIDVRRPSLKLNATASTVNITELSAFTERGILQATAAVSQLPQRQVNLSF

SGRGVPLNILQAWGWPSLPISGDGNLQLTASGSVQADAPLKPTINGQLSAVNMEKQQVAQIMRNGEVSPA

PAAPAPAPVTP

>lcl|NZ\_FO834906.1\_prot\_WP\_002922950.1\_98 [locus\_tag=BN49\_RS01625] [protein=uracil-xanthine permease family protein] [protein\_id=WP\_002922950.1] [location=complement(98928..100319)] [gbkey=CDS]

MSVNTAESENAQPVAHKPASELIYRLEDRPPLPQTLFAAFQHLLAMFVAVITPALLICQALGLPAQDTQH

IISMSLFASGVASIIQIKAWGPVGSGLLSIQGTSFNFVAPLIMGGTALKTGGADVPTMMAALFGTLMLAS

CTEMVLSRILHLARRIITPLVSGVVVMIIGLSLIQVGLTSIGGGYAAMADHTFGAPKNLLLAGIVLALII

ILNRQRNPYLRIASLVIAMAAGYLAAWFLDMLPANTAPTNSSLITVPTPLYYGLGIDWSLLLPLMLVFMI

TSLETIGDITATSDVSEQPVSGPLYMKRLKGGVLANGLNSFVSAVFNTFPNSCFGQNNGVIQLTGVASRY

VGFVVALMLIVLGLFPAVSGFVQHIPEPVLGGATLVMFGTIAASGVRIVSREPLNRRAILIIALSLAVGL

GVSQQPLILQFAPDWLKNLLSSGIAAGGITAIVLNLIFPPEKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529540.1\_99 [gene=gltS] [locus\_tag=BN49\_RS01635] [protein=sodium/glutamate symporter] [protein\_id=WP\_016529540.1] [location=100604..101806] [gbkey=CDS]

MFHLDTLSTLVAATLVLLLGRKLVQTVPFLKKYTIPEPVAGGLLVALALLALKKSMDIEIDFDMSLKDPL

MLAFFATIGLNANLASLRAGGKVLGTFLIVVVGLLLLQNALGIGMATLLGLDPLMGLLAGSITLSGGHGT

GAAWSKLFVERYGFANATEVAMACATFGLVLGGLIGGPVARYLVKHSSSPDGTPDDQVAPTAFEKPDVGR

VITSLVLIESIALIAICLTLGKVVAQLLAGSVFELPTFVCVLFIGVILSNSLALAGLYRVFDRAVSVLGN

VSLSLFLAMALMSLKLWELASLALPMIIILAVQALAMALYAVFVTYRMMGKNYDAAVLAAGHCGFGLGAT

PTAIANMQAITDRFGPSHMAFLVVPLVGAFFIDIVNALVIKLYLLLPMFG

>lcl|NZ\_FO834906.1\_prot\_WP\_002922944.1\_100 [gene=glpK] [locus\_tag=BN49\_RS01640] [protein=glycerol kinase GlpK] [protein\_id=WP\_002922944.1] [location=complement(101921..103432)] [gbkey=CDS]

MTDKKYIVALDQGTTSSRAVVMDHDANIVSVSQREFEQIYPKPGWVEHDPMEIWASQSSTLVEALAKADI

NSDQIAAIGITNQRETVVVWERETGKPIYNAIVWQCRRTAEICEQLKRDGMEEYIRKATGLVVDPYFSGT

KVKWILDHVEGSRERAKRGELLFGTVDTWLIWKMTQGRVHVTDYTNASRTMLFNIHDLDWDDKMLDALDI

PRAMLPEVRKSSEVYGQTNIGGKGGTRIPIAGIAGDQQAALFGQLCVKEGMAKNTYGTGCFMLMNTGEKA

VTSTHGLLTTIACGPRGEVNYALEGAVFMAGASIQWLRDEMKLISDAFDSEYFATKVKDTNGVYVVPAFT

GLGAPYWDPYARGAIFGLTRGVNSNHIIRATLESIAFQTRDVLEAMQADSGIRLHALRVDGGAVANNFLM

QFQSDILGTRVERPEVREVTALGAAYLAGLAVGFWQNLDELQEKAVIEREFRPGIETTERNYRYSGWKKA

VKRALAWEEHDEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002922941.1\_101 [locus\_tag=BN49\_RS01645] [protein=aquaporin] [protein\_id=WP\_002922941.1] [location=complement(103454..104305)] [gbkey=CDS]

MSQTSTLKGQCIAEFLGTGLLIFFGVGCVAALKVAGASFGQWEISIIWGLGVAMAIYLTAGVSGAHLNPA

VTIALWLFACFEGRKVVPFIISQFAGAFCAAALVYGLYYNLFLDYETTHHMIRGSVESLDLAGIFSTYPN

PHINFVQAFAVEMVITAILMGVILALTDDGNGIPRGPLAPLLIGLLIAVIGASMGPLTGFAMNPARDIGP

KAFAWLAGWGDVAFTGGKDIPYFLVPLCAPVVGAALGAFSYRKLIGRHLPCDTCVEEEQQSPSSSTAQHK

ASL

>lcl|NZ\_FO834906.1\_prot\_WP\_004150222.1\_102 [gene=zapB] [locus\_tag=BN49\_RS01650] [protein=septal ring assembly protein ZapB] [protein\_id=WP\_004150222.1] [location=104748..104993] [gbkey=CDS]

MTMSLEVFEKLESKVQQAIDTITLLQMEIEELKEKNNTLVQEVQSAQHGREELERENSQLKEQQQGWQER

LQALLGRMEEV

>lcl|NZ\_FO834906.1\_prot\_WP\_002922936.1\_103 [locus\_tag=BN49\_RS01655] [protein=sulfate ABC transporter substrate-binding protein] [protein\_id=WP\_002922936.1] [location=105145..106134] [gbkey=CDS]

MNKWGVGLTLLLASASVLAKDIQLLNVSYDPTRELYEQYNKAFSAHWKQETGDNVVIRQSHGGSGKQATS

VINGIEADVVTLALAYDVDAIAERGRIDKNWLKRLPDNSAPYTSTIVFLVRKGNPKQIHDWNDLIKPGVS

VITPNPKSSGGARWNYLAAWGYALHQNHGDQAKAQEFVKALYKNVEVLDSGARGSTNTFVERGIGDVLIA

WENEALLATNELGKDKFEIVTPSESILAEPTVSVVDKVVDKKGTRQVAEAYLKYLYSPEGQEIAAKNFYR

PRDPNVAKKYANEFPKLKLFTIDQEFGGWTKAQKEHFSNGGTFDQISQR

>lcl|NZ\_FO834906.1\_prot\_WP\_020803798.1\_104 [locus\_tag=BN49\_RS01660] [protein=CDP-diacylglycerol diphosphatase] [protein\_id=WP\_020803798.1] [location=106297..107067] [gbkey=CDS]

MKMRRVRYFLLALLVAILAALAGGYYWLHSGNPDALRKIVLQQCVPHQQQQQNPSPCAEVNLKGGYVLFK

DRNGPLQYLLMPTYRINGTESPLLLEPLTPNFFWQAWQGREIMSQRHGAPVPDNAVSLAINSRSGRTQNH

FHIHISCLRPDVRAQLDKDAAAISSRWLPLPGGLQGHEYLARRVTEAELAQRSPFLMLAEEVPEAREHMG

RFALAMAQQSDGSLVLLATERNLLTLNRASAEEIQDHRCAILNANH

>lcl|NZ\_FO834906.1\_prot\_WP\_004151505.1\_105 [locus\_tag=BN49\_RS01665] [protein=SLC13 family permease] [protein\_id=WP\_004151505.1] [location=107132..108436] [gbkey=CDS]

MSLWLTHPLFLPSLIVGVTIVLWATSLLPEFITALLFFAAAMMAKIAPPEVIFGGFASSAFWLVFSGFVL

GIAIRKTGLADRAAQALSARLTDSWPRMVASVVLLSYALAFVMPSNMGRIALLMPIVAAMARRAGIADGS

RGWFGLALAVGFGTFQLSATILPANVPNLVMSGAAEGSYGIHLNYVPYLLLHTPVLGWLKGAVLVALICW

LFPGKPHPPRDLAPLPPMSRDEKRLAWLLAVVLSLWVTESWHGVGPAWTGLAAAVITLLPRVGFINGEEF

ASGVNMRTCIYVAGILGLAIAVTQTGIGGAVGNALLQVMPLDKDNPFTSFLALTGITSALNFIMTANGVP

ALYTTFAQSFADATGFPLLSVIMIQVLGYSTPLLPYQASPIVVAMGLGKVPARAGMQLCLALAAVSYLIL

LPLDYAWYQLLGKL

>lcl|NZ\_FO834906.1\_prot\_WP\_002922909.1\_106 [gene=tpiA] [locus\_tag=BN49\_RS01670] [protein=triose-phosphate isomerase] [protein\_id=WP\_002922909.1] [location=complement(108529..109296)] [gbkey=CDS]

MRHPLVMGNWKLNGSRHMVNELVANLRTELAGVSGCAVAIAPPEMYLDLAKRAAEGSHIHLGAQNVDVNL

SGAFTGETSAEMLKDIGAQYIIIGHSERRTYHKESDELIAKKFAVLKEQGLTPVLCIGETEAENEAGKTE

EVCARQIDAVLKTQGAAAFEGVVIAYEPVWAIGTGKSATPAQAQAVHKFIRDHIAKADAKIAEQVIIQYG

GSVNAGNAAELFTQPDIDGALVGGASLKADAFAVIVKAAEAAKKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002922908.1\_107 [locus\_tag=BN49\_RS01675] [protein=YiiQ family protein] [protein\_id=WP\_002922908.1] [location=complement(109406..110008)] [gbkey=CDS]

MKKWTILWLSGLMGLAVGPHALSAESESTTAAAPYLLAGAPSFDQSISQFREKFNADNPKLPLNEFRSIA

TSRDRANLTRAASKINENLYASTALERGTLKIKSMQITWLPIQGPEQKAARTKALEYMSAMIRAFVPTFS

QAQSQQKLQKLLAAGKGKRYFADTEGAVRYVVADHGEKGLTFAIEPIKLALSETLEGNNK

>lcl|NZ\_FO834906.1\_prot\_WP\_002922907.1\_108 [locus\_tag=BN49\_RS01680] [protein=DUF805 domain-containing protein] [protein\_id=WP\_002922907.1] [location=110121..110549] [gbkey=CDS]

MTLQQWLFSIKGRIGRRDFWIWIAIWLVTMSALFTLAGSNLLNLQTAAFIIVCLLWPTAAVVVKRLHDRG

KSGLWALLMVLAWMLLAGNWAMLPQVWQWGVGRFVPTLIIVMMLIDLGAFVGTQGENKFGKETQDVRWKA

DA

>lcl|NZ\_FO834906.1\_prot\_WP\_004173895.1\_109 [gene=fpr] [locus\_tag=BN49\_RS01685] [protein=ferredoxin--NADP(+) reductase] [protein\_id=WP\_004173895.1] [location=complement(110550..111296)] [gbkey=CDS]

MADWVSGKVTKVEYWTDALFSLYVRAPVHPFTAGQFTKLGLEIDGERVQRAYSYVNAPGNPDLEFYLVTV

PEGKLSPRLAALKPGDEVLVVSEAAGFFVLEEVPDCDTLWMLATGTALGPYLSILQEGKDLERFNNLVLV

HAVRYAADLSYLPLMRELEQRYAGKLRIQTVVSRETVEGSLTGRVPFLIETGALEEAVGLPMTTDTSHVM

LCGNPQMVRDTQQLLKETRQMTKHLRRRPGHMTAEHYW

>lcl|NZ\_FO834906.1\_prot\_WP\_002922903.1\_110 [gene=glpX] [locus\_tag=BN49\_RS01690] [protein=class II fructose-bisphosphatase] [protein\_id=WP\_002922903.1] [location=complement(111447..112457)] [gbkey=CDS]

MKRELAIEFSRVTEAAALAGYKWLGRGDKNTADGAAVNAMRIMLNLVNIDGTIVIGEGEIDEAPMLYIGE

KVGTGKGDAVDIAVDPIEGTRMTAMGQANALAVMAVGDKGCFLNAPDMYMEKLIVGPGAKGAIDLNLPLE

ENLHNIARALNKPLGELTVTVLAKPRHDAVIAQLQQLGVRVFAIPDGDVAASILTCMPDSEVDVLYGIGG

APEGVVSAAVIRALDGDMQGRLLARHHVKGDNEENRRIGENELARCKTMGIEAGKVLRLDEMARSDNVVF

SATGITKGDLLDGITRKGNMATTETLLIRGKSRTIRRIQSIHYLDRKDPDIQQHIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151504.1\_111 [gene=recG] [locus\_tag=BN49\_RS01695] [protein=ATP-dependent DNA helicase RecG] [protein\_id=WP\_004151504.1] [location=complement(112506..114587)] [gbkey=CDS]

MSGRLLDAVPLSSLTGVGAAQSSKLAKIGLHTVQDLLLHLPLRYEDRTHLYPIAELLPGVYATVEGEVLN

SNITFGGRRMMTCQISDGTGILTMRFFNFNAAMKNSLATGRRVLAYGEAKRGKYGAEMIHPEYRVQGDMS

TPELQETLTPVYPTTEGIKQATLRKLTDQALELLETCAISELLPPELAQGMMSLPEALRTLHRPPPSLQL

SELESGKHPAQQRLILEELLAHNLSMLALRAGAQRYHALPLGANDTLKNQLLASLPFKPTGAQARVTAEI

EHDMALDVPMMRLVQGDVGSGKTLVAALAALRAIVHGKQVALMAPTELLAEQHANNFRNWFEPLGIEVGW

LAGKQKGKARQAQQEAIASGEVQMIVGTHAIFQEQVQFNGLALVIIDEQHRFGVHQRLALWEKGQQQGFH

PHQLIMTATPIPRTLAMTAYADLDTSIIDELPPGRTPVTTVAIPDTRRSDIIDRVRNACTHEGRQAYWVC

TLIEESDLLEAQAAEATWEELKLALPELNIGLVHGRMKPAEKQAVMQAFKQGEMHLLVATTVIEVGVDVP

NSSLMIIENPERLGLAQLHQLRGRVGRGAVASHCVLLYKSPLSKTAQKRLQVLRDSNDGFVIAQKDLEIR

GPGELLGTRQTGNAEFKVADLLRDQAMIPDVQRIARHIHERYPLQAQALIERWMPETERYSNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181538.1\_112 [gene=trmH] [locus\_tag=BN49\_RS01700] [protein=tRNA (guanosine(18)-2'-O)-methyltransferase TrmH] [protein\_id=WP\_004181538.1] [location=complement(114593..115282)] [gbkey=CDS]

MNSKRYERICEMLARRQPDLTVCMEQVHKPHNVSAVIRTADAVGVHEVHAVWPSSRMRTMASAAAGSNSW

VQVKTHRTIADAVGHLKGQGMQILATHLSDKAIDFREIDYTRPTCILMGQEKTGITQEALALADQDIIIP

MIGMVQSLNVSVASALILYEAQRQRQNAGMYQRANSMLPPQEQQRLLFEGGYPVLARVARQKGLPYPHVN

EQGEVEADAAWWATMQAAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004150214.1\_113 [gene=spoT] [locus\_tag=BN49\_RS01705] [protein=bifunctional GTP diphosphokinase/guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase] [protein\_id=WP\_004150214.1] [location=complement(115287..117407)] [gbkey=CDS]

MYLFESLNQLIQNYLPEDQIKRLRQAYLVARDAHEGQTRSSGEPYITHPVAVACILAEMKLDYETLMAAL

LHDVIEDTPATYQDMEQLFGKSVAELVEGVSKLDKLKFRDKKEAQAENFRKMIMAMVQDIRVILIKLADR

THNMRTLGSLRPDKRRRIARETLEIYSPLAHRLGIHHIKTELEELGFEALYPNRYRVIKEVVKAARGNRK

EMIQKILSEIEGRLQEAGIPCRVSGREKHLYSIYCKMVLKEQRFHSIMDIYAFRVIVHDADICYRVLGQM

HSLYKPRPGRFKDYIAIPKANGYQSLHTSMIGPHGVPVEVQIRTEDMDQMAEMGVAAHWAYKEHGGESST

TAQIRAQRWMQSLLELQQSAGSSFEFIESVKSDLFPDEIYVFTPEGRIVELPAGATPVDFAYAVHTDIGH

ACVGARVDRQPYPLSQPLSSGQTVEIITAPGARPNAAWLNFVVSSKARAKIRQLLKNLKRDDSVSLGRRL

LNHALGGSRKLAEIPPENIQRELDRMKLASLDDLLAEIGLGNAMSVVVAKNLQQGEAAAAPVPANASNHG

HLPIKGADGVLITFAKCCRPIPGDPIIAHVSPGKGLVIHHESCRNIRGYQKEPEKFMAVEWDKETAQEFI

TEIKVDMFNHQGALANLTAAINTASSNIQSLNTEEKDGRVYSAFIRLTARDRVHLANIMRKIRVMPDVIK

VTRNRN

>lcl|NZ\_FO834906.1\_prot\_WP\_000135058.1\_114 [gene=rpoZ] [locus\_tag=BN49\_RS01710] [protein=DNA-directed RNA polymerase subunit omega] [protein\_id=WP\_000135058.1] [location=complement(117426..117701)] [gbkey=CDS]

MARVTVQDAVEKIGNRFDLVLVAARRARQMQVGGKDPLVPEENDKTTVIALREIEEGLINNQILDVRERQ

EQQEQEAAELQAVTAIAEGRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002922664.1\_115 [gene=gmk] [locus\_tag=BN49\_RS01715] [protein=guanylate kinase] [protein\_id=WP\_002922664.1] [location=complement(117756..118379)] [gbkey=CDS]

MAQGTLYIVSAPSGAGKSSLIQALLKTQPLYDTQVSVSHTTRAPRPGEVHGEHYFFVNHDEFRSMIGENA

FLEHAEVFGNYYGTSRKAIEQVLATGVDVFLDIDWQGAQQIRKSMPGARSIFILPPSKDELDRRLRGRGQ

DSEEVIAKRMAQAVAEMSHYAEYDYLIVNDDFDTALSDLKNIIRAERLRMSRQKQRHGALITKLLAD

>lcl|NZ\_FO834906.1\_prot\_WP\_020864855.1\_116 [gene=ligB] [locus\_tag=BN49\_RS01720] [protein=NAD-dependent DNA ligase LigB] [protein\_id=WP\_020864855.1] [location=118638..120314] [gbkey=CDS]

MRKGGWWLALGMFSASVLATCPDWPPARGRQETSRLHQQIVAWKEAYWRQGASGVSDDVYDQLTLRLAQW

RQCFPGATPEDDDLPPPTGDARHPVAHTGVRKLADEDSVARWMKNKSDLWIQPKVDGVAVTLVYRQGRLV

QAISRGDGLRGEAWTARARQIPALEKVMTGELADSVLQGELFLRRDGHVQQQAGGMNARAKVAGLMMRAD

AAAALSQLDVFIWAWPDGPSDMRRRQKLLAQAGFKYSGQYTHPVSRIEQVAQWRQRWYRSPLPFVSDGVI

VREGREPPGRVWSPGKGEWLAAWKYPPASRVMQVRAIRFSIGRSGRLNVVAELEPQRLDDKRVQRVNVGS

VSRWQMLDIGVGDQLQISLAGQGIPRVDAVVWRTAERHKPTPPPAKFNALTCYFATHECSEQFLSRLIWL

SSKSALNVDGVGENLWRVIQQQNPMTHIFSWLALTVEQLQAVPGISAARGQHLWHQFDLVRKRPFIRWVL

AMGIPVPQGALAQLESENWHLLAAKSEAQWRTLPGVGEIRARQLVAFLHHPDVVALAQWLSGQRIPGF

>lcl|NZ\_FO834906.1\_prot\_WP\_002922654.1\_117 [locus\_tag=BN49\_RS01725] [protein=trimeric intracellular cation channel family protein] [protein\_id=WP\_002922654.1] [location=complement(120320..120937)] [gbkey=CDS]

MLLHVLYLIGITAEAMTGALAAGRRRMDTFGVIIIATATALGGGSVRDILLGHYPLGWVKHPEYVIIVAV

AAVLTTIAAPVMPHLRRLFLVLDALGLIVFSIIGAQIALDMGEGPVIASIAAVITGVFGGVLRDMFCKRI

PLVFQKELYAGISFAAAVLYIALQHYVSSHDVVVLATLLFGFTARMLALRWKLGLPVFHYTHDAH

>lcl|NZ\_FO834906.1\_prot\_WP\_009308789.1\_118 [locus\_tag=BN49\_RS01730] [protein=chloride channel protein] [protein\_id=WP\_009308789.1] [location=121213..122463] [gbkey=CDS]

MSVAAGNKNHLIRLIAVVLTGILAGLSGMVLALILHAIQHLAFGYSYGQIVGSVSFLQGVTESSWPRRIV

AIVAGGAVAGFGWWLLGRYGQRRVSIAAAVANPCVPMPAGTTTIHALLQIVTVALGSPLGREVAPREMGA

LGAGMVARKLRLLEDETRTLIACGAGAGLAAVYNVPLAGALFSLEVMLLSFSWEKTLAAIMTSAIAAWTA

TLGLGDESQYHFVSSALPHTFLWWAILAGPILGTGAWLFRKATSAARSRARSNWQMPVFCLLGFSLLAIL

SLYFPELPGNGKGPMQLALSDGLPLSMVAVLLVLKMVVILAVLRGGAEGGLLTPGLAVGGLVSLLLCALW

QLGFPGGDKSSFAVVGAAAFLAASMQMPLTAVALVMEFTHMDHSYLAPALLCAAGAFLTCRVLDKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004151500.1\_119 [locus\_tag=BN49\_RS01735] [protein=methylated-DNA--[protein]-cysteine S-methyltransferase] [protein\_id=WP\_004151500.1] [location=complement(122519..123577)] [gbkey=CDS]

MKITDSMQCDIWYQALLERAVEFTGVFFVGVKTTGVFCISVCRARKPRRENVEFYNDFKSALDAGFRPCK

VCRPTENARTAPAFVEQALRLLREAPKVRLSDSELRQHDISPERVRRWFLQNHGITFQAFQRMQRLNMAL

QELKAGRSTTDVAFDSGYESLSGFGYTCKKLTGFAPSAQRQVVLIHRFTTPLGPMFVCATQRGICLLEFV

DRRALESEFSDLQRRFNASIIAGENAHTRQAQQEITEYFAGQRQSFEVALDTPGSEFQRAVWRRLQHVSF

GETTHYQSIAMEIGKPTATRAVAAANGANRVAIIIPCHRIIGKDGSMTGYGGGIARKIWLINHEATIREK

RG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530011.1\_120 [locus\_tag=BN49\_RS01740] [protein=isocitrate lyase/phosphoenolpyruvate mutase family protein] [protein\_id=WP\_016530011.1] [location=complement(123580..124326)] [gbkey=CDS]

MDFNALRQQHQPLLLANVWDASSAQAAQQAGYQALGSSSAAIAAMLGYEDGEEMSFDELFYVVSRIKTVS

ELPLSVDLEAGYGATTSHIIDNIRRLAHLGVSGINLEDSHVVDGTRRLDDAERFAVKLQEITRACPGLFV

NVRTDTFLLNVQDALVQTLYRGQLYAKHGACGFFVPCVTRAEDITAIVHHVPLPLNVMCMPELADFSTLS

TLGVKRISMGNFIYAATQARLKDLLCQVQTQHSFSGVF

>lcl|NZ\_FO834906.1\_prot\_WP\_002922636.1\_121 [locus\_tag=BN49\_RS01750] [protein=YicC family protein] [protein\_id=WP\_002922636.1] [location=complement(124509..125372)] [gbkey=CDS]

MIRSMTAYARREIKGDWGSAAWELRSVNQRYLETYFRLPEQFRSLEPVVRERIRARLTRGKVECTLRFEQ

DPSAQGELILNEKLAKQLVNAANWVKMQSDEGEINPVDILRWPGVMAAKEQDLDAIAADILAALDGALDD

FIVARETEGQALKALIEQRLEGVSGEVAKVRAHMPEILQWQRERLVAKLEDAEVQLENNRLEQELVLMAQ

RIDVAEELDRLEAHVKETYNILKKKEAVGRRLDFMMQEFNRESNTLASKSINAEVTNSAIELKVLIEQMR

EQIQNIE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530791.1\_122 [locus\_tag=BN49\_RS01760] [protein=lysophospholipid acyltransferase family protein] [protein\_id=WP\_016530791.1] [location=125872..127572] [gbkey=CDS]

MDAIFDRVVREFFPNTTIPFWKKWLFRTAFGNKVFSRLIYNERLVNKNGVEWVNAVVELLELKCESEHHQ

FNNIPEHGATVVISNHPTVIDGLSLIHTVSRVRSDIKIIANHVLPIIFPQVSELTIGIENMAGKMSHKKF

REMNDHLRKGGVLIICPAGKLANWSLSGLQEHKWNPGFLQLAMRNNAALVPIHITGANSKIYYLTATFWR

QLSNMMVIREALRHHGKTMKINIGQQIALSSFKEYNKDLSAAANVCLTHLQSIAKNGPAMLDTIAPQELE

PGKKELISAIEECEILRQFEDGRKLVIYRCNTNRTSPIIDELGRLRERCYRDIGAGTGNDRDNDVFDESY

YHIILWDPSDVEILGAYRVMPVGEQLAQHGVTGLYSNSLFKYHDNAYSCLEKCVEIGRGFIQKPYQKSKV

LDYLWQGIFDFIKRYPDYKYLLGVLTIPGAFPEKVQKLIISFYNIYFPSTADFCTPIALFTAENVQDDTP

FCGEDFRADWSMLNHLLREEGYELPWPFKQSAKWFSSGGSSILAFTKDYSFNSIAGLNLSSIDKLNESYV

KHYLRD

>lcl|NZ\_FO834906.1\_prot\_WP\_065809828.1\_123 [locus\_tag=BN49\_RS30825] [protein=hypothetical protein] [protein\_id=WP\_065809828.1] [location=complement(127610..127741)] [gbkey=CDS]

MLSGLLSHAVSISTDISIINTFIGFRIKTHPYAYHFPYHYGLD

>lcl|NZ\_FO834906.1\_prot\_WP\_165456913.1\_124 [locus\_tag=BN49\_RS01765] [protein=HlyD family efflux transporter periplasmic adaptor subunit] [protein\_id=WP\_165456913.1] [location=127740..128627] [gbkey=CDS]

MLSGYSHGEFVYLSYSGNEKIERILINKGDNVATGQELVKIESFDAQNIFLRAEEKLSAESALLRNLESG

ERPEELDIIRSQIKKAQSAESQVKRQLGRYRNLYANHAISLAEWEDIRDELTQKGAQVEELINQLKARQL

PARQDEISKQRSMVAAAKLERDKALWDVQQTTIVSPVNAKVFDIIYRAGERPSAGKPIISLLPPENIKVR

FFIPEAKLGKFKIGSKVKLICDGCAEPIAGVINYISPEAEFTPPVIYSTKRREKLIFMAEAIPALQQAGR

MKIGQPFDVEIIGDE

>lcl|NZ\_FO834906.1\_prot\_WP\_004152982.1\_125 [locus\_tag=BN49\_RS01770] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004152982.1] [location=128620..129537] [gbkey=CDS]

MNNLCIDVKNLNKHFGEHHVVKDFSLQVAKGEIYGFLGPNGSGKTTSIRMMCGLITPDSGEGTCLGMDIF

TQREKIKKKIGYMTQYFSMWGNLTIRENLLFIARLYSLDRRRDRVERALSELGLTARQHQLAKELSGGWK

QRMALAACMLHEPVLLFLDEPTAGVDPKARREFWQMLHQLSDRGISILVSTHYMDEAERCHKVAYLSYGR

LLANGTIASIIASQNLITMRTSGAGLTLLESQLQRLPDIEQTVIFGNQLYITSRDEAKLKSALFAFTQQG

YEFCKVDTNLEDAFTYLMKNNCEKN

>lcl|NZ\_FO834906.1\_prot\_WP\_004150202.1\_126 [locus\_tag=BN49\_RS01775] [protein=ABC transporter permease] [protein\_id=WP\_004150202.1] [location=129569..130663] [gbkey=CDS]

MVIKEIHELRRDKVSISMVLLTPLFQLIILGYAINMDPHNLPTALLNYDTERMSQIFVTEAQNTGYFSMI

PVDSEEAAQKAFVRGDVTFIVTIPEGFTRKLLRGEKPQLLIQGDAIDPITTGNALSALVQVAKSMFQHDL

PGDMRVVQKEDDFELIIHRMFNPEGITQFNTIPGIMGSILSTTLILMTALSITRERENGALENLLVSPLS

GLEVIIGKITPFVIIGLFQATLILIAAVLLFDIPLHGSVFLLFFVLLIYVFLCLSIGIGISGLAQNQLQA

LQMSSFYFIPSIMLSGFISPFISMPDWAKAIGSCLPLTYFIRLVKGIMLKGYSATALLPDLLPLIGLAVI

VIGVGLKSYRKTLD

>lcl|NZ\_FO834906.1\_prot\_WP\_002922602.1\_127 [gene=rph] [locus\_tag=BN49\_RS01780] [protein=ribonuclease PH] [protein\_id=WP\_002922602.1] [location=130760..131476] [gbkey=CDS]

MRPAGRSANQVRPVTLTRNYTKHAEGSVLVEFGDTKVLCTASIDEGVPRFLKGQGQGWITAEYGMLPRST

HTRNAREAAKGKQGGRTMEIQRLIARALRAAVDLKALGEFTITLDCDVLQADGGTRTASITGACVALADA

LNKLVAAGKLKTNPMKGMVAAVSVGIVNGEAICDLEYIEDSAAETDMNVVMTEDGRIIEVQGTAEGEPFT

HEELLTLLALARGGIESIITTQKAALEN

>lcl|NZ\_FO834906.1\_prot\_WP\_002922600.1\_128 [gene=pyrE] [locus\_tag=BN49\_RS01785] [protein=orotate phosphoribosyltransferase] [protein\_id=WP\_002922600.1] [location=131587..132228] [gbkey=CDS]

MKPYQRQFIEFALSKQVLKFGEFTLKSGRKSPYFFNAGLFNTGRDLALLGRFYAEALVDSGIEFDLLFGP

AYKGIPIATTTAVALAEHHDRDLPYCFNRKEAKTHGEGGNLVGSPLQGRVMLVDDVITAGTAIRESMEII

QAQGAQLAGVLISLDRQERGRGEISAIQEVERDYGCQVISIITLKELITYLEEKPEMAEHLASVRAYREA

YGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002922598.1\_129 [gene=slmA] [locus\_tag=BN49\_RS01790] [protein=nucleoid occlusion factor SlmA] [protein\_id=WP\_002922598.1] [location=complement(132276..132872)] [gbkey=CDS]

MAEKQTAKRNRREEILQSLALMLESSDGSQRITTAKLAASVGVSEAALYRHFPSKTRMFDSLIEFIEDSL

ITRINLILKDEKDTTARLRLIVLLILGFGERNPGLTRILTGHALMFEQDRLQGRINQLFERIEAQLRQVM

REKKMREGEGYTLDETLLASQLLAFCEGMLSRFVRSEFKYRPTDDFDARWPLVAAQLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_019725185.1\_130 [gene=dut] [locus\_tag=BN49\_RS01795] [protein=dUTP diphosphatase] [protein\_id=WP\_019725185.1] [location=complement(132997..133455)] [gbkey=CDS]

MMKKIDVKILDPRVGQQFPLPTYATSGSAGLDLRACLDDAVELAPGATTLLPTGLAIHIADPSLAAVILP

RSGLGHKHGVVLGNLVGLIDSDYQGQLMVSVWNRSQQSFIIEPGERIAQMVFVPVVQAEFNLVESFDATD

RGEGGFGHSGRK

>lcl|NZ\_FO834906.1\_prot\_WP\_004188117.1\_131 [gene=coaBC] [locus\_tag=BN49\_RS01800] [protein=bifunctional phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase CoaBC] [protein\_id=WP\_004188117.1] [location=complement(133433..134647)] [gbkey=CDS]

MTLAGKKIVLGVSGGIAAYKTPELVRRLRERGAEVRVAMTEAAKAFITPLSLQAVSGYPVSDSLLDPAAE

AAMGHIELGKWADLVILAPATADLIARVAAGMANDLVSTICLATPSPVAVVPAMNQQMYRAQATQHNLQT

LATRGLLLWGPDSGSQACGDVGPGRMLDPLTIVDMAAQHFASPVKDLQHLNLMITAGPTREPLDPVRYIT

NHSSGKMGFAIAAAAAQRGANVTLISGPVSLPTPPFVQRIDVTTALEMEAAVQAGAQQQHIFIGCAAVAD

YRAAVIAEDKIKKQGDELTIKMVKNPDIVAGVAALKSHRPYVVGFAAETNNVEEYARQKRARKNLDLICA

NDVSQPNQGFNSDSNALHLFWQDGEKRLPLERKELLGQLLLDEIVTRYDEKNRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529877.1\_132 [gene=radC] [locus\_tag=BN49\_RS01805] [protein=DNA repair protein RadC] [protein\_id=WP\_016529877.1] [location=134820..135485] [gbkey=CDS]

MNGMENLMPREKMLQYGIETLTDVELLALFLRVGTRRQDVLSYAQALLQRFGSLYALLSADKAQLIAVDG

LGLAKYAQLKGIAELARRYFSSQLVEEAALVTPSMTREFLQSQLTEEEREIFMVIFLDNQNRVLKHSRLF

SGTLSHVEVHPREIVREAIKVNAAAVILAHNHPSGSPEPSQADRLITERVIKCCRFMEIRVLDHLVIGRG

AYVSFAERGWI

>lcl|NZ\_FO834906.1\_prot\_WP\_000091955.1\_133 [gene=rpmB] [locus\_tag=BN49\_RS01810] [protein=50S ribosomal protein L28] [protein\_id=WP\_000091955.1] [location=135702..135938] [gbkey=CDS]

MSRVCQVTGKRPVTGNNRSHALNATKRRFLPNLHSHRFWVESEKRFVTLRVSAKGMRVIDKKGIDTVLAE

LRARGEKY

>lcl|NZ\_FO834906.1\_prot\_WP\_002922510.1\_134 [gene=rpmG] [locus\_tag=BN49\_RS01815] [protein=50S ribosomal protein L33] [protein\_id=WP\_002922510.1] [location=135959..136126] [gbkey=CDS]

MAKGIREKIKLVSSAGTGHFYTTTKNKRTKPEKMELKKYDPVVRQHVIYKEAKIK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529878.1\_135 [locus\_tag=BN49\_RS01820] [protein=VWA domain-containing protein] [protein\_id=WP\_016529878.1] [location=136331..137008] [gbkey=CDS]

MASFIPDVSFIDNSEQRTPLILVLDCSGSMQGQPIAQLNEGLKLLEEELKQDVIAAKRVRLLVIKYGGYD

ECELYGDWCDAMDFTAPVLEANGLTPTGQAVSLALDEIEAEKQRLKAAGVPYTRPWLFLMSDGEPTDNWQ

AAAQACRDAQAANKVAVFPISVGLEATESMGQFSRSGINGVKQLKGLQFRELFLWLSASMQVVSQSTPGG

KAQLPPTDSWSEISV

>lcl|NZ\_FO834906.1\_prot\_WP\_042940972.1\_136 [locus\_tag=BN49\_RS01825] [protein=protein phosphatase 2C domain-containing protein] [protein\_id=WP\_042940972.1] [location=137043..137738] [gbkey=CDS]

MGSSHRQNQLPCQDAFCYRNLGDRLVAVVCDGAGSAAYSEQGAAMVAHDLANRLATFTTAPDEKQLVALV

GSVRETVLLQAQAQDISPGDFACTVLAAWLGETASVIVHIGDGAAALGLDAEQHFSLPENGEYANQTWFL

TSDDWREHLHISPFSGRATRLVMMTDGVQPFALNRRGDALFSPFIDPVLRYLQQSSEAEGSEALRATLDD

PRTWAITGDDKTLLVALRHEP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529880.1\_137 [locus\_tag=BN49\_RS01830] [protein=protein kinase] [protein\_id=WP\_016529880.1] [location=137728..139101] [gbkey=CDS]

MNHKKLPVCYTEQRRAVRLGKLIKSGGAGSVYFLADDPSRVAKIYHPHTDTAYYQRKLSAMLAQRPEIPA

PAENASIVQLAWPDYLLYDERKRVVGFVMPVLDTQRTIELEYILQARQAKAHHLPEGIGAKVSLACNLAT

LVSTLHARQHRVIDMKPVNLRFYRDSLYIALLDCDGFSIQGEGERFPAGQFTPDYLAPEFQRIGQVPGEQ

EEAQDRFSLAVIIFQLLNHGIHPFSGRSISAKVPDDLPGRIAAGCYAYGINAAKSSVPVPGSTHHLLPVE

LRKLFDRAFSGSPARRPSADEWAQELRPYALRSTQKIILCHQKHQHFAGMPCLVCVRKKQVVAGIKQAKQ

RKQAETDRPRVAPVVRQPRRAPAAAVARQPTGPGPLTLLWRSIRSSVPSFAWHGALALMSTLIMGGLARS

FARLNDAGPAWFDIAALLIIFIWVAALIFRSIIRSKP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529881.1\_138 [locus\_tag=BN49\_RS31355] [protein=hypothetical protein] [protein\_id=WP\_016529881.1] [location=139102..139824] [gbkey=CDS]

MTLKLRYLILFFALLMAFVAPDLVSLLWSAPFRLMDKLPLLPAALNDPQRLYLYGLWLGGTIYFSALMWV

AVTRRNKGYLIVAVAQLVFVMGITLFKVPIGEQNQRRWQSMNQLETPAWSDFLYKRHARFIQIALQGGPL

DQHKITEQFLAQKKPLAALPLGWNEEDAEAADTLWQQALGYREREAKALPKMMDYLAWMPDRGDLTLATA

ILTLTSEADKAQAETAFRRAIAIAPENPDA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529882.1\_139 [locus\_tag=BN49\_RS31360] [protein=TonB family protein] [protein\_id=WP\_016529882.1] [location=139924..141435] [gbkey=CDS]

MAEGLKESPRQPALQQRLAAYIAQMPVDDRQILHILQARMQTRSCDLPLDKYATEQGEASKVLPLAKSIV

FKTAPVRSVSPINERFPGHVSIDSEHYGIRKESLQAMPYPAIHKYIKSATTILSLDTDASGELLNGVVEC

SSGIPEFDQAALYYAQQWRLGSHRQGKRVLLPVSFISDRVPPEEYYEEMEARAMRISRLAARHNKTAMES

ASKEMIAQFTRMKTLFPQQKLSAEEARQLQLIYLKKRDKTTKGRIESFTEMTQAMEALVDTHPYYAPLLK

DLAFRKSYASFEKKRATWSQLLALAPEDPQVWMAWGSVWADRDPELYMGAMIASMLLQPFTEDTEQKIEN

IKTKLLMRVGMGPRKAILSAKVYADYGDILGERAKGENTAKAAEILPASEKLDRQEAVAPLDPAQRMTVD

IDRDEVLNAALFNVEWKAPQRPDGQRVELTVDIDDTGMPTLVLVSKSSTVEQYDAQAVDMLWRWNFKPLP

DARRITVGVNFLH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529883.1\_140 [gene=mutM] [locus\_tag=BN49\_RS01840] [protein=bifunctional DNA-formamidopyrimidine glycosylase/DNA-(apurinic or apyrimidinic site) lyase] [protein\_id=WP\_016529883.1] [location=141499..142308] [gbkey=CDS]

MPELPEVETSRRGIEPHLVGATILHAVVRNGRLRWPVSEEIYRLSDVPVLSVRRRAKYLLLELPDGWIIV

HLGMSGSLRILSEELPAEKHDHVDLVMSNGKVLRYTDPRRFGAWLWTKTLEGHPVLAHLGPEPLSDEFNA

DYLQQKCAKKKTAIKPWLMDNKLVVGVGNIYASESLFSAGIHPDRLASSLSREECEQLVKVIKLVLLRSI

EQGGTTLKDFLQSDGKPGYFAQELQVYGRKGEPCRICGTPVVGTKHAQRATFYCRQCQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002922501.1\_141 [gene=coaD] [locus\_tag=BN49\_RS01845] [protein=pantetheine-phosphate adenylyltransferase] [protein\_id=WP\_002922501.1] [location=complement(142388..142867)] [gbkey=CDS]

MSTKAIYPGTFDPITNGHIDIVTRAASMFDKVVLAIAASPSKKPMFSLDERIALAEQATAHLVNVEVIGF

SDLMANFARAQQANILIRGLRAVADFEYEMQLAHMNRHLMPTLESVFLMPCKEWSFISSSLVKEVARHQG

DVSHFLPANVHQALLNKLK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529884.1\_142 [locus\_tag=BN49\_RS01850] [protein=glycosyltransferase family 2 protein] [protein\_id=WP\_016529884.1] [location=complement(142864..143640)] [gbkey=CDS]

MSNRLSVVMIAKNAADLLPDCLGSVSWADEIIVLDSGSTDNTVELARRLGAQVYTHTDWRGYGIQRQRAQ

DYATGDWVLMIDTDERVTPELRQAILKVLDASQRGAIYSIARRNYFLGRFMRHSGWYPDRVLRLYERARY

RYNDNLVHESLDSLGAEVIPLTGDLLHLTCRDFAGFQQKQLAYAAAWALERHQKGKKTSMAGIFSHTLGA

FLKTLLLRGGVLDGKQGWLLAMVNAQYTFTKYTELWALSHGYSEKESS

>lcl|NZ\_FO834906.1\_prot\_WP\_004145263.1\_143 [gene=waaA] [locus\_tag=BN49\_RS01855] [protein=lipid IV(A) 3-deoxy-D-manno-octulosonic acid transferase] [protein\_id=WP\_004145263.1] [location=complement(143640..144914)] [gbkey=CDS]

MELLYTTLLYLIQPLVWLRLLLRSRKAPAYRKRWAERYGFCQNKVEPDGILLHSVSVGETLAAIPLVRAL

RHRYPSLPITVTTMTPTGSERAMSAFGKDVHHVYLPYDLPGAMNRFLNTVQPKLVIVMETELWPNMVAAL

HKRKIPLVIANARLSERSAKGYAKLGGFMRRLLSRITLIAAQNEEDGNRFLSLGLKRNQLAVTGSLKFDI

SVTPELAARAVTLRRQWAPHRKVWIATSTHDGEEQIILQAHKKLLETFPNLLLILVPRHPERFPDAREMV

QKAGMSFTLRSTGEIPSSSTQVVIGDTMGELMLLYGIADLAFVGGSLVERGGHNPLEPAAHAIPVLMGPH

TFNFKDICAKLQQDDGLITVTDADSLVREVSTLLTDEDYRLWYGRHAVEVLHQNQGALSRLLQLLQPYLP

QRSH

>lcl|NZ\_FO834906.1\_prot\_WP\_004173909.1\_144 [locus\_tag=BN49\_RS01860] [protein=glycosyltransferase] [protein\_id=WP\_004173909.1] [location=complement(145006..145995)] [gbkey=CDS]

MSQTPLLSIVAAVYNGEKFLAQFFECIEQQQLDSYELILVNDGSTDNSLAVIAEWQERLQNVQVLEQENQ

GVSVARNTGLAAASGKYLAFPDIDDKLYPGMYRTLLEMAEKEHLDIATCNGTYVYEKRRESHPIFPLDRL

PSTDVLPGHVWLKQALDSRKFLHVTWLNIYRHDFIRQHHFHFEPGLRHQDIPWTTEALLAAERVQYTSQQ

FYDYYIHSESVSHKPDNDDTLMRSARHYMKILEMLEAINQRYPDKVRHIAACRWQIAKEGLGIIHTFDSM

KDESKKHVIINEFFDRGIWRLIWKNACTFRLRWRLGRRYLRIKRYRHAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529885.1\_145 [locus\_tag=BN49\_RS01865] [protein=glycosyltransferase] [protein\_id=WP\_016529885.1] [location=complement(146025..147119)] [gbkey=CDS]

MRILFVIDGLPGGGAEKVVLTLAAQFLRDGDRVSLISLRDVCEYPLPEGLDYQVVADRCRKPWRKLTELS

RRARQLDAAVVRAEQQGQFDLVLSNLHKTDRIVARSRALRERNVWFCLHGVFSASYLGHRTGFDRWMKQQ

KIKRIYQGRNVVTVSDAVGRDLVEEFALRPAQLKTIYNPFDITALRAEAEADSERPDGDYLIHVGRFHPG

KRHDRLLEAYAQSGIDAPLVLLGQGKPEQEQRLRQLAKTLHIDDRVWFKGFQKNPLPWIKGARMLVLSSD

SEGFGNVVVEALLLHIPVASTRCPGGVTEILTGELARGLADLTSPALAQTMQSIYHNPPAIDDAALEKFS

VVSICQQYRQLQRT

>lcl|NZ\_FO834906.1\_prot\_WP\_016529886.1\_146 [locus\_tag=BN49\_RS01870] [protein=glycosyltransferase family 4 protein] [protein\_id=WP\_016529886.1] [location=complement(147122..148249)] [gbkey=CDS]

MSKFRLALVRQKYRPDGGAERFVSRALEALDSSHLQLNVITREWQGPVKPDWQIHICNPRKWGRISRERG

FANAARELWQRESFDLVQSHERIPGCDLYRAGDGVHRRWLQQRSRILPAWKSRLLFADRYHRYVMQAERE

MYEDSHLRGVICNAEMIKREIIEDFGLPAEKIHVIYNAIDNQRFLPPDEETFAALRAKWQLPLQATCLIY

VGSGFERKGLAAAIRAIAPTDRYLLVVGKDKDQPRYQALAKSLNCEARVRFFGMQSETLPFYQMADGLLL

PTLYDPFPNVILEAMACGLPVITTTGCGGAEFIVDGHNGYVCDALDIPALQQAVMALPARALSSAEGGHA

RERIMACTSERLSTQLLSLYQDLVN

>lcl|NZ\_FO834906.1\_prot\_WP\_004181527.1\_147 [gene=rfaQ] [locus\_tag=BN49\_RS01875] [protein=putative lipopolysaccharide heptosyltransferase III] [protein\_id=WP\_004181527.1] [location=complement(148246..149322)] [gbkey=CDS]

MTPETLSRGPLNPARILVIKLRHHGDMLLITPLIHALKQQYPAASVDVLLYEETRDMLAANPDIHHIYGL

DRRWKKQGKRYQLKMQWQLIQTLRQQRYDMVLNLADQWPSAVISKLTGAATRIGFDFPKRRHPVWRYCHT

ALASTQQHNQLHTVQQNLSILAPLGLQLNDAPARMGYSEADWAASRALLPEDFREHYIVIQPTSRWFFKC

WREDRMSALINALSAEGYAVVLTSGPDAREKKMVDTIIAGCPQARLHSLAGQLTLRQLAAVIDHARLFIG

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AAAKKVLA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529887.1\_148 [locus\_tag=BN49\_RS01880] [protein=polysaccharide deacetylase family protein] [protein\_id=WP\_016529887.1] [location=149434..150387] [gbkey=CDS]

MHNPAFLITIDTEGDNLWQKHDSITTENARYLPRFQQLCEKYGFKPVYLTNYEMAIDPFYIEFARDVIAR

GTAEVGMHLHAWNSPPTEPLTADDWRHKPYLIEYSDAMMREKVDYMTRLLEDTFQTKMVSHRAGRWAFDE

RYARLLVEYGYQVDCSVTPRVNWKTAKGAPQGDGGTDYRRFPQHAYFLDENDISREGHSPLLEVPMSIQY

KHSAWMNSVKQGYDRLRGKVRSPSVHWLRPMGGNVETMKKVVEQTLTQGNDYVEYMLHSSEYMPGGSPTF

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529888.1\_149 [locus\_tag=BN49\_RS01885] [protein=glycosyltransferase] [protein\_id=WP\_016529888.1] [location=complement(150388..151371)] [gbkey=CDS]

MSDKRPLLSIIIPVFNNELYIKQTLTSVFEQIDNDVEVIIVNDGSTDNSAALIQKAIDEYQGTGDLHFIS

QQNAGVSVARNVALDKAQGRWIGFIDGDDLWCPHFLQTIKPLLLEDEGDLIDFQYHYFAQHPPTSSVPTL

VKRTDITQVNHDALYEIFRRSHWHIWSRIYRHELINQRRFHVGRRYEDMMFTPWLYLEAHHIISLDQVLY

WYRDNAQGITRNIQPSDVNDMVFALNQIIDNARTQPPSQMPSRIITPLIINCFNEIKGIHAKLYGFYNYS

EHTISTLKAAAGLLPSGSLSLKRRLHLRYPGLWKRVSQLRHILRRGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004901359.1\_150 [locus\_tag=BN49\_RS01890] [protein=O-antigen ligase family protein] [protein\_id=WP\_004901359.1] [location=complement(151364..152614)] [gbkey=CDS]

MHRVLNTRLKIKNMVLNLAVLLYLFTFMLFYAAPVEMRKIYYLAGYLTFFVALLGCRSLTSWKNNRDIAG

ATALFGLTLLGWYALNFTHSEYWSIYDSYKETGKVLLITALIVFLVSNLRFSFPAERFSWLLIVAGLATN

AYAIYQGLEIESVRLQIELDRATVIAYIFTMTNIVMLAAILELKSQYRYFLFLLAALSGFAAIAYTETRA

ALLTFPVLIILLLIVHPRVRKKQLLKLGTAFIVMLALLAIAFHQKLTDRYQGLRNDVSQYQDNNSVSSIG

SRLAMFQSGLQAALDAPFGESAERRNDNIKRQVEKKPKLTGALDYMDVHMHNELIENFSLRGVGGVITLI

IFYATLLINAWRKCNVMQGMLTLSVIIYGLSDVIFFGKEAVIIFSTALILSILYQKIVIHKDENHE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529889.1\_151 [locus\_tag=BN49\_RS01895] [protein=glycosyltransferase] [protein\_id=WP\_016529889.1] [location=complement(152598..153770)] [gbkey=CDS]

MRKLHIINLEKMGGVERLFLQYIQDVTTNQDCIFCISNQIGPEIAQHLTGRKVTFVNRILNNYPIKFPPF

LRKYALQTKTWLANPEAIIVWDLVPVFVAKPTRGKVIYYDHGCSWRYPHNKKTMNFFAALDGTISASYAS

KRVMELRFNLSCPSQVLINRILPPANIFTGDKPLTAPLRLGIAARLVGLKGISVALLTLKNLLDRGINVT

LDIAGKGPDEHQFIQLAQKLGIAGNVNFLGFRDDLSDFFNSIHIYLSTPVTEPFGLSCLESLFYGVPVIY

PLIDGQPEVVKNGVCGIGITPDITPEAHFEQCGINVNFPYDVYFPGQDALHPPRLLAPEKCADAVLRIVN

GDYEAFRKNAFEHVKSNFDASVFMSDFNSTISEILDASRA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042178.1\_152 [gene=rfaC] [locus\_tag=BN49\_RS01900] [protein=lipopolysaccharide heptosyltransferase RfaC] [protein\_id=WP\_046042178.1] [location=complement(153770..154732)] [gbkey=CDS]

MRVLIVKTSSMGDVLHTLPALTDAAQAIPGIRFDWVVEEGFAQIPSWHESVERVIPVAIRRWRKAWFSAP

IKAERQAFREAVQAVKYDAIIDAQGLVKSAALVTRLAHGVKHGMDWQTAREPLASLFYNRRHHIAKQQHA

VERTRELFAKSLGYAKPQTQGDYAIARHFLQHEASAAAPYLVFLHATTRDDKHWPETRWQELLDLLADSG

VHIKLPWGAPHEEARAKRLAEGREYVEVLPRMSLEQVAQVLAGARAVVSVDTGLSHLTAALDKPNFTLYG

PTDPGLIGGYGKNQHTLISPTKETKDISATTIMQAIQEVI

>lcl|NZ\_FO834906.1\_prot\_WP\_004196077.1\_153 [gene=rfaF] [locus\_tag=BN49\_RS01905] [protein=ADP-heptose--LPS heptosyltransferase RfaF] [protein\_id=WP\_004196077.1] [location=complement(154736..155794)] [gbkey=CDS]

MKILVVGPSWVGDMMMSQSLYRTLRARYPQAIIDVMAPAWCRPLLSRMPEVNEAIPMPLGHGALAIGERR

KLGHSLRERRYDRAYVLPNSFKSALVPFFANIPLRTGWRGEMRYGLLNDARVLDKDAWPLMVERYVALAY

DNGVMRCAKDLPQPLLWPQLQVNEGEKSQACSAFNLSYDRPIVGFCPGAEFGPAKRWPHYHYAALAKKLI

DDGYQIALFGSAKDNEAGKEIIAALSSEQQAWCRNLAGETQLEQAVILIAACKAVVTNDSGLMHVAAALD

RPLVALYGPSSPDFTPPLSHKARVIRLITGYHKVRKGDAAEGYHQSLIDITPERVLQELNELLAEKTEHE

EA

>lcl|NZ\_FO834906.1\_prot\_WP\_004210780.1\_154 [gene=rfaD] [locus\_tag=BN49\_RS01910] [protein=ADP-glyceromanno-heptose 6-epimerase] [protein\_id=WP\_004210780.1] [location=complement(155804..156736)] [gbkey=CDS]

MIIVTGGAGFIGSNIVKALNDKGITDILVVDNLKDGTKFVNLVDLNIADYMDKEDFLIQIMAGEEFGEIE

AIFHEGACSSTTEWDGKYMMDNNYQYSKELLHYCLEREIPFLYASSAATYGGRTSDFIESREYEQPLNVY

GYSKFLFDEYVRQILPEANSQIVGFRYFNVYGPREGHKGSMASVAFHLNTQLNNGESPKLFEGSDGFKRD

FVYVGDVADVNLWFWENGVSGIFNLGTGRAESFQAVADATLAYHKKGSIEYIPFPEKLKGRYQAFTQADL

TNLRKAGYDKPFKTVAEGVTEYMAWLNRDA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042184.1\_155 [gene=kbl] [locus\_tag=BN49\_RS01915] [protein=glycine C-acetyltransferase] [protein\_id=WP\_046042184.1] [location=156950..158143] [gbkey=CDS]

MRGDFYKQLTSNLETARAEGLFKEERIITSAQQADITVGDSHVINFCANNYLGLANHPELIAAAKSGMDS

HGFGMASVRFICGTQDTHKQLEKKLADFLGMEDAILYSSCFDANGGLFETLLGPEDAIISDALNHASIID

GVRLCKANRFRYANNDMQELEARLKEAREAGARHVLIATDGVFSMDGVIANLQGVCDLADKYDALVMVDD

SHAVGFVGENGRGSHEYCDVMGRVDIITGTLGKALGGASGGYTAARKEVVEWLRQRSRPYLFSNSLAPAI

VAASIKVLEMVEEGADLRDRLWANARLFREKMTAAGFTLAGADHAIIPVMLGEAVVAQNFARELQKEGIY

VTGFFYPVVPKGQARIRTQMSAAHTPEQIERAVEAFTRIGKQLGVIA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529894.1\_156 [gene=tdh] [locus\_tag=BN49\_RS01920] [protein=L-threonine 3-dehydrogenase] [protein\_id=WP\_016529894.1] [location=158156..159181] [gbkey=CDS]

MKALSKLKAEEGIWMTDVPEPEVGHNDLLIKIRKTAICGTDVHIYNWDEWSQKTIPVPMVVGHEYVGEVV

GIGQEVRGFKIGDRVSGEGHITCGHCRNCRAGRTHLCRNTIGVGVNRPGCFAEYLVIPAFNAFKIPDNIS

DDLASIFDPFGNAVHTALSFDLVGEDVLVSGAGPIGVMAAAVAKHVGARNVVITDVNEYRLELAHKMGVT

RAVNVAKENLNDVMAELGMTEGFDVGLEMSGAPPAFRSMLDTMNHGGRIAMLGIPPSDMSIDWTKVIFKG

LFIKGIYGREMFETWYKMAALIQSGLDLSPIITHRFGIDDFQKGFDAMRSGQSGKVVLSWD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529895.1\_157 [locus\_tag=BN49\_RS01925] [protein=glycosyltransferase family 2 protein] [protein\_id=WP\_016529895.1] [location=159350..160138] [gbkey=CDS]

MLKLSVCLLTCNSARLLMEVLPPLLKVADECIVVDSGSTDETVAICQQFGLTVHHHAYKAHGAQMNYAIG

LASHDWVLCMDSDEILDNDVVTAIQALKAGEEPDPTCAWRLPRYWFVLGKQVRTIYPISSPDDPVRLFNR

QQARFNDRPVDDQVVGHASSVRLPGFVRHDTFYSLHEVFNKLNSYTTRLVKYQQIKPSLTRGIVSAIGAF

FKWYLFSGAWRYGKVGVVTGLYATFYSFLKYFKAWYAHEDNQAPVAQKRTDP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529896.1\_158 [locus\_tag=BN49\_RS01930] [protein=divergent polysaccharide deacetylase family protein] [protein\_id=WP\_016529896.1] [location=complement(160144..161091)] [gbkey=CDS]

MLQFRAIALAVAGSLALAAPAFAGKLSIVIDDFGYRPQTENQVLALPATISVAVLPNAPHAREMATKAHN

QGHEVLIHPPMAPLSKQPLEKDTLRPEMSSEEIERIIREAYGKVPYAVGLNNHMGSAMTSNLFGMQKVMQ

ALERYNLYFLDSVTIGNTQAMRAAQGTGVKVIKRKVFLDDTQNEADIRNQFNRAIALARRNGSAIAIGHP

HPTTVRVLQQMVYNLPPDITLVRPSSLLNEPQVDNSTPNYAQPPAQQTQQKPRNPFHGVKSCKPKRPLEP

VNASRFFTILSDSISQSALIQYYRLKWQGWDNPGN

>lcl|NZ\_FO834906.1\_prot\_WP\_002922458.1\_159 [gene=envC] [locus\_tag=BN49\_RS01935] [protein=murein hydrolase activator EnvC] [protein\_id=WP\_002922458.1] [location=complement(161095..162366)] [gbkey=CDS]

MRGKAMYSTTWIAAAVRSVLYASALSAGVLLCASSAHADDRDQLKSIQADIAARQRAIKQQQQQRASLLA

QLKAQEEAIAAAARKLRETQDSLNQLNKQIDEMNAALAKLERQRASQERNLAAQLDAAFRQGPHTGIQMV

LSGEEGQRNQRMQVYFSYFNQARQETIAELKKTREEMAVQKSMLEEKQSQQQTLVYEQKAQQAKLEQARN

ERKKTLSGLESSIQQGQQQLSELRANESRLRGRIAQAEAAAKARADREARDAQAVRDRQQEASRKGTTYK

PTESERSLMSRTGGLGSPRGQAFWPVRGPLLHRYGEQLQGELRWKGMVIAASEGTEVRAIADGRVILADW

LQGYGLVVVVEHGKGDMSLYGYNQSALVSVGTQVRAGQPIALVGSSGGQGRPSLYFEIRRQGQAVNPQPW

LGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004152046.1\_160 [gene=gpmM] [locus\_tag=BN49\_RS01940] [protein=2,3-bisphosphoglycerate-independent phosphoglycerate mutase] [protein\_id=WP\_004152046.1] [location=complement(162376..163920)] [gbkey=CDS]

MSVSKKPMVLVILDGYGYREDQQDNAIYSAKTPVMDALWAKRPHTLIDASGLEVGLPDRQMGNSEVGHVN

LGAGRIVYQDLTRLDVEIKERTFFANPVLTAAVDKAVAAGKAVHIMGLMSPGGVHSHEDHIMAMVELAAE

RGAEKIYLHAFLDGRDTPPRSAEKTLATFEAKFAALGKGRIASLIGRYYAMDRDNRWDRVEQAYDLLTLA

KGEFQADTAVAGLQAAYARDENDEFVKATVIRAAGQADAAMEDGDALIFMNFRADRAREITRAFVNADFD

GFARKKVVNLDFVMLTEYAADIKVACAYPPASLANTFGEWMAKHDKTQLRISETEKYAHVTFFFNGGVEE

PFKGEERILINSPKVATYDLQPEMSSAELTEKLVAAIKGGKYDTIICNYPNGDMVGHTGVMEAAVKAVEA

LDRCIDQVAQAVESVGGQLLITADHGNAEQMRDPATGQAHTAHTNLPVPLIYVGNKAVKAVNGGKLSDIA

PTMLSLMGMEIPQEMTGKPLFIVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002922436.1\_161 [locus\_tag=BN49\_RS01945] [protein=rhodanese-like domain-containing protein] [protein\_id=WP\_002922436.1] [location=164166..164597] [gbkey=CDS]

MQEIMQFIGRHPVLSIAWIALLGAVVFTTFKGLMSKVKVITRGEATRLINKEDAVVVDLRQRDDFRKGHI

AGAINLLPSDIKANNVGELEKHKSQPIIVVDGSGMQAQEPASALNKAGFEKVFVLKEGIAGWSGENLPLV

RGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002922429.1\_162 [gene=grxC] [locus\_tag=BN49\_RS01950] [protein=glutaredoxin 3] [protein\_id=WP\_002922429.1] [location=164702..164953] [gbkey=CDS]

MANIEIYTKATCPFCIRAKALLNSKGVTFHELPIDGDAAKREEMIQRSGRTTVPQIFIDAQHIGGCDDLY

ALDSRGGLDPLLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002922428.1\_163 [gene=secB] [locus\_tag=BN49\_RS01955] [protein=protein-export chaperone SecB] [protein\_id=WP\_002922428.1] [location=165014..165481] [gbkey=CDS]

MSEQNSTEMTFQIQRIYTKDISFEAPNAPQVFQKDWQPEVKLDLDTASTQLAEGVYEVVLRVTVTAALGE

ETAFLCEVQQGGIFSIDGIEGTQMAHCLGAYCPNILFPYARECITSLVSRGTFPQLNLAPVNFDALFMNY

LQQQAGEGAEQHQDA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529899.1\_164 [gene=gpsA] [locus\_tag=BN49\_RS01960] [protein=NAD(P)H-dependent glycerol-3-phosphate dehydrogenase] [protein\_id=WP\_016529899.1] [location=165481..166500] [gbkey=CDS]

MNALNAAMTVIGAGSYGTALAITLARNGHHVVLWGHDPKHIATLQHDRCNAAFLPNVPFPDTLHLESDLA

TALAASRDILIVVPSHVFGQVLRQIKPLMRSDARLVWATKGLEAETGRLLQDVAREALGDDIPLAVISGP

TFAKELAAGLPTAISLAATDPQFAEDLQRLLHCGKSFRVYINPDFIGVQLGGAVKNVIAIGAGMSDGIGF

GANARTALITRGLVEMSRLGAALGADPETFMGMAGLGDLVLTCTDNQSRNRRFGMMLGQGMDVQSAQDKI

GQVVEGYRNTKEVRVLAQRLGVEMPITEEIYQVLYCGKIAREAALTLLGRARKDERSSN

>lcl|NZ\_FO834906.1\_prot\_WP\_002922426.1\_165 [gene=cysE] [locus\_tag=BN49\_RS01965] [protein=serine O-acetyltransferase] [protein\_id=WP\_002922426.1] [location=166574..167395] [gbkey=CDS]

MPCEELDIVWNNIKAEARALADCEPMLASFYHATLLKHENLGSALSYMLANKLASPIMPAIAIREVVEEA

YAADPEMIASAACDIQAVRTRDPAVDKYSTPLLYLKGFHALQAYRIGHWLWTQGRRALAIFLQNQVSVSF

QVDIHPAAKIGRGIMLDHATGIVVGETAVIEDDVSILQSVTLGGTGKTSGDRHPKIREGVMIGAGAKILG

NIEVGRGAKIGAGSVVLQPVPPHTTAAGVPARIVGKPESDKPAMDMDQHFNGIHHTFEYGDGI

>lcl|NZ\_FO834906.1\_prot\_WP\_004181521.1\_166 [gene=trmL] [locus\_tag=BN49\_RS01970] [protein=tRNA (uridine(34)/cytosine(34)/5-carboxymethylaminomethyluridine(34)-2'-O)-methyltransferase TrmL] [protein\_id=WP\_004181521.1] [location=complement(167477..167950)] [gbkey=CDS]

MLNIVLFEPEIPPNTGNIIRLCANTGFSLHIIEPMGFTWDDKRLRRAGLDYHEFTAVQRYADYAAFVASA

QPQRLFALTTKGTPAHSAVSYQDGDFLMFGPETRGLPASILDALPPEQKIRIPMMPDSRSMNLSNAVSVV

VYEAWRQLGYPGAVLRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002922420.1\_167 [gene=lldD] [locus\_tag=BN49\_RS01975] [protein=FMN-dependent L-lactate dehydrogenase LldD] [protein\_id=WP\_002922420.1] [location=complement(168043..169227)] [gbkey=CDS]

MIISAASDYRAAAQRILPPFLFHYIDGGAYAEHTLRRNVEDLSDVALRQRILRNMSDLSLETTLFNEKLA

MPTALAPVGLCGMYARRGEVQAAGAADDKGIPFTLSTVSVCPIEEVAPTIKRPMWFQLYVLRDRGFMRNA

LERAKAAGCSTLVFTVDMPTPGARYRDAHSGMSGPNAALRRYWQAVTHPQWAWDVGLNGRPHDLGNISAY

LGKPTGLEDYIGWLANNFDPSISWKDLEWIRDFWDGPMVIKGILDPEDARDAVRFGADGIVVSNHGGRQL

DGVLSSARALPAIADAVKGDITILADSGIRNGLDVVRMIALGADSVLLGRAYLYALATHGKQGVANLLNL

IEKEMKVAMTLTGAKSIREISRDSLVQNAEALQTFDALKQNNAA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042187.1\_168 [gene=lldR] [locus\_tag=BN49\_RS01980] [protein=transcriptional regulator LldR] [protein\_id=WP\_046042187.1] [location=complement(169227..169988)] [gbkey=CDS]

MIVMPKRLADDVARRVRALIEEQQLEAGMRLPAERQLAAQLGVSRNSLREALAMLVNEGVLLSRRGGGTF

VRFQHEPWSEQNIVQPLKTLLADDPDYSFDILEARHAIEASTAWHAAMRATDADKEKIRLCFEATQSEDP

DIASQADVRFHLAIAEASHNVVLLQTMRGFFDLLHSSVKQSRQRMYQVPPVFARLTEQHQAVMEAIVAGD

AEAARQAMMGHLGFVHGFDEDQARQARITRLPGDHNENSRENS

>lcl|NZ\_FO834906.1\_prot\_WP\_002922413.1\_169 [gene=lldP] [locus\_tag=BN49\_RS01985] [protein=L-lactate permease] [protein\_id=WP\_002922413.1] [location=complement(169985..171640)] [gbkey=CDS]

MNLWQQNYDPAGNIWLSSLIASLPILFFFFALIKLKLKGYIAATWTVAIALVVALLFYKMPVDRALASVV

YGFFYGLWPIAWIIIAAVFVYKISVKTGQFDIIRSSILSITPDQRLQMLIVGFSFGAFLEGAAGFGAPVA

ITAALLVGLGFNPLYAAGLCLIVNTAPVAFGAMGIPILVAGQVTGIDSFAIGQMVGRQLPFLTIIVLFWI

MAIMDGWRGIKETWPAVIVAGGSFAIAQYLSSNFLGPELPDIISSLVSLVCLTLFLKRWQPVRIFRFGDL

GASQVDMTLARTRYTAGQVIRAWSPFLFLTATVTLWSVPPFKALFAPGGAMYDFVINISVPFLDKMVARM

PPVVSAATPYAAVYKFDWLSATGTAILFAALLSIVWLRMKPKDALTTFAGTLKDLALPIYSIGMVLAFAF

ISNYSGLSSTLALALAHTGHAFTFFSPFLGWLGVFLTGSDTSSNALFAALQATAAQQIGVSDILLVAANT

TGGVTGKMISPQSIAIACAAVGLVGKESDLFRFTVKHSLIFTCMVGLITTLQAYVLTWMIP

>lcl|NZ\_FO834906.1\_prot\_WP\_002922410.1\_170 [locus\_tag=BN49\_RS01990] [protein=YibL family ribosome-associated protein] [protein\_id=WP\_002922410.1] [location=complement(171926..172288)] [gbkey=CDS]

MKEVEKNEIKRLSDRLDAIRHQQAELSLVEAADKYAELEKEKATLETEIERLRSVQSQKLSKEAQKLMSL

PFRRAITKKEQADMGKLKKSVRGLVVVHPMTALGREMGLKEMTGFARSEF

>lcl|NZ\_FO834906.1\_prot\_WP\_002922402.1\_171 [locus\_tag=BN49\_RS01995] [protein=hypothetical protein] [protein\_id=WP\_002922402.1] [location=172561..172785] [gbkey=CDS]

MAKIGDGVPRLIDKAVDFMASSQAFMEYLKKSPRLQHVPRDIPQDKEALFLQRLEYYRQLYRPTCDQTEP

ESER

>lcl|NZ\_FO834906.1\_prot\_WP\_002922401.1\_172 [gene=mtlR] [locus\_tag=BN49\_RS02000] [protein=mannitol operon repressor MtlR] [protein\_id=WP\_002922401.1] [location=complement(172774..173370)] [gbkey=CDS]

MHNLARPTSRPLRLLSDMQAMMEETQAFENRVLERLNAGKTVRSFLIATVELLTEAVNILVLQVFRKDDY

AVKYAVEPLLEGSGPLGDLSVRLKLIYGLGVISRAEYEDAELLMALREELNHDGNEYSFTDDEIIGPFGE

LHCVAALPPTPQFDDSDAELLAMQKLRYQQMVRSTMVLSLTELISRISLKKAFQKSTL

>lcl|NZ\_FO834906.1\_prot\_WP\_004145239.1\_173 [gene=mtlD] [locus\_tag=BN49\_RS02005] [protein=mannitol-1-phosphate 5-dehydrogenase] [protein\_id=WP\_004145239.1] [location=complement(173370..174518)] [gbkey=CDS]

MKALHFGAGNIGRGFIGKLLADAGIELTFADVNQTVLDALNARHSYQVHVVGENEQVDTVSGVNAVSSIG

DEVVDLIAEVDLVTTAVGPVVLERIAPAIAKGLAQRKAQGTERPLNIIACENMVRGTTQLKGHVFNALAE

EDKAWVEAHIGFVDSAVDRIVPPSASATHDPLEVTVETFSEWIVDKTQFKGALPTIPGMELTDNLMAFVE

RKLFTLNTGHAITAYLGKLAGHQTIRDAILDEKIRAVVQGAMEESGAVLIKRYAFDPQKHAAYIQKILGR

FENPYLKDDVERVGRQPLRKLSAGDRLIKPLLGTLEYGLPHRNLVKGIAAAMHFRSEDDPQAQELAALIA

DKGPQAALAQISGLDAASDVVAEAVNDYNAEK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529902.1\_174 [gene=mtlA] [locus\_tag=BN49\_RS02010] [protein=PTS mannitol transporter subunit IICBA] [protein\_id=WP\_016529902.1] [location=complement(174619..176526)] [gbkey=CDS]

MSSDIKIKVQSFGRFLSNMVMPNIGAFIAWGIITALFIPTGWLPNETLAKLVGPMITYLLPLLIGYTGGK

LVGGERGGVVGAITTMGVIVGADMPMFLGSMIAGPLGGYCIKKFDNWVDGKIKSGFEMLVNNFSAGIIGM

ILAILAFLGIGPAVEVLSKILAAGVNFMVAHDMLPLASIFVEPAKILFLNNAINHGIFSPLGIQQSHELG

KSIFFLIEANPGPGMGVLLAYMFFGRGSAKQSAGGAAIIHFLGGIHEIYFPYVLMNPRLILAVILGGMTG

VFTLTILNGGLVSPASPGSILAVLAMTPKGAYFANIAAIIAAMAVSFVVSAVLLKTSKVKEEDNIEAATR

RMHDMKAESKGASPLAAGNVTNDLSHVRKIIVACDAGMGSSAMGAGVLRKKVQDAGLSNISVTNSAINNL

PPDVDLVITHRDLTERAMRQVPQAQHISLTNFLDSGLYTSLTERLVAAQRHIDNEVKVTDSLKDSFDDTN

NNLFQLGADNIFLGRKAATKEEAIRFAGEQLVKGGYVEPEYVQAMLDREKLTSTYLGESIAVPHGTIEAK

DRVLKTGVVFCQYPEGVRFGEEEDEVARLVIGIAARNNEHIQVITSLTNALDDETVIERLAKTTSVDEVL

ALLNK

>lcl|NZ\_FO834906.1\_prot\_175 [locus\_tag=BN49\_RS31365] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=<177255..177386] [gbkey=CDS]

LSALLDGIYA\*IAVYSDHFTHVSVMRKVLLRMTSWMHYLYLDH

>lcl|NZ\_FO834906.1\_prot\_WP\_004145238.1\_176 [locus\_tag=BN49\_RS02015] [protein=glutathione S-transferase] [protein\_id=WP\_004145238.1] [location=177493..178101] [gbkey=CDS]

MKLIGSYTSPFVRKISVILLEKRIPFEFVNESPYSESNGVARYNPLGKVPALVTDDGECWFDSPVIAQYL

ELLGVAPPMIPADPRAALRMRQLEALADGVMEAAQALVREKARPGAQQSEQELLRQREKVARGLDRLEAC

AADGTLRGDEVNLATISTACAIAYLNFRRVAPGWCATRPQLVKLVDALFQRASFARTEPPRT

>lcl|NZ\_FO834906.1\_prot\_WP\_032103599.1\_177 [gene=selA] [locus\_tag=BN49\_RS02020] [protein=L-seryl-tRNA(Sec) selenium transferase] [protein\_id=WP\_032103599.1] [location=178207..179595] [gbkey=CDS]

MTTEIRALYTRLPAIDRLLRDPAFSSLLAQHGHSQVVAQLRQMLDEAREQIRQYQTLPDWSHDWPSACAQ

RLTAGRQSALRPVFNLTGTVLHTNLGRAIQAESAVEAVASAMRAPVTLEYDLDDAGRGHRDRAIADLLCQ

ITGAEDACIVNNNAAAVLLMLAATASGREVVVSRGELVEIGGAFRIPDVMRQAGCQLHEVGTTNRTHAKD

YRQAVNDNTALLMKVHTSNYSIEGFTKAVDEAELAAIGRELDVPVVADLGSGSLVDLSQYGLPKEPMPQE

MIAAGVSMVSFSGDKLLGGPQAGIIVGKRALIAQLQSHPLKRALRADKMTLAALEATLRLYQHPEALREK

LPTLRLLTRPAEEIRRLAERLQPDLAAHYADFAVSVAACQSQIGSGSLPVDRLPSAALTFTPHDGRGSRL

EALAARWRALPCPVIGRIYDGRLWLDLRCLENETRFMEMLLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004173923.1\_178 [gene=selB] [locus\_tag=BN49\_RS02025] [protein=selenocysteine-specific translation elongation factor] [protein\_id=WP\_004173923.1] [location=179592..181433] [gbkey=CDS]

MIIATAGHVDHGKTTLLQAITGVNADRLPEEKARGMTIDLGYAYWPQPDGRVLGFIDVPGHEKFLSNMLA

GVGGIDHALLVVACDDGVMAQTREHLAILQLTGKPTLTVALTKTDRVAAARVAEVQAEVEQTLGELGFDA

VAFFPTAAAENIGIAELRSHLLQLAERPRPQQQRFRLALDRAFTVKGAGLVVTGTALSGEVRVGDTLWLT

GVNTPMRVRGLHAQNQAVEQAHAGQRIALNIVGDAQKEAVHRGDWLLSSPPPEPAERVIVELQCHTPLSQ

WQPLHIHHAASHITGRVSLLEGNLAELVLDTPLWLADNDRLVLRDISARLTLAGARVVTLDPPRRGKRKP

EYLQWLHALAAVGADDAQALELHLQRDAVRLEHFAWARQLSEAGMAALIQRPDYLQAGQRLLSAPLAARW

QRKLLDALARYHEQHRDEPGPGRERLRRIALPMEDEALVLLLIEQMRESGLVHSHHGWLHLPEHKAGFTD

EQQAVWQKVETLFGDDPWWVRDLAREVHVEESLMRAVLRQAAQQGMITAIVKDRYYRNDRIVQFAQRVRE

LDRLRGSTCAADFRDTLNVGRKLAIQILEYFDRIGFTRRRGNDHILRDKALFR

>lcl|NZ\_FO834906.1\_prot\_179 [locus\_tag=BN49\_RS29880] [protein=IclR family transcriptional regulator] [pseudo=true] [partial=5'] [location=<181476..181568] [gbkey=CDS]

GEKNLLKPLRETAEAISRELGFTVREASGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002922360.1\_180 [locus\_tag=BN49\_RS02030] [protein=4Fe-4S binding protein] [protein\_id=WP\_002922360.1] [location=181678..182163] [gbkey=CDS]

MNQFLIANAQRCIGCRTCEVACAVAHQQAQDVAALSTNHFAPRIRVVKSGDISTAMACRQCEDAPCASVC

PQGAIQRDNDVWWVDQRRCIGCKSCMVACPYGAMTVTVMNQQAQALKCDLCHHRAEGPACVAACPTQALR

VMVPAELEALCAQKRQRLALA

>lcl|NZ\_FO834906.1\_prot\_WP\_002922359.1\_181 [gene=avtA] [locus\_tag=BN49\_RS02035] [protein=valine--pyruvate transaminase] [protein\_id=WP\_002922359.1] [location=complement(182206..183462)] [gbkey=CDS]

MTFSLFGDKFTRHSGITRLMEDLNDGLRTPGAIMLGGGNPAQIPEMNDYFQQLLADMLDNGKALDALCNY

DGPQGKSELLALLANMLRDELGWEIEPQNIALTNGSQSAFFYLFNLFAGRRADGTTRKVLFPLTPEYIGY

ADAGLEEDLFVATRPNIELLPEGQFKYHVDFEHLQVTEETGMICVSRPTNPTGNVITDEELIKLDALANQ

HGVPLVIDNAYGVPFPGIIFSDARPLWNPNIVLCMSLSKLGLPGSRCGIIIANEKIITAISNMNGIISLA

PGGIGPAMMCEMIKRQDLLRLSETVIKPFYYQRVQETIAIIRRYLPEERCLIHKPEGAIFLWLWFKDLPI

STELLYQRLKKRGVLMVPGDYFFPGLDKPWPHTHQCMRMNYVPDPQKIEAGVKILAEEVEFAWREQEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004901315.1\_182 [locus\_tag=BN49\_RS02040] [protein=alpha-amylase] [protein\_id=WP\_004901315.1] [location=complement(183633..185666)] [gbkey=CDS]

MKLAALATLFVPGMAFAAWTTTDFPAFTEEGTGRFISQKVVEKGTRPLQLNFDQQCWQPSGGIKLNQMLS

MEPCRGTPPQWRIFRQGLYTLEVDTRSGTPTMMISLEEKETSAAAPQIRQCPKWDGKPLTIDVSKTFAEG

SKVRDFYSGNVATVSGGKITLQPAFGSNGLLLLERAETAAPAPFDWHNATVYFVLTDRFVNGNPANDNSY

GRHKDGMQEIGTFHGGDLQGLTSKLDYLQQMGVNALWISSPLEQIHGWVGGGTKGDFPHYAYHGYYTQDW

SKLDANMGTEADLRRLVDEAHKRGIRILFDVVMNHAGYATLADMQEFQFGSLYLQGDELKKTLGERWTDW

KPGAGQTWHSFNDYINFSDKAGWEKWWGKKWIRTDIGDYDNPGYDDLTMSLAFLPDLKTESKEVSGLPNF

YSHKPDTAAKAIPGYTPRDYLTHWLSQWVRDYGIDGFRVDTAKHVEMDAWQQLKTQATAALAEWKKANPD

KALDAAPFWMTGEAWGHGVMQSDYYRHGFDAMINFDYQDQAAKAATCMANIDLTWQQMADKLQSFNVLSY

LSSHDTRLFREGGTTAAELLLLAPGAVQIFYGDESSRPFGPTGSDPLQGTRSEMNWQDVNGKAARSVTHW

QKIGQFRARHPAIGMGKQTTLSMPRGYGFVRESGEDKVMVIWAGQQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004188166.1\_183 [locus\_tag=BN49\_RS02045] [protein=protein bax] [protein\_id=WP\_004188166.1] [location=185981..186799] [gbkey=CDS]

MISNPIRRYGAAILMLLTCIFSGSVLATTHTATKSHKAPTVKKISSTKVSSKQEYSRNSVKSSSLPDLRK

YPSGTPRKKAFLRTVMPYITKQNQAITADRNWLISKQYDARWSPTEKARLKDIASRYKVKWSGNTRHVPW

NALLERVDIIPNSMVATMAAAESGWGTSRLARENNNLFGMKCGAGRCRGAMKGYSQFESVEQSVQAYVTN

LNTHPAYSSFRKSRLQLRKADQEVTASTMIHKLKGYSTKGSSYNNYLFAMYQDNQRLIAAHL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530898.1\_184 [locus\_tag=BN49\_RS02050] [protein=XylR family transcriptional regulator] [protein\_id=WP\_016530898.1] [location=complement(186839..188017)] [gbkey=CDS]

MFEKRHRITLLFNANKAYDRQVVEGVGEYLQASQLEWDIFIEEDFRARIENIKEWLGDGVIADYDDPEIE

KLLADVHVPIVGVGGSYHQPEQYPPVHYIATDNAALVESAFLHLKEKGVHRFAFYGLPISSGKRWAVERE

YAFCQLVAKEKYRGVVYQGLETAPENWQHAQNRLADWLQTLPPQTGIIAVTDARARHVLQACELLHIPVP

EKLCVIGIDNEELTRYLSRVALSSVAQGTRQMGYQAAKLLHRLLNNEALPLQRQLIPPMRVVERRSTDYR

SLNDPSVIQAMHYIRNNACKGIKVEQVLDAVGISRSNLEKRFKEEVGETIHTVIHSEKLEKARSLLVSTS

LSINEISQMCGYPSLQYFYSVFKKEYDVTPKEYRDRHSEVML

>lcl|NZ\_FO834906.1\_prot\_WP\_002922349.1\_185 [locus\_tag=BN49\_RS02055] [protein=sugar ABC transporter permease] [protein\_id=WP\_002922349.1] [location=complement(188250..189431)] [gbkey=CDS]

MSKNTSSEIKLTPTAPAALPALKGLNLQVFVMIAAIVVIMLFFTWVTDGAYLSARNISNLLRQTAITGIL

AVGMVFVIISAEIDLSVGSMMGLLGGAAAIFDVWLGWPLPLTILVTLVMGLLLGAWNGWWVAYRKVPSFI

VTLAGMLAFRGILIGITNGTTVSPTSPAMSQIGQSYLPDGIGFGIGVVGMAVFIVWQWRGRMRRQALGLA

TSSSTAAVGRQAITAVIVLGAIWLLNDYRGVPTPVLILAALLLAGLFMATRTAFGRRIYAIGGNLEAARL

SGINVERTKLAVFAINGLMVAIAGLILSSRLGAGSPSAGNIAELDAIAACVIGGTSLAGGIGSVAGAVMG

AFIMSALDNGMSMMDVATFWQYIVKGAILLLAVWMDSATKRRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002922346.1\_186 [locus\_tag=BN49\_RS02060] [protein=xylose ABC transporter ATP-binding protein] [protein\_id=WP\_002922346.1] [location=complement(189409..190950)] [gbkey=CDS]

MTWLLEMKNITKTFGAVKAVDNVSLRLNAGEVVSLCGENGSGKSTLMKVLCGIYPHGSYEGEIIFAGETL

QANHIRDTERKGIAIIHQELALVKHLTVLENIFLGAEISRHGLLDYETMTLRCQKLLAQVNLPISPDTRV

GDLGLGQQQLVEIAKALNKQVRLLILDEPTASLTEQETATLLAIVRDLQNHDIACIYISHKLNEVKAISD

TICVIRDGQHIGTRDASGMSEDDIITMMVGRELTALYPSEPHAHGEEILRVEHLTAWHPVNRHIKRVNDV

SFSLRRGEILGIAGLVGAGRTEAVQCLFGVWPGRWQGEIFIDGQPVSISNCQQAIAHGIAMVPEDRKKDG

IVPVMAVGKNITLAALNQFTGAMSSLDDAAEQHCIQQSIQRLKIKTSSPELAIGRLSGGNQQKAILARCL

LLNPRILILDEPTRGIDIGAKYEIYKLINQLVQQGIAVIVISSELPEVLGLSDRVLVMHEGRLKANLVNQ

HLTQEQVMEAALRSERHVEEHVV

>lcl|NZ\_FO834906.1\_prot\_WP\_004152040.1\_187 [gene=xylF] [locus\_tag=BN49\_RS02065] [protein=D-xylose ABC transporter substrate-binding protein] [protein\_id=WP\_004152040.1] [location=complement(191015..192010)] [gbkey=CDS]

MKIKNLCLTLCASSLLLASMAGMAKEVKIGMAIDDLRLERWQKDRDIFVNKAESLGAKVFVQSANGNEET

QMSQIENMINRGVDVLVIIPYNGQVLSNVIKEAKQEGIKVLAYDRMINNADIDFYISFDNEKVGEMQAQS

LVDKVPQGNYFLMGGSPVDNNAKLFRAGQMKVLKPYVDDGKIKIVGDQWVDGWLPENALKIMENALTANN

NKIDAVVASNDATAGGAIQALTAQGLAGKVAISGQDADLAGVKRIISGTQTMTVYKPITTLATNAAEIAV

ELGNDKQPKADTTLNNGLKDVPSRLLTPIEVNKENIDATVIKDGFHKKSEL

>lcl|NZ\_FO834906.1\_prot\_WP\_002922139.1\_188 [gene=xylA] [locus\_tag=BN49\_RS02070] [protein=xylose isomerase] [protein\_id=WP\_002922139.1] [location=192505..193827] [gbkey=CDS]

MQTYFDQLDRVRYEGPKSTNPLAFRHYNPDELVLGKRMEDHLRFAACYWHTFCWNGADMFGVGSFDRPWQ

QPGDALEMAKRKADVAFEFFHKLNVPYYCFHDVDVSPEGASLKEYSNNFARMVEVLAEKQQQSGVKLLWG

TANCFTNPRYGAGAATNPDPEVFSWAATQVVTAMNATHQLGGENYVLWGGREGYETLLNTDLRQEREQIG

RFMQLVVEHKHKIGFKGTLLIEPKPQEPTKHQYDYDASTVYGFLKQFGLEKEIKLNIEANHATLAGHSFH

HEIATAIALGLFGSVDANRGDPQLGWDTDQFPNSVEENALVMYEILKAGGFTTGGLNFDAKVRRQSTDKY

DLFYGHIGAMDTMALSLKVAARMIEDGELDKRVARRYAGWNGELGQQILNGQMTLSDIAQYAAQHQLAPQ

HRSGQQEQLENLVNHYLFDK

>lcl|NZ\_FO834906.1\_prot\_WP\_046042192.1\_189 [gene=xylB] [locus\_tag=BN49\_RS02075] [protein=xylulokinase] [protein\_id=WP\_046042192.1] [location=193920..195374] [gbkey=CDS]

MYIGIDLGTSGVKAILLNEQGEVVASHTEKLTVSRPHPLWSEQDPEQWWLATDTAMKALGAQHSLRDVKA

LGIAGQMHGATLLDKSLQVLRPAILWNDGRCAEECQLLEDKVSASRQITGNLMMPGFTAPKLLWVQRHEA

AVFSQVDKVLQPKDYLRLRMTGELASDMSDAAGTMWLDVARRDWSDEMLAACDLSRDAMPALFEGSDVTG

QLRPEVAQAWNMPPALVVGGGGDNAAGAVGVGMADAGQAMLSLGTSGVYFAVSEGFLSKPESAVHSFCHA

LPGRWHLMSVMLSAASCLDWAAKLTGLASVPALIAAAQTADESAGPVWFLPYLSGERTPHNNPQAKGVFF

GLTHQHGPAELARAVLEGVGYALADGMDVVHACGIKPQSITLIGGGARSAYWRQMLADISGLQLDYRTGG

DVGPALGAARLAQLAVHDEADRPGLLKPLPLEQAHRPDDRRVAHYAPQRETFRQIYQQLKPLMS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529858.1\_190 [locus\_tag=BN49\_RS02080] [protein=inner membrane protein YiaB] [protein\_id=WP\_016529858.1] [location=195543..195914] [gbkey=CDS]

MITKRNIARGMMATGSLVYLLGIWRTCPLFRGKGYFLGVLVMGMFAVLAHQRASQWQEQDDGFIALCRLV

LLLSVGLLLVGAWYVPADWHEKAVYIAAWFVCLYGASATPERTRIARAMQKTE

>lcl|NZ\_FO834906.1\_prot\_WP\_004188180.1\_191 [locus\_tag=BN49\_RS02085] [protein=inner membrane protein YiaA] [protein\_id=WP\_004188180.1] [location=195946..196392] [gbkey=CDS]

MMENKHATYSPAFHLISWIALIGGIVTYLVGLWNADMQLNEKGYYFAVLVLGLFAAASYQKTVRDKYEAI

PTTALYYTTCLVVFVIAVGLLVIGLWNATLLLSEKGFYGLAYFLSLFGAVAVQKNVRDVWDPTRLREPLS

VTEEGPET

>lcl|NZ\_FO834906.1\_prot\_WP\_016529859.1\_192 [locus\_tag=BN49\_RS02090] [protein=acyltransferase] [protein\_id=WP\_016529859.1] [location=complement(196419..197414)] [gbkey=CDS]

MQEKIHWITNLRGIACMMVVMIHSTSWYITHPHAITLLQWDIANLLNSASRVSVPLFFMISGYLFFGERS

AQPRHFWRIGLCIAFYSALSLLYITLFTHINVELSLKNLLQKPVFYHLWFFFAITVIYLLSPLLQVKSTS

STMLLALMAILGILANPNMVSVKAAGIEWLPVNLYINGDTFYYVLYGVLGRAIGTLNTDKKWLTPLCAAL

FIAAVWVISRGTLHELRWRGDFGDTWYLYCGPAVFVCAVTLLTLAKNWLNARPLPGIACIARHSLGIYGF

HALIVHALRASHLELSRWPLLDIVWIFSAALLGSLLLSGLVQRIDSRRLVS

>lcl|NZ\_FO834906.1\_prot\_WP\_072198203.1\_193 [locus\_tag=BN49\_RS02095] [protein=YsaB family lipoprotein] [protein\_id=WP\_072198203.1] [location=197594..197893] [gbkey=CDS]

MKGVVSVMLVLLLAGCSETVSPPTQKAQRARITPQTTLNMAQLCKDQAAIRYNTQTQFVDVNHFEQFQAS

YELSGRTGKNERFICSFDPDGQFMHLSMR

>lcl|NZ\_FO834906.1\_prot\_WP\_002922128.1\_194 [gene=glyQ] [locus\_tag=BN49\_RS02100] [protein=glycine--tRNA ligase subunit alpha] [protein\_id=WP\_002922128.1] [location=198021..198932] [gbkey=CDS]

MQKFDTRTFQGLILTLQDYWARQGCTIVQPLDMEVGAGTSHPMTCLRALGPEPMATAYVQPSRRPTDGRY

GENPNRLQHYYQFQVVIKPSPDNIQELYLGSLKELGMDPTIHDIRFVEDNWENPTLGAWGLGWEVWLNGM

EVTQFTYFQQVGGLECKPVTGEITYGLERLAMYIQGVDSVYDLVWSDGPLGKTTYGDVFHQNEVEQSTYN

FEYADVDFLFTCFEQYEKEAQQLLALETPLPLPAYERILKAAHSFNLLDARKAISVTERQRYILRIRTLT

KAVAEAYYASREALGFPMCNKNK

>lcl|NZ\_FO834906.1\_prot\_WP\_002922127.1\_195 [gene=glyS] [locus\_tag=BN49\_RS02105] [protein=glycine--tRNA ligase subunit beta] [protein\_id=WP\_002922127.1] [location=198942..201011] [gbkey=CDS]

MSENTFLVEIGTEELPPKALRSLAESFAANVTAELDNAGLAHGKVEWFAAPRRLALKVANLAAAQADREV

EKRGPAIAQAFDAEGKPSKAAEGWARGCGITVDQAERLTTDKGEWLLYRAHVKGESTEALLPNMIASSLA

KLPIPKLMRWGASDVHFVRPVHTVTLLLGDKVIPATILGIPSDRVIRGHRFMGEPEFTIDHADQYPQILL

ERGKVIADYEQRKAKIKADAQEAARKIGGQADLSESLLEEVTSLVEWPVVLTAKFEEKFLAVPSEALVYT

MKGDQKYFPVYDNAGKLLPNFIFVANIESKDPQQIISGNEKVVRPRLADAEFFFNTDRKKRLEDNLPRLE

TVLFQQQLGTLRDKTDRIQALAGWIAEQIGADVNHATRAGLLSKCDLMTNMVFEFTDTQGVMGMHYARHD

GEAEDVAVALNEQYQPRFAGDALPSNPVACAVAIADKMDTLAGIFGIGQHPKGDKDPFALRRAALGVLRI

IVEKNLDLDLQTLTEEAVRLYGEKLTNANVVDDVIDFMLGRFRAWYQDEGYGVDTIQAVLARRPTRPADF

DARMKAVSHFRTLEESSALAAANKRVSNILAKSDETLNDIVHASVLKEAAEIKLAGNLVVLRDKLQPYFA

AGRYQDALIELAALREPVDEFFENVMVNAEDKDVRINRLTLLSKLRELFLQVADISLLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_087661561.1\_196 [locus\_tag=BN49\_RS29885] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_087661561.1] [location=join(201308..201797,201797..202677)] [gbkey=CDS]

MSRRKYTFQQRLEVVMHYFATDEGYRLTSARFNVPRTQVRIWVAAYDAYGEEGLKPRDKGVSIDPDIRVE

AVKAVLTGQISQTQAAAKFNVAGSASVGKWMKVFSEHGEEGLRSLRVGKKRALHMIDDPVALEVELERSK

DKRIQELEQKVRRLELRILYLKKFESLSSVRDKVRIIDELRQHYSFDQLLQIAQIPRSTFYYHLKALRSP

GKYDEVKCRIKEIYDENLGRYGYRRIALALRREGGALNHKVVQRLMNVLRLKAAIRVKRYSSWRGEHGRA

ADNILQRNFKASRPNEKWVTDVTEFAVSGRKLYLSPIIDLFNNEVISYSISEHPTMPMIDDMLIKAFARL

DAGTNPVLHSDQGWQYRHRWYQYQLREFGIIQSMSRKGNCLDNACAECFFGTLKSECFYTSKFKDIDELK

IVIEDYIRYYNTRRISLKFKGLSPVEYRLKSYPGRN

>lcl|NZ\_FO834906.1\_prot\_WP\_004901287.1\_197 [locus\_tag=BN49\_RS28540] [protein=GFA family protein] [protein\_id=WP\_004901287.1] [location=202878..203306] [gbkey=CDS]

MNGSCLCGTIEFELTHKPAVFYRCHCSLCRKQSGVGYNLATLVKDSEFRWIKGKNCVASWSKPTGYRTDF

CNVCGSTVPNSLRDVPYVWVPVGLIDERLDMECAGDFCTDDAMPWDETRSPSGHAGPVESLASLLKCLKL

NS

>lcl|NZ\_FO834906.1\_prot\_WP\_003026799.1\_198 [locus\_tag=BN49\_RS02120] [protein=DUF1778 domain-containing protein] [protein\_id=WP\_003026799.1] [location=203440..203706] [gbkey=CDS]

MKSDVQLNLRAKESQRALIDAAAEILHKSRTDFILEMACKAAENVILDRRVFNFNDEQYAEFIDMLDAPV

EDEPAINKLLARKPQWDV

>lcl|NZ\_FO834906.1\_prot\_WP\_115217266.1\_199 [locus\_tag=BN49\_RS02125] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_115217266.1] [location=complement(join(203719..204632,204632..204947))] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_WP\_227504837.1\_200 [locus\_tag=BN49\_RS02135] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_227504837.1] [location=204958..205515] [gbkey=CDS]

MTSLKTSIKTITYLSDIGCLEIQGASLITAPEPLSSAHQLAEFVSGETVLDEWLKQRGLKNQALGAARTF

VVCKKGTKQVAGFYSLATGSVNHTEATGSLRRNMPDPIPVIILARLAVDVSLRGKGLGADLLHDAVLRCY

RVAENIGVRAIMVHALTEEAKNFYIHHGFKPSQTQPRTLFLRLPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002922102.1\_201 [gene=hokA] [locus\_tag=BN49\_RS02140] [protein=type I toxin-antitoxin system toxin HokA] [protein\_id=WP\_002922102.1] [location=205859..206011] [gbkey=CDS]

MPQKYLLFGLVVICFTILLLTWMVRDSLCELQRRQGNIELVAFLACDIKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042196.1\_202 [locus\_tag=BN49\_RS02145] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_046042196.1] [location=206313..207923] [gbkey=CDS]

MAHCAHIPAFVLHQVTCQFATGQTLFGPLSVSLEPSLCGLVGRNGVGKTRLLAGLDSPAGGHIERAAAVA

WVAQQPTLTPETTLATLLGYASVFAALSRLEQGQGLADDFDLLDGHWDLTDRLSLAFREADLPPFSADRP

AFSLSGGERMKALLCGAFVSGADYLLLDEPTNHLDRQGREWLYHQLESWQGGALIASHDRELLTRMPRII

ELTPTVLRSYGGNYDEYQRQRMAEQQAARAALEHAVTDRRRTRARMHKEHDAAQRRSAQTLRTVDTLNIA

SFERVKYKGAAKERPGALRRQHREQNSSLNAAVQQARERVEEETPVMFTLPGSEVAAGKQVLVVESLQLD

HAPAAPLNWRIDGPMRIALKGPNGCGKTTLLKTLLGLEQAASGDVRLSVSAAYLDQHLTQLDLSLSVMAH

LSLEDTPLDEGLLRTRLAQLQLGADKVTLPLSALSGGERLKAALACVLWRREPAQLLLLDEPTNHLDLAS

TQAIESALAAFPGAMLVVSHDEAFLQGLKLTHSLAWRETSWHFSLL

>lcl|NZ\_FO834906.1\_prot\_WP\_000014594.1\_203 [gene=cspA] [locus\_tag=BN49\_RS02150] [protein=RNA chaperone/antiterminator CspA] [protein\_id=WP\_000014594.1] [location=complement(208022..208234)] [gbkey=CDS]

MSGKMTGIVKWFNADKGFGFITPDDGSKDVFVHFSAIQNDGYKSLDEGQKVSFTIESGAKGPAAGNVTSL

>lcl|NZ\_FO834906.1\_prot\_WP\_002921931.1\_204 [locus\_tag=BN49\_RS02155] [protein=HTH-type transcriptional regulator] [protein\_id=WP\_002921931.1] [location=complement(208487..208777)] [gbkey=CDS]

MEYKDPVFELLSSLEHIVFKDDNQKLTSNRKSTVFSEFEQLRKGTGLKIDDFANVMGVSVAMVREWESRR

VRPSPTELKLMRLIQANPQLSRQLLD

>lcl|NZ\_FO834906.1\_prot\_WP\_004901270.1\_205 [locus\_tag=BN49\_RS02160] [protein=aromatic acid/H+ symport family MFS transporter] [protein\_id=WP\_004901270.1] [location=complement(209023..210378)] [gbkey=CDS]

MTKTTIDIQAFINEHPFTRYQWMILALCFITVAMDGFDTAIIGFIASDLVQEWGVEKSALGPVMSAALVG

LAVGALTAGPLADRIGRKKVLIMSIVVFGGFSLLTAFATSLNQLTLLRFLTGLGLGAAMPNAATLMSEYA

PERRRALLVNLMFVGFPMGSSLGGFLSAWMIPHYGWQSVLVLGGVMPLLLAVALIFLLPESVRYLVVKQH

PAQRIAAILRHIAPLPKAVEFVLREAGQVKEKSAIGVIFSPRYAVGTVMLCLTYFMGLLIFYLLTSWLPL

LIRETGASMSQASIITALFPLGGGIGVLILGALMDKINPNKVVAVGWLLTGVFVCLVGFSTSSLALMGVM

VFIAGSIMNGAQSSMPALAAGFYPTQGRATGVAWMLGIGRFGGILGAFSGAFLMQAQLSFETIFTLLAIP

AFLSAFALLIKYRVSKSVPATTDEARSLQKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002921929.1\_206 [locus\_tag=BN49\_RS02165] [protein=DUF3053 domain-containing protein] [protein\_id=WP\_002921929.1] [location=210819..211529] [gbkey=CDS]

MATGKSCSRWFAAMAALLMVVSLSGCFDKEGDQRKAFIDFLQNTAMRSGERLPTLTADQKKQFGPFVSDY

AVIYGYSQQVSQAMDAGLRPVVDSVNAIRVPQDYMTQREPLRQANGALGVLSQQLQNAKMQADAAHGALK

QADDLKPVFDQVYAKVVTAPADALQPLIPAAQIFTQQLVQVGDFVAQQGTQVSFVANGIQFPTSQQASQY

NALIGPLAAQHQAFNQAWTAAVNATR

>lcl|NZ\_FO834906.1\_prot\_WP\_004186083.1\_207 [gene=ghrB] [locus\_tag=BN49\_RS02170] [protein=glyoxylate/hydroxypyruvate reductase GhrB] [protein\_id=WP\_004186083.1] [location=complement(211638..212609)] [gbkey=CDS]

MKPSVILYKTLPDDLLQRLEEHFSVTQVKNLRPETVSQHAEAFAQAEGLLGSSEKVDAALLEKMPKLRAT

STVSVGYDNFDVEALNARRVLLMHTPTVLTETVADTVMALVLSTARRVVEVAERVKAGEWTKSIGPDWFG

TDVHHKTLGIVGMGRIGMALAQRAHFGFGMPILYNARRQHPQAEERFNARYCDLDTLLQEADFVCLILPL

SEETHHLFGQAQFAKMKSSAIFINAGRGPVVDEQALIAALQNGEIHAAGLDVFEHEPLAKDSPLLSLPNV

VALPHIGSATHETRYNMAACAVDNLINALNGNVEKNCVNPQVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002921927.1\_208 [locus\_tag=BN49\_RS02175] [protein=MFS transporter] [protein\_id=WP\_002921927.1] [location=complement(212634..213914)] [gbkey=CDS]

MNSSTNATKRWWYIMPIVFITYSLAYLDRANFSFASAAGITEDLGITKGISSLLGALFFLGYFFFQIPGA

IYAERRSVRKLIFICLILWGGCASLTGIVHNIPALAAIRFILGVVEAAVMPAMLIYISNWFTKSERSRAN

TFLILGNPVTVLWMSVVSGYLIQAFGWREMFIIEGVPAVIWAFCWWVLVKDKPSQVSWLAESEKAALQEQ

LDREQQGIKAVRNYGEAFRSRNVILLCAQYFAWSIGVYGFVLWLPSIIRSGGENMGMVEVGWLSSVPYLA

ATIAMIVVSWASDKLQNRKLFVWPLLLIGGLAFIGSWAVGANHFWVSYTLLVVAGAAMYAPYGPFFAIIP

EMLPRNVAGGAMALINSMGALGSFCGSWFVGYLNGATGSPAASYIFMGVALFASVWLTLIVKPANNQNLP

LGAHHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002921921.1\_209 [locus\_tag=BN49\_RS02180] [protein=sugar kinase] [protein\_id=WP\_002921921.1] [location=complement(214019..214954)] [gbkey=CDS]

MENLDVITIGEAMAMFVATETGDLAEVEHFMKRVAGAELNVATGLARLGLKVGWVSRVGNDSFGRFVLQS

LAKEGIDSHAVAIDNRFATGFQMKSKVENGTDPIVEYFRKGSAASHLSPDDFRADYFTSARHLHLSGVAA

ALSESSYALLEHAAKVMKAEGKTLSFDPNLRPVLWKSEAEMVEKLNRLAFQADWVLPGLKEGVILTGQQT

PEGIADFYLSRGVKAVVIKTGCDGAWFKSASGEQGTVDAIKVDNVVDTVGAGDGFAVGVISALLEGKTLL

QAVNRGNKIGSLAIQVQGDSEGLPTRDALGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002921919.1\_210 [locus\_tag=BN49\_RS02185] [protein=hypothetical protein] [protein\_id=WP\_002921919.1] [location=complement(214958..215707)] [gbkey=CDS]

MARKIIVVTAAYGNDHVKSLGGQAAVLPFIANAGADGVEIRRELCSAEELNALPSLAATIERHGLLACYS

APQALFTDNGELNPDLPTLLAEAQTLNALWLKLSLGHFLHNQQLDELRDILSDSGMALVVENDQTDCGQL

APMQRFKAACRVHQLPITLTFDMGNWLWVGDSPEEAARHLAPAVSYIHVKAAEPHHEKFRAVPPDQAAER

WLALLDNLPADAPRGIEFPLTGHDLTAVTRRYVNLLRED

>lcl|NZ\_FO834906.1\_prot\_WP\_002921918.1\_211 [locus\_tag=BN49\_RS02190] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_002921918.1] [location=complement(215819..216835)] [gbkey=CDS]

MAKAARATISDVAKAAKTGKTSISRYLNGEKHLLSDDLLSRIEKAIAELDYRPSLMARGLKHGRTRLIGL

IIADITNPYSVNVMSGIEAACREKGFTLLVCNTNNELDQELHYLDLLRSYQVEGIVVNAVGMREDGLNRL

QQSALPMVLIDRKIPDFACDVVGLDNAQAATTATEHLVEKGFEAILFLSEPLGSVNTRRERLSAFRATLA

RHHGVVAENAEVQLNDGAMLDNVLRQFHARHRGMRKAVISANGALTLQVARALKRVGLIWGSDIGLLGFD

ELEWAELAGVGITTLKQPTWQIGYAAVEQVIRRIAGTNDPIRERVFSGELIVRGSTSR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042200.1\_212 [locus\_tag=BN49\_RS02200] [protein=OmpA family lipoprotein] [protein\_id=WP\_046042200.1] [location=complement(216939..217601)] [gbkey=CDS]

MKKRVLMIAALVSGTLAISGCTTNPYTGEREAGKSGIGAGIGSLVGAGVGALSSSKHDRGKGALIGAAAG

AALGGGIGYYMDVQEAKLRDKMQGTGVSVTRNGDNIVLNMPNNVTFDSNSANLKPAGANTLTGVAMVLKE

YEKTAVNVVGYTDSTGSKDLNMRLSQQRADSVASALITQGVAANRIRTTGMGPANPIASNSTAEGKAQNH

RVEITLSPLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_029884694.1\_213 [locus\_tag=BN49\_RS02205] [protein=molybdopterin guanine dinucleotide-containing S/N-oxide reductase] [protein\_id=WP\_029884694.1] [location=217769..220099] [gbkey=CDS]

MPTSSATKTILTAAHWGPMLVETDGENVLSSRGALATPFANSLQTAVRDQVHSKTRVRYPMVRKGFLASP

DKPQGVRGQDEFVRVSWEQALDLIDAQHRRIRDSYGPASIFAGSYGWRSNGVLHKAATLLQRYMSLAGGY

TGHLGDYSTGAAQAIMPYVVGGNEVYQQQTSWPLVLEHSEVVVLWSANPLNTLKIAWNASDEQGIPWFDR

LRQSGKRLICIDPMRSETVDFFGDSMEWIAPHMGTDVALMLGIAHTLVENDWQDDAFLTRCTSGYDIFAR

YLTGESDGVAKTAEWAAAICGVKADKIRELAQLFHENTTMLMAGWGMQRQQYGEQKHWMLVTLAAMLGQI

GTPGGGFGLSYHFANGGNPTRRAAVLGSMQGSVAGGVDAVEKIPVARIVEALENPGAEYQHNGMARRFPD

IRFIWWAGGANFTHHQDTNRLIQAWQKPELIVISECFWTAAARHADIVLPATTSFERNDLTMTGDYSNQH

LVPMKQVVAPRDEARDDFAVFADLSERWEAGGRERFTEGKSDLQWLETFYQMAARRGAQQQVTLPPFAEF

WQANQLIEMPEEPENARFARFAAFRADPQANPLKTASGKIEIHSPTIAAFGYADCPPHPMWLEPGEWHGN

AEAGQLQLLSAHPAHRLHSQLNHTALRERYAVAGREPVTIHPQDAQARGIVDGDLVRVWNARGQVLAGAV

VTEGIRPGVICLHEGAWPDLDPQVGICKNGAVNVLTKDIPTSRLGNGCAGNTALAWLEKYTGPALPLTAF

DPPANA

>lcl|NZ\_FO834906.1\_prot\_WP\_015959126.1\_214 [locus\_tag=BN49\_RS02210] [protein=N-acetyltransferase] [protein\_id=WP\_015959126.1] [location=complement(220068..220508)] [gbkey=CDS]

MIRKWDTKDTAPLLALWLDSTIHAHPFISESYWRDSVAVVRDVYLPAASTWVWEQDGELKGFVSVLDSRF

VGALFVAPGATRQGIGRALLDEVKQHYAWLSLEVYQKNESAVSFYHAQGFRIEDCAWQDDTQHPTWIMRW

PADQMP

>lcl|NZ\_FO834906.1\_prot\_WP\_002921914.1\_215 [gene=tag] [locus\_tag=BN49\_RS02215] [protein=DNA-3-methyladenine glycosylase I] [protein\_id=WP\_002921914.1] [location=complement(220486..221067)] [gbkey=CDS]

MQRCGWVSQDPLYIEYHDTEWGVAQKEGRQLFEMICLEGQQAGLSWITVLKKRQNYRQAFHQFDPVRVAA

MGDDDIERLLQDTGIIRHRGKIQAIIGNARAYLAMEENGESFTDFVWSFVDNAPQVTRAATLAEIPTTTP

ASDALSKALKKRGFKFVGSTICYSFMQACGLVNDHVTGCFCHPGGQDDPQVGH

>lcl|NZ\_FO834906.1\_prot\_WP\_004220756.1\_216 [locus\_tag=BN49\_RS02220] [protein=lipase] [protein\_id=WP\_004220756.1] [location=221273..221854] [gbkey=CDS]

MSCVSGANAWQQEYIAIDTKSNTSERYTWDSDHQPRYEDILAERMKSSETPGGLALNQGLAPPDSGRGLS

IGWNYPLANGVTSGPVASLRSDVTAPTVRSAGEAGYVNTLGWRMDYQALWGVHPWAQVSYNQSLASDVWA

PMSRAREGGWSDVTLGADMRLGSHVAAWATLSQADNLPSGENTLYLMGVSANF

>lcl|NZ\_FO834906.1\_prot\_WP\_002921907.1\_217 [locus\_tag=BN49\_RS02225] [protein=MFS transporter] [protein\_id=WP\_002921907.1] [location=222096..223301] [gbkey=CDS]

MNAANRQSTRWLTLIGTIITQFALGSVYTWSLFNSSLSDKLGEPVSQVAFSFGLLSLGLALSSSVAGKLQ

ERFGVKRVTMASGILLGLGFFLTAHSSSLMMLWLSAGVLVGLADGAGYLLTLSNCVKWFPERKGLISAFS

IGSYGLGSLGFKFIDSHLLATVGLEKTFVIWGAIVLVMIVFGATLMKDAPNHPAATAANGVVENDFTLAE

SMRKPQYWMLAVMFLTACMSGLYVIGVAKDIAQGMVHLDVATAANAVTVISIANLSGRLVLGILSDKISR

IRVITIGQVVSLVGMAALLFAPLNALTFFAAIACVAFNFGGTITVFPSLVSEFFGLNNLAKNYGVIYLGF

GIGSICGSLIASLFGGFYVTFCVIFALLILSLALSTTIRQPKSTVYNEAHA

>lcl|NZ\_FO834906.1\_prot\_WP\_032105386.1\_218 [gene=eptB] [locus\_tag=BN49\_RS02230] [protein=kdo(2)-lipid A phosphoethanolamine 7''-transferase] [protein\_id=WP\_032105386.1] [location=223544..225217] [gbkey=CDS]

MKYIRTMTQQKLSFWLALYIGWFMNVAVFFRRFDGYAQEFTFWKGLSGVVELVATVFVTFFLLRLLSLFG

RRIWRILATLIVLFSAAASYYMTFLNVVIGYGIIASVMTTDIDLSKEVIGWHLILWLVAVSAPPLLFIWS

NRCRHTLLRQLRTPGQRVKNVLIVVLAGLIVWGPIRLLELRQHDVERHSEVDMPSYGGVIANSYLPSNWL

SALGLYAWAQVDESSDNKSLINPAKKFTYVAPEGLDDTYVVFIIGETTRWDHMGILGYSRNTTPELEKEK

NLVAFRGYSCDTATKLSLRCMFVREGGAEDNPQRTLKEQNVFAVLHQLGFSGNLYAMQSEMWFYSNTMAN

NIAYREQIGAEPRNRGKSVDDMLLVDEMKRGMAQGNASGKHLIILHTKGSHFNYTQRYPRSFAQWKPECV

GVDNKCSKAELINSYDNSVAYVDHFIVSVLDQLRDKKAIVFYAADHGESINEREHLHGTPRKMAPPEQFR

VPMMVWMSDKYLENPDHAAAFAHLQQQAAMKVPRRHVELYDTIMGCLGYTSPDGGINENNNWCRWKK

>lcl|NZ\_FO834906.1\_prot\_WP\_032105387.1\_219 [locus\_tag=BN49\_RS02235] [protein=ankyrin repeat domain-containing protein] [protein\_id=WP\_032105387.1] [location=225409..226803] [gbkey=CDS]

MKVIKGLVLLCLMMLAGCQSEEETSQFLLACKYDAPATIAAMLDNGIDVDGQDKTGLSGLMVAAAENRRD

VVELLLKRRAKPNLQTRQGVTALMLAAARGSDTAIIGDLLQAGASVNQTSIDKSTALMSAISDGGDVRND

YQHILAMKKPDAPVEEESTLDKIVGVTAAKSLATGNRALMTEDMALQLAPGAFKKNVDEIVALLLKHGAD

VKAVNASGESAFFLAVDHARSAETITTLANAGADTSLADKSGTTPLMLAAAGDDPDLVLALSASGVEVDK

PNREGLTALQVAAGQGAPAVIAALVQRGAKLDQLSANDLSPLMLAVKMNNKANVEALLAAGASVNLSNKA

GYTAIGYSRAGEVRQLLLAQHAELKGQAAHMAQSELQFCANAFADKLAYSDIARAVNNDTRPDIMRHQQS

CPELGELTMLLGEFTFTPAGATYLGEPVTCKVSEYRKTFEVNCR

>lcl|NZ\_FO834906.1\_prot\_220 [locus\_tag=BN49\_RS30190] [protein=IS3-like element ISKpn1 family transposase] [pseudo=true] [location=227161..228524] [gbkey=CDS]

MAKPKYSPETKLAVVNHYLSGKDGEQSTADLFGIERTSVRRWVRAWQFHGAEGLTAKNNHYSDEFKLVVV

RAVISDRLTMREAAARFNLSAEILVRRWLDVYNDAGAEGLLNMQCGRPGQMTKPKNIPPLTDKELEKLSP

EELRAELRYLRAENAYLKKLKALVQSEKNGKKP\*\*SVN\*GMNTLCGTFCGRPVCPVARGITI\*MH\*SKGT

GMRVLKRTSGRYTTITKVVRATAGSRSH\*ENRGCG\*TIKQCSG\*WQNCHSGL\*\*GRKNIVPGKGERARPR

PIS\*AGTSVRQKPTKNG\*QM\*QSSRYREKSFTCRQFSICLTGRLSPTACRKGR\*WRW\*IRCWTVRSRSSD

REMLRCCTRIRAGITG\*GAIRNV\*RRMG\*RRVCRVKETAWIMQ\*WKTSSGP\*NRSVFI\*GSSGVSVR\*EK

P\*RTISITTTTSG\*A\*N\*KA\*VR\*STEPRL\*EPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529074.1\_221 [locus\_tag=BN49\_RS02260] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016529074.1] [location=229164..230771] [gbkey=CDS]

MSISLKKSGMLKLGLSLVAMTVAASVQAKTLVYCSEGSPEGFNPQLFTSGTTYDASSVPIYNRLVEFKTG

TTEVIPGLAEKWEVSADGKTYTFHLRQGVKWQDNKDFKPTRDLNADDVVFSFDRQKNTNNPYHKVSGGSY

EYFEGMGLPDLISEVKKVDDNTVQFVLTRPEAPFLADLAMDFASILSKEYADNMLKAGTPEKVDLNPIGT

GPFQLLQYQKDSRILYKAFPGYWGTKPKIDRLVFSITPDASVRYAKLQKNECQVMPYPNPADIARMKEDK

NITLLEQPGLNVGYLSFNTEKKPLDNVKVRQALTYAVNKEAIIKAVYQGAGQSAKNLIPPTMWGYNDDVK

DYTYDPEKAKQLLKEAGMEKGFTIDLWAMPVQRPYNPNARRMAEMIQADWAKVGVQAKIVTYEWGEYLKR

AKAGEHQTVMMGWTGDNGDPDNFFATLFSCAAAKDGSNYSRWCYKPFEDLIQPARATDDHNKRIELYKQA

QVVMHDQAPALIIAHSTVYEPVRKEVKGYVVDPLGKHHFDNVSVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002921786.1\_222 [gene=dppB] [locus\_tag=BN49\_RS02265] [protein=dipeptide ABC transporter permease DppB] [protein\_id=WP\_002921786.1] [location=230906..231925] [gbkey=CDS]

MLQFILRRLGLVIPTFIGITLLTFAFVHMIPGDPVMIMAGERGISPERHAQLLAEMGLDKPLWQQYAHYI

WGVLHGDLGISLKSRIPVWQEFVPRFKATLELGVCAMIFAVAVGIPVGVLAAVKRGSIFDHTAVGLALTG

YSMPIFWWGMMLIMLVSVQLNLTPVSGRISDTVFLDDTLPLTGFMLIDTAIWGEQGDFIDALMHMILPAI

VLGTIPLAVIVRMTRSSMLEVLGEDYIRTARAKGLTRMRVIVIHALRNAMLPVVTVIGLQVGTLLAGAIL

TETIFSWPGLGRWLIDALQRRDYPVVQGGVLLVATMIILVNLLVDLLYGVVNPRIRHKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004145207.1\_223 [gene=dppC] [locus\_tag=BN49\_RS02270] [protein=dipeptide ABC transporter permease DppC] [protein\_id=WP\_004145207.1] [location=231935..232837] [gbkey=CDS]

MSQVTENKVIAAPVPMTPLQEFWHYFKRNKGAVVGLVYVVVMIVIAVFANFLAPYNPADQFRDSLLAPPF

WQDGGSMAHLLGTDDVGRDILSRLMYGARLSLLVGCLVVVLSLILGVVLGLVAGYFGGVVDSIIMRVVDI

MLALPSLLLALVLVAIFGPSIVNASLALTFVALPHYVRLTRAAVLVEVNRDYVTASRVAGAGAMRQMFVN

ILPNCLAPLIVQASLGFSNAILDMAALGFLGMGAQPPTPEWGTMLSDVLQFAQSAWWVVTFPGVAILLTV

LAFNLMGDGLRDALDPKLKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002921785.1\_224 [gene=dppD] [locus\_tag=BN49\_RS02275] [protein=dipeptide ABC transporter ATP-binding protein] [protein\_id=WP\_002921785.1] [location=232848..233831] [gbkey=CDS]

MALLNVDKLSVHFGDENAPFRAVDRISYSVKQGEVVGIVGESGSGKSVSSLAIMGLIDYPGRVMADKLEF

NGRDLQRISEKERRQLVGAEVAMIFQDPMTSLNPCFTVGYQIMEAIKVHQGGNKQTRRQRAIDLLNLVGI

PDPASRLDVYPHQLSGGMSQRVMIAMAIACRPKLLIADEPTTALDVTIQAQIIELLLDLQQQENMALVLI

THDLALVAEAAHKIIVMYAGQVVETGDAKDIFRAPRHPYTQALLRALPEFAQDKARLASLPGVVPGKYDR

PNGCLLNPRCPYATDKCRSEEPALADLTGGRQSKCHYPLDDAGRPGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002921784.1\_225 [gene=dppF] [locus\_tag=BN49\_RS02280] [protein=dipeptide ABC transporter ATP-binding subunit DppF] [protein\_id=WP\_002921784.1] [location=233828..234841] [gbkey=CDS]

MSTQKAATPQPLLQAIDLKKHYPVKKGLFAPERLVKALDGVSFTLERGKTLAVVGESGCGKSTLGRLLTM

IEIPTGGELYYQGQDLLKHDPQAQKLRRQKIQIVFQNPYGSLNPRKKVGQILEEPLLINSSLSKEQRREK

ALAMMAKVGLKTEHYDRYPHMFSGGQRQRIAIARGLMLDPDVVIADEPVSALDVSVRAQVLNLMMDLQQD

LGLSYVFISHDLSVVEHIADEVMVMYLGRCVEKGTKDQIFNNPRHPYTQALLSATPRLNPDDRRERIKLT

GELPSPLNPPPGCAFNARCRRRFGPCTQLQPQLKDYGGQLVACFAVDQDENPQKSHA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145206.1\_226 [locus\_tag=BN49\_RS02285] [protein=hypothetical protein] [protein\_id=WP\_004145206.1] [location=234860..235039] [gbkey=CDS]

MAGSFSPAVDKTWRLRILPQFMSRSQSILRRLSEKISLSVHFYRIKEKLKWFRFILSLI

>lcl|NZ\_FO834906.1\_prot\_WP\_016531323.1\_227 [gene=bcsO] [locus\_tag=BN49\_RS02290] [protein=cellulose biosynthesis protein BcsO] [protein\_id=WP\_016531323.1] [location=235356..235895] [gbkey=CDS]

MSHYDDLQRFQEKTRTQNLNFQDLSSQAATREHGDWAILNQLNPGAEKPSSLALGGSVSAPLPQSVPADL

FRQVEAAVAAAPTSDPVVSAASAAPATSQPVVETAAAAPEPVRQEPAPTPAPSIPVSEPAMAPPPRMAPR

PAPAAENYAHLFAAKSAEPVAKNKDQPLKSLLERIATCR

>lcl|NZ\_FO834906.1\_prot\_228 [locus\_tag=BN49\_RS02295] [protein=AAA family ATPase] [pseudo=true] [location=235897..236689] [gbkey=CDS]

MRLFTERRRRENDPGGQFSLFAGADGQQSSGAGF\*CPERAAFAFWRTAER\*AGLCGEGAGAARLEPVRVE

RRQ\*YFRPAIWRSE\*GAASGV\*\*ATDP\*\*PFPPARSVRAA\*LSRAYHHRRYAPWTFARAKGADGAGGPAS

YPAAGGYRLDVDPGARRKAAPDRRGAEL\*ARALFRH\*PKR\*PSPGQPGRHQPDGRETGRATAWRDPS\*\*K

RGGGQCLAEVDPGL\*RFLGSGLRY\*NHG\*KNIFAVGYSYWRWHGAQPATHVRAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004901226.1\_229 [gene=bcsA] [locus\_tag=BN49\_RS02300] [protein=UDP-forming cellulose synthase catalytic subunit] [protein\_id=WP\_004901226.1] [location=236709..238820] [gbkey=CDS]

MKKSLFWLLALVLSPVAVLVVITPMDSQKQYIFGLLSIGILFLMGFSKRRSVSVIMVVTSLLMSTRYMYF

RLTQTLHFNSSIEAILGMGLFLAEVYIWVMLLLNYLQTVWPLKRGIVPLPDDMSKWPTVDIYIPSYNEPL

EVVRDTVLAAQCIDYPKDKMKIYLLDDGKRSEFAVFAADVGVGYITRNDNKHAKAGNLNHALTLTQGELI

CVFDCDHVATRVFLQATVGGFLKDPMLALVQTPHYFYSPDPFERNLSVGRNIPNEGMLFYGPIQQGNDNW

NATFFCGSCAVIRREALAQIGGFAVETVTEDAHTALKFQRLGWKSAFLDIPLAAGLATERLVVHVIQRTR

WARGMTQIFRVDNPLFGRGLTFQQRLCYLSAMLYYQFALPRVVFVTAPLAYLLFNLNIIYSSASLIVSYA

LPHLFLAIYVGSRMNGRYRYSFWGEIYDIVLAFHLVLPTLVTMIFPKRGKFNVTDKGGLLDVGYFDFTVV

RPHLVVACLLALGVIVGIVRAIGHDYFGSDPNVIALNVGWGIYSLIFLLAAIAVARETRQVRKTIRIDVD

IPVVIHYASGIVSRSHTADLSMGGCRVVALDNRHLEDDIEEIELILQSGAISIPAQLVTSDERFLRLKFD

EDIPLSRRRELVRVVLARADAWINPPRPQDNPFRSFFTILRCVFELFWLTWKTRRSQRNRATVAKTAQED

GTL

>lcl|NZ\_FO834906.1\_prot\_230 [gene=bcsB] [locus\_tag=BN49\_RS02305] [protein=cellulose biosynthesis cyclic di-GMP-binding regulatory protein BcsB] [pseudo=true] [location=238817..241251] [gbkey=CDS]

MKRLTTLALLAGMLSAPALHSEEPGSGSAAPLSFPQLNDAADSEPGDEPPAASPEEGASPAAPATAGDAA

ATAPAPVMPDLPPPVSGTAATEVIPVAPVWGGDLNLAQMGMPDGIILSGGQRQGGGSFTLPADQVVIHSQ

LSLAVRVSPEMASRNATLQLMLNGQPLGTLPLGADGEDVSHYQLDIPPALMVSSNNLSVKINDGDTLQCQ

RDIHDTSRVTVLPTSHFSWESQQLNISDDLSHFPRPFFDSMQMTPADIAVAYGAKPSADVFSAAALISSW

LGIQADYRGIAFSALRDRLPERHGIVIGHPGEQVGGMMLPETDKPLLRIIANPANPAYKLLLIVGKNDTA

LRMAAWRLTRGNFAPQTATLDVEPQTIPVGKAYDAPRWIPTDRPVKLSELLRKDQSPTVSGVWHEPLRIA

FRAAPDLYLWDGETIPLQVGYRFPSESWINEDKSLLSVTLNGTFLNNLPMNKQGPLEKVWRYLGGDARQE

RFTIPLAPYLIYGDNQLSMYFNVVPKDDVPCSVLLNNNIKSRITDDSWIDLSKTRHFSLLPNLSYFVGAS

FPFSRLADYSQTTLLLPADPSETQVATLLNLAARSGNATGTALANNRVVLGMPTGGGDLQSLRERDVLAV

TALDQQAFNQSLLADSPYRPVDNVLSVREPDLWQKVQRRLTGDWTSASLDADRYFSSSSAWRGFISYRSP

WNSTRLVVVALASNDDQLARLKTDLDSPRINAGIRGDTAVITSDNGVRSFQVSTPFPSGQMPWYMMAVWY

ASQHSGFLAVLG\*LPPR\*WDWR\*PRCLNVTPVSVWVRGITN

>lcl|NZ\_FO834906.1\_prot\_231 [locus\_tag=BN49\_RS02310] [protein=BCSC C-terminal domain-containing protein] [pseudo=true] [location=241248..245300] [gbkey=CDS]

MKRKIIITMKNTRRLTTFCLTGALTLAASGGALAAGNDAALQALFAQANYWHEKSHDELAMESLQKVLSV

DANNTQALYLMALWSQQGGDMQAAAQWRARLAKAAPDSPGLQDLDNAKKMSQVPQGQLSLARQQARGGNI

PGALATWRSMFNGNTPPAGLAAEYYLTMASDKSLYPQAISELRQYVAQHPQENAPRVALGKALTWREETR

REGIALLEPMASGNKEADSGLRQALLWLGPQAGDEQYYDTWMQRHPQDSEVQNYFRERRSGQARGQGYAN

LNSGNTAAAKQQFEEVLQTNPQDADALAGMGYIAQRSGDYQAASQYLSRAADLGGDASATRRQQAADALF

YGQLAQAQQAYKQGNISQALALSAPLAQQSGAQGASAKLFRADVLRHNKDLPQAEQTLRSLLNDDPQNAA

ARENLYYVLREQNKSAEAQAMLQTLPQSLRQKLQPRVVAGMPGDALRRQAQAQVSSGNPAGAIATLREGV

ARYPDDPWLRLDLARLLQKSGNGSEASSLMSAAYRPGASNSALYAAALFASENGAWQQAQTLLARIPGGS

QTSDMRDLRQRVNYNLQLVTAENYLAQGNTIAASNTLRAMASTPPKAPADAGKLARLLAESGDLTTAVSL

VRNNISSGVSGNAGDYADQIAVLNQAGLTGEAQNLISNPQLQASSTPTQLASIRNGYVINKADRLREQGN

YAAAYDKLIRAMQSDPQNTDLMFAMARLYQSGKMNKEAGVVYDYLMTRDTPNQDARAGAIDVALSAGNND

RAEQLAGGLRQDNSPDRLLLLARVAEAQGHHQQAMTYLRSARGKLLGMQSTNSSETPTVGGVLAADNPFI

GVSQTSAPTRTASAYGQYMPWQVAQSAAVPGSTLPGIQRTDLPVDTAQTRMLRQVDTMMESLQEKTGSWL

QGGMDVRGRDG\*SGTSKLTELRTPLTWSSSPFGDSRFDFTVTPVSLNAGTASGDAWRRYGANPLANAVSN

MVSTATSEQAAIASMTEAERTAYFASNPGAEALSGLGTLNAADFNPTTSSGMENLAKLGSYDAGQVASYL

SSSSRKPNVDQTSGSTDSQKANGVELALALSGDDYRVDIGSTPLGQDLNTVVGGVKWSPKLTNYLSLILT

GERRSLTDSLLSYVGLKDAYSGKTWGQVTKNGGTLQLSYDDGDAGFYVGGGGYSYLGQNVASNTSINANA

GVYLRPYHDEYRQLQAGLSMSYMDYSKNLSYFTYGQGGYFSPQNYVSVSLPVSLTEKYDNWTMKLGGSVG

YQSYSQDKSAYFPTNSEWQQTLETAVSNGFAKEAYYSATSKSGIGYTLRAGADYKVNKQMTLGGQIGYDT

FGDYNESTAGLYIRYMLGDH

>lcl|NZ\_FO834906.1\_prot\_WP\_002921529.1\_232 [locus\_tag=BN49\_RS02315] [protein=hypothetical protein] [protein\_id=WP\_002921529.1] [location=245300..245776] [gbkey=CDS]

MMTENNNPVVMTWFQQQQTPAGWFDLLIIMIEGMLNNAGELESQPFLRQMGASLAETHPLPASETVGDLE

ANINRLLTHFHWGVVTIDVGEDGLRLRHQALPVSRDEAGRVRWCNAFCAILEGLYSRWLQSQGGSAHVIL

QRERVFSVSDVQFLYYHP

>lcl|NZ\_FO834906.1\_prot\_WP\_004188233.1\_233 [locus\_tag=BN49\_RS02320] [protein=glycosyl hydrolase family 8] [protein\_id=WP\_004188233.1] [location=245788..246789] [gbkey=CDS]

MPLRALVAVIVTTVVMLVPRAWADTAWERYKARFMMPDGRIIDTANGNVSHTEGQGFAMLLAVANNDRPA

FDKLWQWTDNTLRNKSNGLFYWRYNPVAPDPIADKNNASDGDTLIAWALLRAQKQWQDKRYAIASDAITA

ALLKSTVVTFAGRQVMLPGVKGFNLNDRLNLNPSYFIFPAWRAFAERTHLTAWRTLQSDGQALLGQMGWG

KSHLPSDWVALRADGKMLPAKEWPPRMSFDAIRIPLYLSWADPHSALLAPWKAWMQSYPRLQTPAWINVS

TNEVAPWYMAGGLLAVRDLTLGEPQEAPQIDDKDDYYSASLKLLVWLAKQDQR

>lcl|NZ\_FO834906.1\_prot\_234 [gene=bcsG] [locus\_tag=BN49\_RS02325] [protein=cellulose biosynthesis protein BcsG] [pseudo=true] [location=complement(246897..248563)] [gbkey=CDS]

MTNKKTTTAPLPLWQYWRGLGGWNFYFLVKFALLWAGYLNFHPMLNLVFLAFLLVPIPREKLHRIRHWIA

IPLGFALFWHDTWLPGPESIFSQGSQIAGFSASYICDLIVRFINWSMVGAFFVLLVLWLFISQWLRVTVF

VSAMIVWLAVSPLLPAFTLWPAGQPTTAAATTAQANTGANAAAGAASSPANSDIPPQTEPPTSANLTNWL

NAFYAAEQKRKTPFPDQLPADAQPFDLLVINICSLSWSDIEAAGLMDHPLWKHFDIVFKNFNSATSYSGP

AAVRLLRASCGQLSHTNLYQPSGADCYLFENLAKLGFNQQLMLGHNGLFGDFLKELRSLGGMQSPLMDQT

GLPVSLQAFDGSPVYEDLAVLNRWLKTEEASSNPRNATFYNTLPLHDGNHFPGQSKTADYKVRAQKLFDD

LDNFFTELEKSGRKVMVVVVPEHGGALKGDKMQVSGLRDIPSPSITNVPTAVKFFGMKGRRLSSISPAVI

WRCRRWWCAPSTAKCSARTASTGSSMSPTCRRARRCPRTPTPSSSSIRASLMSS\*MAVAGCLIRN

>lcl|NZ\_FO834906.1\_prot\_WP\_002921518.1\_235 [gene=bcsF] [locus\_tag=BN49\_RS02330] [protein=cellulose biosynthesis protein BcsF] [protein\_id=WP\_002921518.1] [location=complement(248560..248757)] [gbkey=CDS]

MMSLADILQLVVLCALLFFPLGYLTRHYQRRIRTTLRLMFFKPRYVKPAGVLRRGTTVKQGKANK

>lcl|NZ\_FO834906.1\_prot\_236 [gene=bcsE] [locus\_tag=BN49\_RS02335] [protein=cellulose biosynthesis protein BcsE] [pseudo=true] [location=complement(248757..250310)] [gbkey=CDS]

MDNVFTLGISSLWDEVCHMPVGGVWWLNVDRYADAVSLFNQTLAAQAKNSHVAALVMGNKPKDIISLDHI

HGPDNIALFTLPNRPQALEEIHRDLVCSLEPGNYLFILLCAENA\*QNINNEKLCAWVEKTSRWAQYHRCA

FLAINSAQEIDRQLTPLLREYRSLSGLASIRYQGDRHIFDIAWWGSDKGISAQQQLMVQHDDAGWRLAQD

AETSVQPRSDEKAILSHVRVLEGAPPLSEYWTLFDTNDEVFNAGRTAQAATILFSITQNTQIEQLGRYIH

TLRRQRGTALKIIVREQTPSLRATDERLLLSSGASLVIPSSASLSRCLTLIESVQNQKFSRHIPEDFATL

LTWSQPLKLRGYQKWDAFCEAVHNVMTNTLLPPDSKGVMVALRPAPGLRVEQALTLCKPNRMGDIMTIGN

NRLVLFLSFCRINDLDTALNHIFPLPTGDIFSNRMVWFEDKQILSEIVIMRGVEPARWNTPLPLSVGKNE

TINATHDGRHWRRYPEPHRLTTREEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002921513.1\_237 [locus\_tag=BN49\_RS02340] [protein=cellulose biosynthesis protein BcsR] [protein\_id=WP\_002921513.1] [location=250479..250667] [gbkey=CDS]

MPAKDPAVPTDATLGYTFQNDFLALSRAFSLPDIDYHDISRREQLNAALKRWPLLAEFAEKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002921510.1\_238 [gene=bcsQ] [locus\_tag=BN49\_RS02345] [protein=cellulose biosynthesis protein BcsQ] [protein\_id=WP\_002921510.1] [location=250679..251410] [gbkey=CDS]

MAILGLQGVRGGTGVTSITAALAWALQLLGESVLAIDASPDNMLRFFFNTDIHHQDGWARALLDGRDWRD

AGLRYTQHIDLLPFGQLSAGERENVDQLQPTLGAIAEAVQQLQGQYRWLLLDLPAGYSPLTRELLTLCDR

SLVVVHPDANSHIRLHQQPLPANGDILINDLRVGSQLQEDLYQLWLESQPRILPVTIHRDEAMAECLAAK

QPLGEYRQDSLAAEEVLTLANWCLIHYSAGRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002921508.1\_239 [gene=bcsA] [locus\_tag=BN49\_RS02350] [protein=UDP-forming cellulose synthase catalytic subunit] [protein\_id=WP\_002921508.1] [location=251407..254025] [gbkey=CDS]

MIRLSTLLLAPPVGERLRARYDDYRQHGASWLSASLGCLWASLVWALMPLETPRWQAILARHETYFPHIN

PHRPRPLDPLRYLLQSLWLLTTRVPEPEKKVNWRSLAALEGVHGRYTQWLEKLPEQMNARTGHLDKQKEL

AHLNPKLRRAILGGVTFCSLVLALMCITQPFNPLSQFIFLMLLWGVALLVRRIPGRFSALMLIVLSLTVS

CRYIWWRYTSTLNWNDPVSLVCGIILLFAETYAWVVLVLGYFQVVWPLNRQPVPLPEDMDLWPTVDIFVP

TYNEDLNVVKNTIYASQGIDWPKDKLNIWILDDGGREAFRQFAKDVGVHYIARTSHEHAKAGNINNALKY

AKGEFVSIFDCDHVPTRSFLQMTMGWFLKEKELAMMQTPHHFFSPDPFERNLGRFRKTPNEGTLFYGLVQ

DGNDMWDATFFCGSCAVIRRGPLDEIGGIAVETVTEDAHTSLRLHRRGYTSAYMRIPQAAGLATESLSAH

IGQRIRWARGMVQIFRLDNPLFGKGLKLVQRVCYANAMLHFLSGIPRLIFLTAPLAFLLLHAYIIYAPAL

MIALFVLPHMIHASLTNSKIQGKYRHSFWSEIYETVLAWYIAPPTFVALINPHKGKFNVTAKGGLVEEEY

VDWVISRPYIYLVLLNLVGVAVGIWRFMYGPENEILTVWVSIVWVFYNLIILGGAVAVSVESKQVRRSHR

VEMSMPAAIAREDGHLFSCTVHDYSDGGLGIKINGDAQVLEGQNARLLLKRGQQEYAFPVRVARVNGSEV

GLQLLPLTNQQHIDFVQCTFARADTWALWQDSFPEDKPMESLLDILKLGFRGYRHLAEFSPPSVKVVFRA

LTSLVAWIASFVPRRPERAAPTLSADPAMAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_071829969.1\_240 [gene=bcsB] [locus\_tag=BN49\_RS02355] [protein=cellulose biosynthesis cyclic di-GMP-binding regulatory protein BcsB] [protein\_id=WP\_071829969.1] [location=254036..256381] [gbkey=CDS]

MKRKLSWMCAVAVGMCSWYPLVSYAAPAAVANAAPVVQPQAATPAAPIVVGEPTATLAEPTAPAALAENV

PQREVKLSFATIAPPPGSIVLRGSRPDASVEFGMRSDELVANALLNLEYTPSPSLLPVQSQLKVYLNDEL

MGVLPVTKEQLGKKIRAQLPIDPLYITDFNRVRLEFVGHYRDVCENPASSTLWLDVGRESYLDLTYQSLK

VNNDLSHFPVPFYDPRDNRPLKLPMIFPGSPAVTQQQAAAIVASWFGSKAGWRGQQFPVYFNELPDRNAI

VFATNDKRPDFLRDHPPVKAPTIEMIDNPNDPYVKLLVIFGRDDNDLLLAAKGIAQGNILFRGSSVTVDG

IKTLQPRQPYDAPNWVRTDRSVTFAELKTYEQQLQSSGLVPDAITVALNLPPDLYLLRANGIDMDLKYRY

TMPPVKDSSRMDISLNDQFLQSFSLNSSQDVNKLILRLPVLQGLLDGKSEVTIPALRLGAVNQLRFDFQY

MNPMPGGSIDNCITFQPVQNHVVIGDDSTIDFSKYYHFIALPDLRVFANAGFPYSRMADLSDTLVVVPKA

PTQGQVATLLQALGGIGSQTGLAAINLQMTDDGNQIKNKDADLLLIGAIPSSLKDDTKINLLVEATKSWV

KMPMRHYDLASIYPDDEARTPNTRTDITSSGPMAAVIGFQSPYNDQRSVVALLADSPRGNELLTNALNDS

GKRAAMFGSVAVIRESGVNSLRVGDIYYVGHLPWFERIWFALSNHPILLAIFAAISIVLLAWVLWRMLRI

ISRRRLSLDDE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042211.1\_241 [gene=bcsZ] [locus\_tag=BN49\_RS02360] [protein=cellulose synthase complex periplasmic endoglucanase BcsZ] [protein\_id=WP\_046042211.1] [location=256385..257494] [gbkey=CDS]

MMKVLCGAVLSALLLAAGQVGAACQWPAWEQFKQAYVSPEGRVIDPSDARKISTSEGQSYGLFFALAAND

RAGFDKLLTWTQNNLAEGDLKQHLPGWLWGKKDDEEWTLLDSNSASDSDLWIAWALLEAGRLWQQPQYTE

TGKALLARIVAEETVAVPGLGTMLLPGKVGFADDSGWRFNPSYLPPQLATYFVRFGAPWPALRDSNLRLL

LETAPKGFTPDWVRYEKGKGWQLKTEKPPIGSYDAIRVYLWVGMLHNGDKQKARLLQRFAPMAAQTTEQG

VPPEKVNIATGKTSGQGPVGFSAAMLPFLQDDEARSVQRQRVADNYPGADAYYSAVLTLFGQGWDQHRFR

FTASGELQPDWNQECASSH

>lcl|NZ\_FO834906.1\_prot\_WP\_046042212.1\_242 [gene=bcsC] [locus\_tag=BN49\_RS02365] [protein=cellulose synthase complex outer membrane protein BcsC] [protein\_id=WP\_046042212.1] [location=257476..260955] [gbkey=CDS]

MRKLSLSLLTLSLGVALLPLAQAATTPAQEHLLEQVRLGEASNREDLVRQSLYRLELIDPNNPELIAARM

RYLLRQGDAAGAQKELERLTKLAPDSPELKASRNEMKSNTGEGRQALQQARLLGVAGKVDEAIAAYEKLY

GGVPDDVDVAIEYWTLVARLPSRHSEGVSQLKKLNASAPGNVSLLTSLAKQMFADNKPQEGFAYLAEMAR

SASGRGIAADMWFSEVKSMPVSKASVQALQQFLLQFPTGSVAANARVLLDQQQAQLQDPTFRARSEGLAA

VKSGNTTQAVADLQKAVQADSRDSDAVGALGQAYSQRGDRARAVAQLSKAIAMDPDSPNRGKWDSLLQTN

RYWLLIKQGDNALKAGQLSQAQNYYAQAQRVDRTDSYAVLGLGDVAAARKEAAAAERYYQQALRLDRGNN

LAVRGLANLYRAESPEKASAWIAGLPPAQRRSIDDIERSLTNDRLEKQAQALESQGNWAQAAEVQRRRLA

LDPDSVWITYRLARDLVSAGERQEADALMRTMVNRQPQDAERVYASGLYLSGNDQDDLALAQIAALPRSA

WTDNIRELEARLQSDRVLRQANQLRDSGDEAQAIALIKRQPASVRYDLTLADWAQQRGDSQTAIADYQRV

LRQEADNGDARLGLAEVYLAEGDKPAARAQVMQLKGAETESMNMQRRVALARAGLGDTADAQRIFNQIVP

QAKAQPPSMESALVLRDAARFATQSGAPQQALTHYREAMVASGITPAQPQDNATFTRLTRNDSHDDWLKR

GIRSDAADLYRQQDLNVTLEHDFWGSSGTGGYSDLKAHTTMLQVDAPLADGRMFFRTDLVNMDAGSFSTH

SDGSYSPSWGTCGEIACTSGSINQTDSGASVAVGWKNDTWSGDIGTTPMGFNVVDVVGGLSYSSDVGPVG

YTVNVHRRPISSSLLSFGGQKDSSSHTGATWGGVRADGGGLSLSYDRGEAHGIWSSLGADSLTGKNVADN

WRVRWMTGYYYKVINENNRRVTVGLNNMIWHYDKDLSGYTLGQGGYYSPQEYLSFAVPVTWRQRTENWSW

ELGGSVSWSHSRTQTQARYPLLNLIPSDYRQRASELTEEGSSSHGFGYTARALVERRVTSNWFVGAAVDI

QQAKDYTPSHALLYVRYSAAGWQGDLDMPPQPLVPYADW

>lcl|NZ\_FO834906.1\_prot\_WP\_004151429.1\_243 [gene=hmsP] [locus\_tag=BN49\_RS02375] [protein=biofilm formation regulator HmsP] [protein\_id=WP\_004151429.1] [location=261198..263204] [gbkey=CDS]

MRVSRSLTIKQMAMVASVSMAFVLVFCTILLFHFVQQSRFTTATQLESIARSVREPLSAAILKADIPEAE

AILSRIQPAGIVSRADVVLPNQFQALRMRFIPERPVPVTVTRLFELPVQISLPIYSLERPANPQPLAYLV

LQADSYRMYKFVMSALATLVTAYLLLVLMLTVALTWCINRLMVRPLRRIARELNDLSQQERLGHQLTLPR

LHHDDEIGMLVRSYNRNQQSLVRQHDELSIQSTRFPVSELPNKAFLLAMLEQTVARPQSAALIVVACETL

QDAAGVLKESQREMLLLTLVEKLRAAIPPQMVLAQVSGYDFAILADGLAEPWQAVTLSKQVLTIINERLP

LHGLQLRPYASVGIAMFHAGLSAEQFYRRAVSAAVTARRKGKNQIEFFDPEQMEKAQRRLMEEHDIMTAL

DNQQFAIWLQPQVACASGEICGAEVLLRQRQADGSWSLPPALIERIESCGLIIPVGYWVMEEACRQLAAW

QSQGIMLPLSVNVSLLQLLEHDRGEEMLKLIARYRIAPGTLILEVTESCRMDDPQDVMARLRPLREAGVQ

IALDDFGMGYAGLHQLQQMKALPVDILKIDKVFIDMLPEDVSMVPAMIQLARGLSLRIVAEGVENDAQRR

WLQAAGVEVLQGHLFGCALPQEAFSARYLSPVREDENL

>lcl|NZ\_FO834906.1\_prot\_WP\_002921438.1\_244 [locus\_tag=BN49\_RS02380] [protein=dicarboxylate/amino acid:cation symporter] [protein\_id=WP\_002921438.1] [location=263361..264647] [gbkey=CDS]

MKTSIFKSLYVQVLTAIAIGILLGHFYPELGAQMKPFGDAFVKLIKMVIAPVIFCTVVTGIAGMESMKAV

GRTGAVALLYFEVVSTIALIIGLIIVNVVQPGAGMNVDPSTLDAKAVAVYAEQAKDQGVVAFLLDVIPGS

VIGAFASGNILQVLLFAVLFGFALHRLGSKGQLIFNVIESFSQVIFGIINMIMRLAPIGAFGAMAFTIGK

YGVGTLVQLGQLIICFYITCILFVVVVLGSIARATGFSIFKFIRYIREELLIVLGTSSSESALPRMLDKM

EKLGCRKSVVGLVIPTGYSFNLDGTSIYLTMAAVFIAQATNSHMDIFHQITLLVVLLLSSKGAAGVTGSG

FIVLAATISAVGHLPVAGLALILGIDRFMSEARALTNLVGNGVATVVVAKWVKELDAKQMDDVLNNRVPA

NKTHELSS

>lcl|NZ\_FO834906.1\_prot\_WP\_004145185.1\_245 [locus\_tag=BN49\_RS02385] [protein=insulinase family protein] [protein\_id=WP\_004145185.1] [location=264867..266369] [gbkey=CDS]

MQGTTIKLLTGGLLMVAAAGYVQAEALQPDPAWQQGTLANGLSWQVLATPQRPSDRIEVRLSVNIGSLSE

STQQSGFSRFIPRLALTQSGSLPTMQARSLWQQSIDPKRPLPPAIVSYDYTMFNLSLPNNRNDLLKEALS

WLADASGKLAITPESINHALQGSDMVATWPLDTKEGWWRYRLKGSTMLGHDPAAPLKQPIDVAQLKDFYQ

KWYTPDAMTLIVVGNVDSRSVAEQINKTFGDLKGKRETPAAVPTLSPLPTVPVSIMTNAVRQDKLSIMWD

APWQPIRDSAALQRYWRDDLAREALFWHVQQSLSKNNVKDIGLGFDCRVLYQRAQCAINIDSPGERLNNN

LSVVSRELAKVRDNGLPQEEFDALIAQKSLELQKLFATYARTDTDILMSQRMRSLQNQVVDIAPEQYQKL

RQEFLNSLTVDMLNQYLRQQLSQDMALVLQQPKGEPEYNMKELQATWEKLMAPNPAATATSGSADTVDAH

SEASDIPPGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004901196.1\_246 [locus\_tag=BN49\_RS02390] [protein=sugar kinase] [protein\_id=WP\_004901196.1] [location=complement(266424..267353)] [gbkey=CDS]

MSKKIAVIGECMIELSEKNGAVNRGFGGDTLNTSVYIARQTDASALSVHYVTALGTDAFSQQMLDSWQQE

NVNTDLIQRMADRLPGLYYIETDDTGERTFYYWRNEAAAKFWLESDRAAAICEELATFDYLYLSGISLAI

LSPASRDKLFTLLRECRANGGKVIFDNNYRPRLWASQAETQQVYQEMLACTDIAFLTLDDEDALWGEKPV

AEVIARTHAAGVEEVVVKRGAEACLVSVSGQPLREVPAVRLAKEKVVDTTAAGDSFSAGYLAVRLTGGDA

ESAARRGHLTASTVIQYRGAIIPREAMPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016532624.1\_247 [locus\_tag=BN49\_RS02400] [protein=AsmA family protein] [protein\_id=WP\_016532624.1] [location=267548..269599] [gbkey=CDS]

MSRTRKTLVIITGTILLLIVLFFIVLATFDWNRLKPTINQKVSAELNRPFAIRGDLGVVWERQPDERGWR

SWIPWPHVHAEDIVLGNPPAIPQVTMIHLPRVEATLAPLALLSKTVYLPWIKLEQPDVRLIRLAEDNNNW

TFQLAGDKRTSGDSAPSSWSFRLDNILFDRGTIAIDDKITRSDITILVDPLGKPLPFSEVTGTKDRHSAA

KPGDYVFGLSLKGRYKGQPVTGNGKIGGMLALRSASAPFPLQGDFHSGNTRVAFSGTVSDPLNVGGIDLR

LKFAGDSLRDLYALTGVLLPETPSFSTDGRLRADFMQKNRMRFNYQNFNGRIGDSDIHGSLTYTTGKPRP

KLSGDMESKQLRLADLGPLIGVDSGKGTKKSAARQAGDRPQPAGKVLPADRFETDKWQVMDADVRFKGRR

IEHGGTLPISDLSTHVILEDGDLRLQPVRFGLANGSIAGSVHLQGDKKPLQGEANLQARRLKLKALMPNV

EMMQKTLGEMNGDVQLRGSGNSVAALLGNSNGNLKLLMNDGLISRNLMEILGLNVGNYLIGQIFGDEEVR

VNCAAANIDVTNGVARPQIFAFDTENALINVTGTASFASEQLDLTIDPESKGFRVITLRSPLYVRGTFKS

PQAGVKAGPLIVRGAVAAALATLVTPAAALLALISPAEGDSNQCRTILSQMKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004150118.1\_248 [locus\_tag=BN49\_RS02405] [protein=MHS family MFS transporter] [protein\_id=WP\_004150118.1] [location=complement(269637..270959)] [gbkey=CDS]

MQATATTLENTQETAPVNSRNKVVVASLIGTAIEFFDFYIYATAAVIVFPHIFFPQGDAAAATLQSLATF

AIAFVARPIGSALFGHFGDRVGRKVTLVASLLTMGISTVVIGLLPGYESIGIVAPMLLALARFGQGLGLG

GEWGGAALLATENAPARKRALYGSFPQLGAPIGFFFANGTFLLLSWLLTDQQFMEWGWRVPFIFSAVLVI

IGLYVRVSLHETPVFAKVAAAKKQVKIPLGTLLTKHVRVTVLGTFIMLATYTLFYIMTVYSMTFSTGAAP

NGLGLPRNEVLWMLMMAVIGFGVMVPVAGLLADAFGRRKSMIIITTMIILFALFAFKPLLGSGNPLLVFA

FLLLGLSLMGLTFGPMGALLPELFPTEVRYTGASFSYNVSSILGASVAPYIAAWLQGNYGLAAVGTYLAA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002921337.1\_249 [gene=yhjD] [locus\_tag=BN49\_RS02410] [protein=inner membrane protein YhjD] [protein\_id=WP\_002921337.1] [location=complement(271231..272262)] [gbkey=CDS]

MTPENDDRRPPQEPDTQPEKSKSTLEALNDTAVGQKASQALKTVTGTAAKVQRNPVIAHLLRAAERFNDR

LGNQFGAAITYFSFLSMIPILMVSFAAAGFVLAWHPTLLQDIFDKILQNVSDPTLAATLKNTINTAVQQR

TAVGLVGLLVALYSGINWMGNLREAIRAQSRDVWERRPQDEEKIWVKYFRDLISLIGLLVALIITLSITS

VAGSAQQMIISALYLDNIEWLKPAWRLIGLAISIFANYLLFFWIFWRLPRHRPRRKALFRGTLIAAIGFE

IIKIVMTWTLPALVKSPSGAAFGSVLGLMAFFYFFARLTLFCAAWIATAEYKDDRRMPGKTHR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145179.1\_250 [locus\_tag=BN49\_RS02415] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004145179.1] [location=complement(272369..273268)] [gbkey=CDS]

MDKIHAMQLFIRVADLESFSRAAETLALPKGSVSRQIQALESHLGVRLLHRTTRRVQLTQDGMVYYERAK

DLLSNLDELDGMFQHDPASISGRLRVDMPVGFAKKMVIPHLPTFLQQYPGIELELSSSDRLVDVIREGFD

CVVRVGALKDSGLIARPLGKLTQINCASPDYLARFGYPQSLEDLADHALIHYASTLGVRPPGFEVMIDGA

VRWVKTGGILTVNSTETYQAACIAGLGIIQVPRTGVREALRAGDLIEILPQYRAEPLPVSLIYPHRRNLS

RRVNLFMEWLGGLMKAYVD

>lcl|NZ\_FO834906.1\_prot\_WP\_002921336.1\_251 [locus\_tag=BN49\_RS02420] [protein=SDR family oxidoreductase] [protein\_id=WP\_002921336.1] [location=273388..274146] [gbkey=CDS]

MTQRIALVTGGSRGLGKNAALKLAAKGTDILLTYHSNRQAALDVVAEIEQKGVKAAALALNVGDSTTFDA

FASEVAQVLAQKWGRTTFDYLLNNAGIGLNAPFAETSEAQFDELMNIQFKGPFFLTQRLLPLLQDGGRIL

NVSSGLARFALPGYAAYAAMKGAMEVLTRYQAKELGGRGISVNIIAPGAIETDFGGGEVRDNAEVNRHIA

AQTALGRVGLPDDIGDAIAALLSDELAWMNAQRVEVSGGMFL

>lcl|NZ\_FO834906.1\_prot\_WP\_004901185.1\_252 [locus\_tag=BN49\_RS02425] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004901185.1] [location=complement(274181..274714)] [gbkey=CDS]

MPELLTPRLRCSPLQLDDWSFFLSLQQDPQVMLYVADPRPQAAIREAFDSRLPPWTPGDEHWLCLVVRDR

LTHTPLGLTGYQHHQRDIAEVGFLFAPAAQGRGYGYESLRALCDYAFTTGGVRRLTASVTAGNETSKQLL

LKAGFRLEGELRENYWLNGRWHNDWLFGRLRGEGDAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004150117.1\_253 [locus\_tag=BN49\_RS02430] [protein=alpha,alpha-trehalase] [protein\_id=WP\_004150117.1] [location=complement(274781..276433)] [gbkey=CDS]

MFSQKLRHVEDDELRIDIDPCYEADPYELKLDEMIDAEPEPEVIEGLPASDALTPADRYLELFTNVQKSR

IFADSKTFPDCAPKHDPLDILRNYRKVKRQPDFDLRQFVEDNFWLPESQSDIYISDPSLTLKEHIDKLWP

VLTREPQDHIPWSSLLALPQAYIVPGGRFSETYYWDSYFTMLGLAESGREDLLKCMADNFAWLIETYGHI

PNGNRTYYLSRSQPPVFALMVELFEEDGVRGAKRYLDHLKMEHAFWMDGAESLIPHQAYRHVVRMPDGSL

LNRYWDDRDTPRDESWREDVETARHSGRPANEVYRDLRAGAASGWDYSSRWLRDITRLASIRTTQFIPID

LNAFLFKLETTIANLSGLKGDRETETAFRQKAQDRRAAVNRYLWDDENGCFRDYDWRREQLALFSAASIV

TLYVGLATHEQAERLADAVRARLLTPGGIMATEYESGEQWDKPNGWAPLQWMAIQGFKRYGQDPLGDEIA

WSWLQTVNHFYKQHHKLIEKYHIATGVPHEGGGGEYPLQDGFGWTNGVVRRLIGLYGEPT

>lcl|NZ\_FO834906.1\_prot\_WP\_016529215.1\_254 [locus\_tag=BN49\_RS02435] [protein=iron-containing alcohol dehydrogenase] [protein\_id=WP\_016529215.1] [location=complement(276673..277821)] [gbkey=CDS]

MLTPFTVLMPANIRFGRGQAESAAPWLAQQGGPILLVHGASPQRAAFLRQQLEALQLAVTTLAISREPWL

SDIEQGVQLAREKGIRAVVSLGGGAVIDAGKAIAALVPAVGPVIDYLEVVGTGRQLEASPLPFVAIPTTA

GTGAEVTKNAVINVPEQQRKVSLRDDRMLPDLAILDPALTDNAPRSITLSSGLDALTQVIEPWLCSRATP

FTDALCQQAIPRGIRALKILMEQECPASRDEMAWVSLCGGLALANAGLGVIHGLAGPLGGLSRASHGALC

GSLLPFGLALNESQINDPGLRQRVNDVRRWLADGLDVPVDQVWDSLREWSHRAGLGTLRDLGVARDALEP

AALAASTSSSMKANPVSLSGEQLLEMLEAAWE

>lcl|NZ\_FO834906.1\_prot\_WP\_002921273.1\_255 [locus\_tag=BN49\_RS02440] [protein=glutathione S-transferase] [protein\_id=WP\_002921273.1] [location=277948..278571] [gbkey=CDS]

MLTILGKRSSINVRKVLWTCEEAGLAYQQEDYGSGFKPLDTPEFQRLNPNSLVPVLLDDDFVLWESNSIC

RYLARKAERWDLLPAEPQPAAEVEHWMDWQATEFNTAWRHAFMGLVRKDPRFQDPVAIKESIAAWTHCVR

IVEAQLQRTGAWIAGERFTLADIVLGLSVHRWKMTPFAHPEMPAVERWYMALNQRPAFMRHGNNGVA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042215.1\_256 [gene=gorA] [locus\_tag=BN49\_RS02445] [protein=glutathione-disulfide reductase] [protein\_id=WP\_046042215.1] [location=complement(278624..279976)] [gbkey=CDS]

MSKHYDYLAIGGGSGGIASINRAAMYGQKCALIEAKELGGTCVNVGCVPKKVMWHAAQIREAIHLYGPDY

GFDTTINHFDWEKLVASRSAYIDRIHTSYDNVLGKNKVDVIKGFARFVDAHTVEVNGEIITADHILIATG

GRPSHPDIPGVEYGINSDGFFELPALPKRVAVVGAGYIAVELAGVINGLGAETHLFVRKHAPLRSFDPLI

VETLVEVMNAEGPQLHTNAIPKAVVKNADGSLTLELEDGRSQTVDCLIWAIGREPATDNFNLAATGVKTN

DKGYIIVDKFQNTNVPGIYAVGDNTGAVELTPVAVAAGRRLSERLFNNKPEEHLDYSNIPTVVFSHPPIG

TVGLTEPQAREQYGDDAVKVYKSSFTAMYTAVTSHRQPCRMKLVCVGPEEKIVGIHGIGFGMDEMLQGFA

VALKMGATKKDFDNTVAIHPTAAEEFVTMR

>lcl|NZ\_FO834906.1\_prot\_WP\_002921269.1\_257 [locus\_tag=BN49\_RS02450] [protein=23S rRNA (adenine(2030)-N(6))-methyltransferase RlmJ] [protein\_id=WP\_002921269.1] [location=complement(280049..280891)] [gbkey=CDS]

MLSYRHSFHAGNHADVLKHTVQSLIIESLKEKEKPFLYLDTHAGAGRYQLSGEHAERTGEYLEGIARIWQ

QDDLPAELEPYISVVEHFNRNGQLRYYPGSPLIARQLLREQDSLQMTELHPSDFPLLRAEFQKDSRARVD

KADGYQQLKAKLPPVSRRGLILIDPPYEIKTDYQAVVTGINEGYKRFATGTYALWYPVVLRAQIKRMIKE

LEATGIRKILQIELAVRPDSDQRGMTASGMIVINPPWKLEQQMNNVLPWLHSKLVPTGTGHATVSWIVPE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529354.1\_258 [locus\_tag=BN49\_RS02455] [protein=phosphatase PAP2 family protein] [protein\_id=WP\_016529354.1] [location=281085..282356] [gbkey=CDS]

MKRQLSLLAVALLLAQPVLAKDIPLNRAAALANSVTPAASSQAYDDLEQQALAQLRHALQGNAATLTRDR

LARTKQNQTQADTAWLKASGYDFQTRANQQAGIALLSAFSTLPETVVKQNLATVTAINRDAVQTTRRQAL

ADAEGISYLYFLSDALGPRLGKAFLTAYDQGALGKAAALIKASEVSTGEAKKHFNNPRPFLVQGNTIHLV

PDDVVVKDNQPYTADGGSFPSGHTNTGYTDALLLAAMIPERYDALVARGARYGYSRIVLGVHYPLDVIGS

RMVAERNVAHYLNDPHYRVLFNEARDQLRAALAKACGTSLAECAKSSVKDDPWRDPAMRDFSRFTMTYDL

PQQKGPQPRLQVPEGAEVLLEDALPHLSAAQRRALMVNTALPAGYPLSGTTPEQQFWQRLNLSAAWEMAQ

KRQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004151426.1\_259 [gene=prlC] [locus\_tag=BN49\_RS02460] [protein=oligopeptidase A] [protein\_id=WP\_004151426.1] [location=282539..284581] [gbkey=CDS]

MTNPLLTPFSLPPFSAIKPEHVVPAVTKALEDCRAAVESAVAHGAPYSWENLCQPLAEVDDVLGRIFSPV

SHLNSVKNSPELREAYEQTLPLLSEYSTWVGQHEGLYKAYRDLRDGDNYATLNTAQKKAVDNALRDFELS

GIGLPPEAQKRYGEIAARLSELGNQYSNNVLDATMGWNKLVTDVADLAGMPESALAAAQAQAQAKEQEGY

LLTLDIPSYLPVMTYCDNQALREEMYRAYSTRASDQGPNAGKWDNSPVMAEILALRHELAQLLGFDSYAY

KSLATKMAKDPQQVLDFLTDLAKRARPQGEKELAQLRAFAKAEFGVDELQPWDIAYYSEKQKQHLYSISD

EQLRPYFPENKAVSGLFEVVKRIYGITAKERTDVDVWHPEVRFFELYDEHNELRGSFYLDLYAREHKRGG

AWMDDCVGQMRKLDGSLQKPVAYLTCNFNRPVNGKPALFTHDEVITLFHEFGHGLHHMLTRIDTAGVSGI

SGVPWDAVELPSQFMENWCWEPEALAFISGHYETGEPLPQELLEKMLAAKNYQAAMFILRQLEFGLFDFR

LHAEYKPEQGAKILETLAEIKKQVAVVPGPTWGRFPHAFSHIFAGGYAAGYYSYLWADVLAADAFSRFEE

EGIFNRETGQSFLDNILSRGGSEEPMELFKRFRGREPQLDAMLEHYGIKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151425.1\_260 [gene=rsmJ] [locus\_tag=BN49\_RS02465] [protein=16S rRNA (guanine(1516)-N(2))-methyltransferase RsmJ] [protein\_id=WP\_004151425.1] [location=284589..285341] [gbkey=CDS]

MKICLIDETGAGDGALSVLAARWGLEQDDDNPMALALTTEHLELRKRDEPKLGGIFVDFVGGAMAHRRKF

GGGRGEAVAKAVGIKGDYLPDVVDATAGLGRDAFVLASVGCRVRMLERNPVVAALLDDGLARGYADAEIG

GWLQERLQLIHASSLTALTDITPRPQVVYLDPMFPHKQKSALVKKEMRVFQSLVGPDLDADGLLAPARQL

ATKRVVVKRPDYAPPLAEVATPNAVVTKGHRFDIYAGTPE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529351.1\_261 [gene=dtpB] [locus\_tag=BN49\_RS02470] [protein=dipeptide/tripeptide permease DtpB] [protein\_id=WP\_016529351.1] [location=complement(285485..286951)] [gbkey=CDS]

MNTTAPTGLLQQPRPFFMIFFVELWERFGYYGVQGILAVFFVKQLGFSQEQAFITFGAFAALVYGLISIG

GYVGDHLLGTKRTLVLGAIVLAIGYFMTGMSLLKPQLIFIALGTIAVGNGLFKANPASLLSKCYPPKDAR

LDGAFTLFYMSINIGSLLSLAPVIAEKFGYAVTYNLCGAGLIIALLVYFACRGMVKDIGSEPDHRPLSLR

NLALVLAGTVVMIFLCAWLMHNVMIANLVLIVLSVVVIAFFFREAFRLDKTGRNKMFVAFILMIEAVLFY

ILYAQMPTSLNFFAINNVHHEILGFTINPVSFQALNPFWVVVASPVLAAIYTHLGHKGKDLTMPVKFTLG

MFLCALGFLTAAAAGMWFADAQGLTSPWFIVLVYLFQSLGELLISALGLAMVAALVPQHLMGFILGMWFL

TQAAAFLLGGYVATFTAVPENITDPLQTLPVYTNVFSKIGLVTLGVTVVMALMVPWLNRMINTPASAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004145166.1\_262 [gene=uspA] [locus\_tag=BN49\_RS02475] [protein=universal stress protein UspA] [protein\_id=WP\_004145166.1] [location=complement(287208..287645)] [gbkey=CDS]

MAYKHILIAVDLSPESKVLVEKAVSMARPYNAKVSLIHVDVNYSDLYTGLIDVNLGDMQKRISEETHHAL

TELSTNAGYPITETLSGSGDLGQVLVDAIKKYDMDLVVCGHHQDFWSKLMSSARQLINTVHVDMLIVPLR

DEEDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002921203.1\_263 [gene=uspB] [locus\_tag=BN49\_RS02480] [protein=universal stress protein UspB] [protein\_id=WP\_002921203.1] [location=288028..288363] [gbkey=CDS]

MISTIALFWALCVVCVVNMARYFSSLRALLVVLRGCDPLLYQYVDGGGFFTSHGQPSKQMRLVWYIYAQR

YRDHHDDEFIRRCERVRRQFILTSALCGLVVVSLIALMIWH

>lcl|NZ\_FO834906.1\_prot\_WP\_002921200.1\_264 [gene=pitA] [locus\_tag=BN49\_RS02485] [protein=inorganic phosphate transporter PitA] [protein\_id=WP\_002921200.1] [location=complement(288419..289915)] [gbkey=CDS]

MLHLFAGLDLHTGLLLLLALAFVLFYEAINGFHDTANAVATVIYTRAMRSQLAVAMAALFNFFGVLLGGL

SVAYAIVHMLPTDLLLNMGSAHGLAMVFSMLLAAIIWNLGTWYFGLPASSSHTLIGAIIGIGLTNALMTG

TSVVDALNIPKVIGIFASLIISPIVGLVIAGGLIFLLRRYWSGTKKRARIHLTPAEREKKDGKKKPPFWT

RIALILSAIGVSFSHGANDGQKGIGLVMLVLIGVAPAGFVVNMNASGYEITRTRDAVNNVETFFQQRPEL

LKKATGVDQLVPSPDTNTAANGEFHCHPANTINALDRVKTMLTGVENYESLKPEQRGQLRRIMLCISDTT

DKVAKLPDVSADDQRLLKKLKTDMLSTIEYAPIWIIMAVALALGIGTMIGWRRVATTIGEKIGKKGMTYA

QGMSAQMTAAVSIGLASYTGMPVSTTHVLSSSVAGTMLVDGGGLQKKTVTSILMAWVLTLPAAIILSGVL

YWLSLKLI

>lcl|NZ\_FO834906.1\_prot\_WP\_016529349.1\_265 [locus\_tag=BN49\_RS02490] [protein=NAD(P)/FAD-dependent oxidoreductase] [protein\_id=WP\_016529349.1] [location=290145..291338] [gbkey=CDS]

MERFDAIVVGAGAAGMFCAAQAGQLGCRVLLLDNGKKPGRKILMSGGGRCNFTNMYVEPAAYLSQNPHFC

KSALARYTQWDFIELVGKYGIAWHEKTLGQLFCDDSAEQIVNLLLAECEKGGVQIRLRSEILSVERDEQG

YRLQVNGETLMTKKLVIASGGLSMPGLGASPFGYKVAEQFGLKVLPTRAGLVPFTLHKPLLEQLQVLSGV

SVPSTITAENGTLFRENLLFTHRGLSGPAVLQISSYWQPGEFVTVNLLPDCDLDDFLNEQRSAHPNQSLK

NTLAMQLPKRLVECLQQLGQIPDVTLKQLNVRDQQTLVETLTAWRVQPNGTEGYRTAEVTLGGVDTNELS

SRTMEARKAPGLYFIGEVMDVTGWLGGYNFQWAWSSAWACAQALVEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002921192.1\_266 [locus\_tag=BN49\_RS02495] [protein=magnesium transporter] [protein\_id=WP\_002921192.1] [location=complement(291378..292391)] [gbkey=CDS]

MSSIQLCAAHQATSGFDGDAIVQYMRTDFITLQEHLSVHEAREHFISQLASDDIPGQVFVVAGKKLRGSL

SVKKLLQETDINQSIRHLMDSCLFRVKPDDERQQVIAELSERGLDLVPVVDKGELVGCLMEKEIAHLLED

DVTEDAQLQGATLPLEKPYLEISPWTLWKKRSVWLLLLFVAEAYTSSVLQHFEEALESAIALAFFIPLLI

GTGGNSGTQITSTLVRSMALGEVRLRDMGRVIRKEVSTSFLIALTLGLAGCLRAWMMGIGMEITLIVSLT

LVCITLWSAIVSSVIPMVLKRIGIDPAVVSAPFIATLIDGTGLIIYFKIAQYFLGLN

>lcl|NZ\_FO834906.1\_prot\_WP\_002921188.1\_267 [gene=nikR] [locus\_tag=BN49\_RS02500] [protein=nickel-responsive transcriptional regulator NikR] [protein\_id=WP\_002921188.1] [location=complement(292717..293115)] [gbkey=CDS]

MQRVTLTLDDDLLAALDALSARRGYHNRSEAVRDILRDALNQDPPSPESRRGYAVLSYVYEHEKRELASR

LVATQHHHHDLSVATLHVHISHDDCLEIAVLKGDMAEVQHFADDVIAQRGVRHGHLQCLADD

>lcl|NZ\_FO834906.1\_prot\_WP\_004173958.1\_268 [gene=nikE] [locus\_tag=BN49\_RS02505] [protein=nickel import ATP-binding protein NikE] [protein\_id=WP\_004173958.1] [location=complement(293103..293894)] [gbkey=CDS]

MNLLSATGVSHDYPHHGRVLHAIHLAIAPGETVALLGRSGCGKSTLARMLVGLETPQHGDIAWRGTPLAA

LKGEAIGAFRRDIQLVFQDAFSAVNPRKTVREIVSEPLRHLLCLSREARARRVEEMLLAVDLAPSLLDKR

PAQVSGGQLQRVCLARALAVRPQLLILDEAVSNLDLLLQAEIIALLKRLQAQFDTACLFITHDLRLVERF

CQRVLVMEHGRIVETATVSLPLRLRSPAGQALQQAVLPPFPATLLNEAMPCSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004173959.1\_269 [locus\_tag=BN49\_RS02510] [protein=nickel import ATP-binding protein NikD] [protein\_id=WP\_004173959.1] [location=complement(293891..294655)] [gbkey=CDS]

MPQKIQLEQISLAADRPLVSDVSFTLRRGQVLALLGSSGCGKSLTCAAALGLLPPGVRQTAGRVLLDGIP

VHGEQLRGATIATIMQNPRSAFNPLQTMAAHARETCRAAGRETNDAVLLAAMEEVGLDNPRALLKRYPFE

MSGGMLQRMMVALALLSRAPFIIADEPTTDLDAIAQARILDLLADIVARRGLGLLLVTHDMGVVARLAHH

VTVMENGRLVEHCDVNTLFSAPRHPLSQRLLAAHLALYGLEKTP

>lcl|NZ\_FO834906.1\_prot\_WP\_004151422.1\_270 [gene=nikC] [locus\_tag=BN49\_RS02515] [protein=nickel ABC transporter permease subunit NikC] [protein\_id=WP\_004151422.1] [location=complement(294655..295488)] [gbkey=CDS]

MRGLQSFRWPVKLAMLVIALLAVIAIGSGWWLPWDPAAIDLQQRLLPPGAAHWLGTDHLGRDIFSRLLAA

TRVSLGAVMACLLLVLLIGLAVGGCAGLLGGRADRGLMRIAELFMTFPTSILSFFMVGVLGTGLTNVILA

IALSHWAWYARMVRNLVVSLRQREFILAARLSGASQWRLFSDHLAGAVIPSLLVLASLDIGHMMLHVAGM

SFLGLGVSAPTAEWGVMINDARQYIWTQPLQMVWPGLALFISVMAFNLLGDALRDRLDPHLIAEHSH

>lcl|NZ\_FO834906.1\_prot\_WP\_002921105.1\_271 [gene=nikB] [locus\_tag=BN49\_RS02520] [protein=nickel ABC transporter permease subunit NikB] [protein\_id=WP\_002921105.1] [location=complement(295485..296429)] [gbkey=CDS]

MLRYILRRLLLLIPLLLAASAIIFLLLRLGAGDPALDYLRLSNLPPTEEMVASTRELLGLNQPLAMQYLH

WLWRALHLDFGLSYATQRPVLDDLLHFLPATLLLTGAALALILVTSLPLGIWAARHRDRLPDYIVRLIAF

LGVSMPNFWLAFLLVMLFSVHLQWLPAMGYGDWQHLILPAVSIAFMSLAINARLLRASMLDAASQRHVIW

ARLRGLSARQVERRHILRNATLPVVTAMGMHIGELIGGTMIIENIFAWPGVGRYAVSAIFNRDYPVIQCF

TLMMVTVFVLANLAVDVLNAALDPRLRRHEEVSA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042218.1\_272 [gene=nikA] [locus\_tag=BN49\_RS02525] [protein=nickel ABC transporter substrate-binding protein] [protein\_id=WP\_046042218.1] [location=complement(296429..297997)] [gbkey=CDS]

MSIIRLTLLALVACVPLLAQAAPYQLTTAWPVNVGPLNPHLYTPNQMFAQSMVYEPLVKYQADGSVQPWL

ATRWRHSADGKTWWFTLRDDVAFSNGEPFNAQAAAANFQAVLANRQRHAWLELANQITDVRALSTTELQI

TLKSAYAPLLQELALPRPFRFIAPSQFIDGGTARGIKAPIGTGPWRLASSQLNQRDVLVRNERYWGRKPA

LQQITIKVIPDATSRAVAFETGEIDMLYGDEGLLPLDTFERFRHHPGYVTRLSAPAETVMLALNASQGPT

REQAVREALNYAVDKQTLVDSVLYGTQQVADTLFAPSVPYAPQNLTPRRYDPTKARALLEQAGWQQLEGQ

PWRQKAGQPLAIELAFIGTDALAKSMAEIIQANLRQVGVQVTLVGEEESSIYARQREGRFGMIFNRTWGA

PYDPHAFLSSMRVPSHADYQAQRGLPDKALIDKEISEVLTTGDEAQRRKLYHDVLTRLHQDAVYLPISYV

SLMSVARQEVGEIPFAPVTSEIPFDQITPVTP

>lcl|NZ\_FO834906.1\_prot\_WP\_004151421.1\_273 [locus\_tag=BN49\_RS02530] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004151421.1] [location=complement(298136..298996)] [gbkey=CDS]

MHKTTLEQWALLEKVVELGSFARAAEETNRSQSSVSYNLALLQERLGVALLAPSGRRAVLTPAGELLLNQ

VKPLLQAFAYVETHAATLRNGARTRLDLVVDSIFPRQRLFAILRQFQQRYPQTQVRLTEVLENLDDESAA

RTEADVMVLTRRQDITGRGEWLMNIDFIAVAHRDHPLAALDGPLEDSALAPWPLVRIADQGGDSQAPRDA

WTFSTIDAAIDAVMYQVGFGWLPEERIRPHLDQGVLKRLPLSHGARRATPLHLIVKRDLAPIDEQVATLL

ALFRTP

>lcl|NZ\_FO834906.1\_prot\_WP\_004181483.1\_274 [locus\_tag=BN49\_RS02535] [protein=phenolic acid decarboxylase] [protein\_id=WP\_004181483.1] [location=299094..299600] [gbkey=CDS]

MMSTFDKHDLSGFIGKHLVYTYDNGWNYEIYVKNGHTLDYRIHSGIVGNRWVKDQEAYIVRVGESIYKIS

WTEPTGTDVSLIVNLGDKLFHGTIFFPRWIMNNPEKTICFQNDHIPLMNSYRDAGPAYPTEVIDEFATIT

FIRDCGADNDEVINCPASELPADFPANL

>lcl|NZ\_FO834906.1\_prot\_WP\_016532496.1\_275 [gene=arnB] [locus\_tag=BN49\_RS02540] [protein=UDP-4-amino-4-deoxy-L-arabinose aminotransferase] [protein\_id=WP\_016532496.1] [location=299973..301112] [gbkey=CDS]

MSDFLPFSRPSMGDAELAALREVLASGWITTGPKNQALEAAFCQLTGNRHAIAVSSATGGMHVTLMALGI

GPGDEVITPSQTWVSTLNMICLLGATPVMIDVDNDNLMIIPDAVEAAITSRTKAIIPVHYAGAPADIDAI

RAVGERHGISVIEDAAHAAGTHYKGRHVGWQGTAIFSFHAIKNMTCAEGGLIVTDDDELASRIRSLKFHG

LGVDAYDRQTHGRAPQAEVITPGFKYNLADINAALALVQLEKLSHANQRRTEIAQRYLRELADTPFKPLS

VPAWEHQHAWHLFIIRVDEAACGISRDALMEKLKAMGIGTGLHFRAAHTQKYYRERFPEVSLPNTEWNSA

RICSLPLFPDMTDDDVTRVISALRQLSGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002921035.1\_276 [gene=arnC] [locus\_tag=BN49\_RS02545] [protein=undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase] [protein\_id=WP\_002921035.1] [location=301114..302097] [gbkey=CDS]

MLTYPPVKKVSVVIPVYNEQDSLPELLRRTDAACATLGRQYEILLIDDGSSDDSARMLTEAAEAEGSHVV

AVLLNRNYGQHSAIMAGFSHVTGDLIITLDADLQNPPEEIPRLVAKADEGYDVVGTVRQNRQDSIFRKTA

SKMINRLIQRTTGKAMGDYGCMLRAYRRHIIDAMLNCHERSTFIPILANTFARRAVEIPVMHAEREFGDS

KYSFMRLINLMYDLVTCLTTTPLRLLSIFGSVIALLGFAFGLLLVVLRLAFGPQWAAEGVFMLFAVLFMF

IGAQFVGMGLLGEYIGRIYNDVRARPRYFIQRVVRQPETASKEEDRS

>lcl|NZ\_FO834906.1\_prot\_WP\_016532497.1\_277 [gene=arnA] [locus\_tag=BN49\_RS02550] [protein=bifunctional UDP-4-amino-4-deoxy-L-arabinose formyltransferase/UDP-glucuronic acid oxidase ArnA] [protein\_id=WP\_016532497.1] [location=302094..304079] [gbkey=CDS]

MKAVVFAYHDMGCTGIQSLLDAGYDIAAIFTHPDNPGENHFFGSVARLAAEQGIPVWAPEDVNHPLWIER

IREMKPDVLFSFYYRNLLGDEILNLAPKGAFNLHGSLLPKYRGRAPLNWVLVNGESETGVTLHRMVNRAD

AGDIVAQQAVAIGADDAALTLHRKLCAAATELLSRALPAILAGTTDERPQDHSQATYVGRRTPEDGRLDW

ELPAQTLHNLVRAVSDPWPGAFGYAGANKFIVWKSRVRHDLPAAKPGTVLSIAPLIVACQDGALEIVTGQ

TERGVYMQGAQLAQALGLVSGAVISSKPVEAIKRRTRVLILGVNGFIGNHLTERLLQDDNYEIYGLDIGS

DAINRFLDCPRFHFVEGDISIHSEWIEYHIKKCDVVLPLVAIATPIEYTRNPLRVFELDFEENLKIIRDC

VKYNKRIIFPSTSEVYGMCTDKNFDEDSSNLVVGPINKQRWIYSVSKQLLDRVIWAYGDKNGLKFTLFRP

FNWMGPRLDNLNAARIGSSRAITQLILNLVEGSPIKLIEGGKQKRCFTDISDGIEALFRIIENKDGRCDG

QIINIGNPDNEASIKELAEMLLACFERHPLRDRFPPFAGFREVESSDYYGKGYQDVEHRKPSIRNAKRCL

NWEPKVEMEETVEHTLDFFLRTVELVDDKNP

>lcl|NZ\_FO834906.1\_prot\_WP\_021469881.1\_278 [locus\_tag=BN49\_RS02555] [protein=4-deoxy-4-formamido-L-arabinose-phosphoundecaprenol deformylase] [protein\_id=WP\_021469881.1] [location=304076..304978] [gbkey=CDS]

MKQVGLRIDVDTFRGTRDGVPRLLELLGRHGIQASFFFSVGPDNMGRHLWRLIKPKFLWKMLRSRAASLY

GWDILLAGTAWPGRRIGAGNEAVIRAAAESHEVGLHAWDHYSWQAWSGVWPQERLALEVERGLLELERII

GRPVTCSAVAGWRADQRVVKAKESFDFLYNSDCRGTRPFLPQLGSGVSGTVQIPVTLPTWDEAVGTAVDI

AGFNRYLLDCIHRDAGVPVYTIHAEVEGIAYADQFNELLTMAAEEEIQFCPLSQLLPADFSELPSGKVVR

GELAGREGWLGREQLLTSGI

>lcl|NZ\_FO834906.1\_prot\_WP\_046042221.1\_279 [gene=arnT] [locus\_tag=BN49\_RS02560] [protein=lipid IV(A) 4-amino-4-deoxy-L-arabinosyltransferase] [protein\_id=WP\_046042221.1] [location=304978..306633] [gbkey=CDS]

MKSIRYGVSLIALFALYYLLPLNFRLLWQPDETRYAEISREMLATGDWVVPHFLGLRYFEKPIAGYWINS

IGQWLFGHNNFGVRFGSVFAITMTALLVAWLAWRIFRDKRVAILSLIIFLTAMLVYAIGTYAVLDPMITL

WLALAMCSFWGAVQAHSRSGKILGYVLLGVACGMGVMTKGFLALAVPVVGVLPWVIARKRWREVLTYGWL

AVIVCTLVVLPWGLAIAQREPDFWRYFFWVEHIQRFAEKDAQHKAPFWYYIPFLIAGSLPWLALLPGALK

RGWLERDEARGALYLLGWVAMPFLFFSIAKGKLPTYILPCFAPLSILMARYALEAAKTGAKALRINGMIN

LGVGLLGLIAVLVVSPWGFMHKPVWTKIELYKCLLAAIAFAVWALMGWLAMKDSGRRWSLAALCPLGLAL

LVGFAIPDRVIDSKQPQFLVDIVSESLQPSRYVLTNNVGIAGGLAWELKRSDIIMFDKQGELKYGLDWPD

AQGSFVSQAGFADWLAAHRQQGPVSLVLLMDKGESMLDLPLPKPDNAYELGRVVFLQYLPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002920864.1\_280 [gene=arnE] [locus\_tag=BN49\_RS02565] [protein=4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnE] [protein\_id=WP\_002920864.1] [location=306630..306968] [gbkey=CDS]

MSVWICLVCASLLSCAGQLCQKQATRPSRRGRRSRHILFWLGMALLCLGCGMLLWLSVLQSIPVSIAYPM

LSLNFVWVTLAGWGIWHEPVARRHWLGVGLIVVGIVILGTSV

>lcl|NZ\_FO834906.1\_prot\_WP\_016532502.1\_281 [locus\_tag=BN49\_RS02570] [protein=4-amino-4-deoxy-L-arabinose-phosphoundecaprenol flippase subunit ArnF] [protein\_id=WP\_016532502.1] [location=306968..307348] [gbkey=CDS]

MGFFWALLSVGLVSAAQLLLRSAMVALPPLTDIAAFLQHLLHFQPGTFGLFFGLLGYLLSMVCWYFALHR

LPLSKAYALLSLSYILVWAAAIWLPGWHEPFYWQSLLGVAIIVAGVLTIFWPVKRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532503.1\_282 [locus\_tag=BN49\_RS02575] [protein=AI-2E family transporter] [protein\_id=WP\_016532503.1] [location=complement(307345..308394)] [gbkey=CDS]

MSPPQADKAGLHILLKLAALVIILAGIHAAADILVQLLLALFFAIVLNPLVTWFIRRGVRRPFAITLVVT

AMLVMLTALLGVLAASLNDFVAMLPDFNRALTRKILQLQEYLPFLNLHINPERMLRRMDSERLMTWATTL

MTQLSGAMASIVLLVMTVIFMLFEVRHLPYKLRFVLNNPRLHIAGLHRALKGVTHYLALKTLISLWTGLI

VWLGLLAMGVQFALMWGVLAFLLNYVPNIGSAISAIPPMLQALLFSGIYECLLVGALFLVVHMVLGNMVE

PRMMGHRLGMSTLVVFLSLLVWGWLLGPVGMLLSVPLTSVCKIWMETTVGGSKLAILLGPGRPKSRLPG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532504.1\_283 [locus\_tag=BN49\_RS02580] [protein=MFS transporter] [protein\_id=WP\_016532504.1] [location=308528..309748] [gbkey=CDS]

MPEPVAEPALNGLRLNLRIVSVVIFNFASYLTIGLPLAVLPGYVHDVMGFSAFWAGLVISLQYFATLLSR

PHAGRYADLLGPKKIVVFGLGGCFLSGLSYLLAAWGSGWPLISLLLLCLGRVILGIGQSFAGTGSTLWGV

GVVGSLHIGRVISWNGIVTYGAMAMGAPLGVLCYSHIGLSGLAGVIMAVALVAILCALPRAAVKAAKGKA

MSFRAVLGRVWPYGMALALASAGFGVIATFITLFYDAKGWDGAAFALTLFSCAFVGARLLFPNAINRLGG

LNVAMLCFSVEAIGLLLVGFADTPMMAKIGTFLTGAGFSLVFPALGVVAVKAVPQHNQGSALATYTVFMD

LSLGVSGPLAGLLLAWTGISMIYLAAAGLVMAALLLGWRLKKRPPVSEPEASAPGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016532505.1\_284 [locus\_tag=BN49\_RS02585] [protein=DcrB family lipoprotein] [protein\_id=WP\_016532505.1] [location=complement(309749..310306)] [gbkey=CDS]

MRNLVKYVGIGLLVMGLAACDNSDSKAPTVGAAAESNASGQAISLLDGKLSFTLPAGMADQSGKLGTQAN

NMHVYSDATGQKAVIVIVGDSTNEDLAVLAKRLEDQQRSRDPQLQVVSNKPLEIKGHTLQQLDSIISAKG

QTAWSSVILGKVDDKLLTLQITLPADNQQQAQTEAESIINTLTIQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002920860.1\_285 [locus\_tag=BN49\_RS02590] [protein=7-cyano-7-deazaguanine/7-aminomethyl-7-deazaguanine transporter] [protein\_id=WP\_002920860.1] [location=complement(310380..311045)] [gbkey=CDS]

MNPFTTVQRKKALVWLSLFHLLVITSSNYLVQLPISIFGFHTTWGAFSFPFIFLATDLTVRIFGAPLARR

IIFAVMVPALAISYGISALFYMGEWQGFAALGTFNLFVARIAVASFMAYALGQILDVHVFNRLRQSRRWW

LAPTASTLFGNISDTVAFFFIAFWRSPDPFMAAHWGEIALVDYSFKVLISIIFFLPMYGVLLNMLLKRLA

DKSDLSALQPS

>lcl|NZ\_FO834906.1\_prot\_WP\_002920858.1\_286 [gene=tusA] [locus\_tag=BN49\_RS02595] [protein=sulfurtransferase TusA] [protein\_id=WP\_002920858.1] [location=311252..311497] [gbkey=CDS]

MSELFSTPDHTLDALGLRCPEPVMMVRKTVRTMPVGETLLIIADDPATTRDIPGFCRFMEHELVAQETEA

LPYRYLIRKSH

>lcl|NZ\_FO834906.1\_prot\_WP\_046042224.1\_287 [gene=zntA] [locus\_tag=BN49\_RS02600] [protein=Zn(II)/Cd(II)/Pb(II) translocating P-type ATPase ZntA] [protein\_id=WP\_046042224.1] [location=complement(311824..314034)] [gbkey=CDS]

MSTPDAQDKKVPQFSSFTMRPATAPAESCCTDHACATESAPAAEALSDARYSWQVDGMDCAACARKVETA

VRQVPGVSQVQVLFATEKLLVNAEGDVRAQVENAVRQAGYTLRDADAPAAEQTRGSLLRDNLPLLTLVIM

MALSWGLEQANHPAGQLAFIATTLVGLWPVARQALRLIKSGSWFAIETLMSVAAIGALFIGATAEAAMVL

LLFLIGERLEGWAASRARQGVSALMALKPDTAIRLRNGVRETVAQRDLRPGDVIEVAAGGRLPADGQLLS

PFASFDESALTGESVPVERQAGERVAAGATSVDRLVQLTVISEPGDSAIDRILKLIEEAEERRAPIERFI

DRFSRIYTPAIMVVALLVAIVPPLFFASAWLPWIYKGLTLLLIGCPCALVISTPAAITSGLAVAARRGAL

IKGGAALEQLGQVRQVAFDKTGTLTVGQPQVTSVIATAEVDDNALLALAAAVEQGSSHPLAQAIVREAQR

RQLSIPLASGQRALAGSGIEAEVNGCRILICAASKAAPAEHEAQIQQLESAGQTVVLVMRGETLLGILAL

RDTLRDDARQAVDALHQLGVQGVILTGDNPRAAAAIASELGLEFRAGLLPADKVNAVIALNADAPLAMVG

DGINDAPAMKAATIGIAMGSGTDVALETADAALTHNRLTGLAQMISLARATHANIRQNIAIALGLKGIFL

VTTLLGLTGLWLAVLADTGATVLVTANALRLLRKKL

>lcl|NZ\_FO834906.1\_prot\_WP\_004173987.1\_288 [locus\_tag=BN49\_RS02605] [protein=lysoplasmalogenase] [protein\_id=WP\_004173987.1] [location=complement(314113..314739)] [gbkey=CDS]

MLWSFIAVCFSAWLYVDASYRGPAWRRWVFKPVTLILLLLLAWQAPMFNAISYLVLAGLCASLLGDALTL

LPRQRVMYAVGAFFLSHLLYTIWFASQLTLSFFWPLPLVLLVFGALLMAVIWSRLEEMKMPVLTFIGMTL

VMVWLAGELWFARPTNTALSGFAGAALLLLSNAVWLVSHYRRRFRADNAIAAAFYFAGHFLIVRALYL

>lcl|NZ\_FO834906.1\_prot\_WP\_004173989.1\_289 [locus\_tag=BN49\_RS02610] [protein=DUF2500 domain-containing protein] [protein\_id=WP\_004173989.1] [location=314890..315240] [gbkey=CDS]

MPLFFVLVVAVIVVAASFRYVQQRREKQANDAAPLLQKRVIVSNKREKVINDRRSRQQTVTPAGSEMRYE

ASFRPENGGLEVVFRLDAPQYHALSVGDRGMLSYKGTAFVAFTPDP

>lcl|NZ\_FO834906.1\_prot\_WP\_002920822.1\_290 [locus\_tag=BN49\_RS02615] [protein=DUF1145 family protein] [protein\_id=WP\_002920822.1] [location=complement(315254..315529)] [gbkey=CDS]

MLINLGRLLMLCVWAFLLLNLFQPFPKPLNIFVNVALIFMILMHGLQLTLLKATQPKEAPPLSRFEQIRI

FIFGVFELVAWQKKLKATLKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920820.1\_291 [gene=rsmD] [locus\_tag=BN49\_RS02620] [protein=16S rRNA (guanine(966)-N(2))-methyltransferase] [protein\_id=WP\_002920820.1] [location=complement(315519..316115)] [gbkey=CDS]

MKKPNHAGSGQIRIIGGQWRGRKLPVPESPGLRPTTDRVRETLFNWLAPSIVDAHCLDCFAGSGALGLEA

LSRYAASTTLLEMERGVAQQLQKNLATLKADRGKVITTNTLSFLSQPGTPHQIVFVDPPFRQGLLEETLR

LLETQGWLADEALVYVESEVENGLPPVPANWQLYREKVAGQVAYRLYQREAQGEHHAD

>lcl|NZ\_FO834906.1\_prot\_WP\_046042226.1\_292 [gene=ftsY] [locus\_tag=BN49\_RS02625] [protein=signal recognition particle-docking protein FtsY] [protein\_id=WP\_046042226.1] [location=316298..317821] [gbkey=CDS]

MAKEKKRGFFSWLGFGQKEQAQETETEQKVEEQQAVAEEIPAVETPAEPSAPKADPEAFAEDVVEVTETV

VESEKAHLAEPASAQEEEWVETPALTEETPVVEPEPAVSEPPEQPAVVEPLAEEVIAEPVVAEAVAEQPV

EGIVVQPQETEAPEEDAPLSDEELEAQALAAEAAEEAAVVVPAPEDEAPLEALAQEQEKPTKEGFFARLK

RSLLKTKQNLGSGFISLFRGKKIDDDLFEELEEQLLIADVGVETTRKIITNLTEGASRKQLRDAEALYGL

LKEEMGEILAKVDEPLNVEGKTPFVILMVGVNGVGKTTTIGKLARQFEQQGKSVMLAAGDTFRAAAVEQL

QVWGQRNNIPVIAQHTGADSASVIFDAIQAAKARHVDVLIADTAGRLQNKSHLMEELKKIVRVMKKLDVD

APHEVMLTIDASTGQNAISQAKLFHEAVGLTGITLTKLDGTAKGGVIFSAADQFGIPIRYIGVGERIEDL

RPFNAGDFIEALFARED

>lcl|NZ\_FO834906.1\_prot\_WP\_002920817.1\_293 [gene=ftsE] [locus\_tag=BN49\_RS02630] [protein=cell division ATP-binding protein FtsE] [protein\_id=WP\_002920817.1] [location=317824..318492] [gbkey=CDS]

MIRFEQVSKAYLGGRQALQGVTFHLQPGEMAFLTGHSGAGKSTLLKLICGIERPSAGKIFFSGHEISRLK

SREVPFLRRQIGMIFQDHHLLMDRTVYDNVAIPLIIAGASGDDIRRRVSAALDKVGLLDKAKNFPIQLSG

GEQQRVGIARAVVNKPAVLLADEPTGNLDEALSEGILRLFEEFNRVGVTVLMATHDLGLISSRPYRVLTL

SDGHLHGGIRGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004173994.1\_294 [gene=ftsX] [locus\_tag=BN49\_RS02635] [protein=permease-like cell division protein FtsX] [protein\_id=WP\_004173994.1] [location=318485..319540] [gbkey=CDS]

MNKRDAMNQIRQFGSKFDRLRNAAGGGGGGRNAPKRPKAAPNPASRKSNVFNEQVRYAWHGALQDLKSTP

LATFLTVMVIAISLTLPSVCYMVYKNVSSAASQYYPSPQITVYLEKTLDDDAAARVVGQLQAEQGVDKVN

YLSRDEALGEFRNWSGFGGALDMLEENPLPAVAIVVPKLDFQSTEALNTLRDRVTRIQGVDEVRMDDSWF

ARLSSLTGLVGRVSAMIGVLMVAAVFLVIGNSVRLSIFARRDTINVQKLIGATDGFILRPFLYGGAMLGF

SGAFLSLILSEILVMRLSSAVTEVAKVFGTQFELSGLGFDECLLMLIVCSMIGWVAAWLATVQHLRHFTP

D

>lcl|NZ\_FO834906.1\_prot\_WP\_002920815.1\_295 [gene=rpoH] [locus\_tag=BN49\_RS02640] [protein=RNA polymerase sigma factor RpoH] [protein\_id=WP\_002920815.1] [location=319810..320664] [gbkey=CDS]

MTKEMQTLALAPVGNLESYIRAANTWPMLSADEERELAEKLHYQGDLEAAKKLILSHLRFVVHIARNYSG

YGLPQADLIQEGNIGLMKAVRRFNPEVGVRLVSFAVHWIKAEIHEYVLRNWRIVKVATTKAQRKLFFNLR

KTKQRLGWFNQDEVEMVARELGVSSKDVREMESRMAAQDMTFDMSSDDESDSQPMAPVLYLQDKTSNFAD

GIEDDNWEEQAANKLTDAMQGLDERSQDIIRARWLDEDNKSTLQELADRYGVSAERVRQLEKNAMKKLRA

AIEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042228.1\_296 [locus\_tag=BN49\_RS02645] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_046042228.1] [location=complement(320717..322240)] [gbkey=CDS]

MRSLVGDLVLVRLQEERDPLLHKRLYNALRRAILDGSLAPQSRLPPSRDLAGELGVSRNTILTTYEQLLA

EGYVVSRRGSGTFVAQTAPESSLTAKGQQENSSIAAPTAHLSRQGQHLLGQVSASPRQWGAFIPGVPDVN

AFPHPLFSKIQARISRRPKPERLSYSCNGGTPELQQALVDYLRVSRGVHCQSDQILITEGIHQAIDLVTR

MLCDNGDLAWVEEPSYWGIRHVLTMNDVRAEPLTVDANGLCPPETVDDAPRLIFVTPSHQYPLGAVMSLE

RRQRLLALARQQGSWIVEDDYDSEFRFSGQPIPALQGLVADAPVVYIGTFSKTLYPGLRLGYVVIPRPLV

SDLKHAHAELYRGGHSLIQMALAEFITAGHYSAHIRRMRLLYSRRRAFLTELIQRHCMPYALSDFSDNAG

LHLILNLPAEADDVAIAREANARHILVRPLSRYYLTAARKKGLLMGFASQPEEQMASAFSVLLGCLQTHC

PQMLLLREDAEKQNAPT

>lcl|NZ\_FO834906.1\_prot\_WP\_002920814.1\_297 [locus\_tag=BN49\_RS02650] [protein=4-aminobutyrate--2-oxoglutarate transaminase] [protein\_id=WP\_002920814.1] [location=322359..323624] [gbkey=CDS]

MKSSELNQRRQQATPRGVGVMCNYFVEKAENATLWDIEGNEVIDFAAGIAVLNTGHRHPKVVAAVADQLQ

AFTHTAYQIVPYESYVSLAERINDLAPIDGPAKTAFFTTGAEAVENAVKIARAYTGRPGLITFGGGFHGR

TFMTMALTGKVAPYKIGFGPFPGSVYHGVYPNAAHGVTTADALKSLERIFKADIAPDQVAAIILEPIQGE

GGFNVAPADFMQALRDLCDTHGILLIADEVQTGFARTGKLFAMQHYEVKPDLMTMAKSLAGGFPLSGVVG

RAEVMDAPAPGGLGGTYAGNPLAVAAAHAVLDVIAEEQLCQRAEQLGSHLQEVLNQARATCPAIVDVRGR

GSMVAVEFNDPQTGEPSPEFTRLVQQKAQENGLLLLSCGVYGNVIRFLYPLTIPDAQFSKALDILARVLK

S

>lcl|NZ\_FO834906.1\_prot\_WP\_032104698.1\_298 [locus\_tag=BN49\_RS02655] [protein=amino acid permease] [protein\_id=WP\_032104698.1] [location=323772..325016] [gbkey=CDS]

MSENSTFSPVLTGRERTAVPAKSLSFIEGVSMIVGTNIGAGVLSIAYASSKAGFLPLLFWLVLVGSLTTV

TMLYVAESTLRTRKHLQLSGLSKRYVGGFGALMMFLSVCVNSVGALTAYMTGSGKLLHSLFGISPALGSV

LFFVPAAGVLYLGLKAIGRGEKFISIGMVVMISVLVIATLLKETTRVGYLLDGNWLYMVPVFNVVAFCFS

AQYIVPEMARGFADKPEKLPKAIMVGMALTFTLLALVPLSVISLNGLDNISDVATISWGRALGEWAFFSA

NLFALCAMLTSYWGLGGSFLTNIFDQFRLGNDEQPARRLMVLLVVAIPPFVLAYSGMVSFVNALYFAGVF

SGVILSIMPILMLKGARQRGDLTPGWTCPAWMTHPLIQCFIVLLYLCSAAYAIASAVGYLPAGW

>lcl|NZ\_FO834906.1\_prot\_WP\_002920812.1\_299 [gene=livJ] [locus\_tag=BN49\_RS02660] [protein=branched chain amino acid ABC transporter substrate-binding protein LivJ] [protein\_id=WP\_002920812.1] [location=325274..326377] [gbkey=CDS]

MNMKGKALLAGCIALVMSSAALAEDIKIAVVGAMSGPVAQYGDQEFTGAEQAVADINAKGGIKGNKLQIV

KYDDACDPKQAVAVANKVVNDGIKYVIGHLCSSSTQPASDIYEDEGILMITPAATAPELTARGYKLILRT

TGLDSDQGPTAAKYILDKVKPQRIAVVHDKQQYGEGLARAVQDGLKKGGANVVFFDGITAGEKDFSTLVA

RLKKENIDFVYYGGYHPEMGQILRQARAAGLKTQFMGPEGVANVSLSNIAGESAEGLLVTKPKNYDQVPA

NKPIVDAIKAKKQDPSGAFVWTTYAALQSLQAGLNQSDDPAEIAKYLKGATVDTVMGPLSWDQKGDLKGF

EFGVFTWHANGTATDAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920810.1\_300 [gene=panM] [locus\_tag=BN49\_RS02665] [protein=aspartate 1-decarboxylase autocleavage activator PanM] [protein\_id=WP\_002920810.1] [location=complement(326523..326906)] [gbkey=CDS]

MKLTIIRLQHFSDQDRIDLGKIWPSQDLSTLTLDENHRLYAARFNERLLGAVRVTLRGVEGELSDLCVRE

VTRRRGVGQYLVEETLRDNPAINSWRVADHGVEDRGVMAAFMQALGFSAQQNGWEKH

>lcl|NZ\_FO834906.1\_prot\_WP\_004150079.1\_301 [gene=livK] [locus\_tag=BN49\_RS02680] [protein=high-affinity branched-chain amino acid ABC transporter substrate-binding protein LivK] [protein\_id=WP\_004150079.1] [location=327329..328438] [gbkey=CDS]

MKRNAKTIVAGIVALAMSHAAMAKDIKVAVVGAMSGPVAQWGDMEFNGARQAIKDINASGGIKGDKLVAV

EYDDACDPKQAVAVANKIVNDGIQYVIGHLCSSSTQPASDIYEDEGILMISPGATNPELTQRGYQYIMRT

AGLDSSQGPTAAKYIVEKVKPQRIAIIHDKQQYGEGLARSVQDNLKKAGANIVFFDGITAGEKDFSALLA

RLKKENIDFVYYGGYYPEMGQMLRQARSVGLKTVFMGPEGVGNASLSNIAGAAAEGMLVTMPKRYDQDPA

NSAIVNALKAEKKDPSGPYVWITYAAVQSLAQAMDRTGSQQPLDLINDLKAHGAKTVIGPLTWDEKGDLK

GFEFGVFQWHADGSSSAAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920807.1\_302 [gene=livH] [locus\_tag=BN49\_RS02685] [protein=high-affinity branched-chain amino acid ABC transporter permease LivH] [protein\_id=WP\_002920807.1] [location=328500..329426] [gbkey=CDS]

MSEQFLYFLQQMFNGVTLGSTYALIAIGYTMVYGIIGMINFAHGEVYMIGSYVSFMIIAALMMMGIDTSW

LLVAAGFVGAIVIASAYGWSIERVAYRPVRNSKRLIALISAIGMSIFLQNYVSLTQGSRDVALPSLFNGQ

WVVGHSDSFSATITTMQLVIWVVTFIAMLALTLFIRYSRMGRACRACAEDLKMASLLGINTDRVIALTFV

IGAAMAAVAGVLLGQFYGVINPYIGFMAGMKAFTAAVLGGIGSIPGAMIGGLILGIAEALSSAYLSTEYK

DVVSFALLILVLLVMPTGILGRPEVEKV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174005.1\_303 [gene=livM] [locus\_tag=BN49\_RS02690] [protein=branched chain amino acid ABC transporter permease LivM] [protein\_id=WP\_004174005.1] [location=329423..330700] [gbkey=CDS]

MKPMQIAMALLSAVMFFILAGVFMGVQLELNGTKLVVDTAADIRWQWIFIGTAVVFFFQLLRPLFQKAVK

NVSGPKFIMPAIDGSTVKQKLFLIALLVIAVAWPFMVSRGTVDIATLTMIYIILGLGLNVVVGLSGLLVL

GYGGFYAIGAYTFALLNHYYGLGFWTCLPLAGLVSAAAGFLLGFPVLRLRGDYLAIVTLGFGEIVRILLL

NNTEITGGPNGISQIPKPTFFGLEFSRSAREGGWDTFSNFFGVKYDPSDRVIFLYLVALLLVVLSLFVIN

RLLRMPLGRAWEALREDEIACRSLGLSPTRIKLTAFTISAAFAGFAGTLFAARQGFVSPESFTFAESAFV

LAIVVLGGMGSQFAVILAAILLVVSRELMRDFNEYSMLMLGGLMVLMMIWRPQGLLPMTRVQLKLKNGQA

KGEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920803.1\_304 [gene=livG] [locus\_tag=BN49\_RS02695] [protein=high-affinity branched-chain amino acid ABC transporter ATP-binding protein LivG] [protein\_id=WP\_002920803.1] [location=330697..331464] [gbkey=CDS]

MSQPLLSVSGLMMRFGGLLAVNNVSLELREREIVSLIGPNGAGKTTVFNCLTGFYKPTGGTILLRDQHLE

GLPGQQIARMGVVRTFQHVRLFREMTVIENLLVAQHQQLKTGLFSGLLKTPAFRRAQSEALDRAATWLER

IGLLEHANRQASNLAYGDQRRLEIARCMVTQPEILMLDEPAAGLNPKETKELDELIAELRNHHNTTILLI

EHDMKLVMGISDRIYVVNQGTPLANGTPEEIRNNPDVIRAYLGEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145133.1\_305 [gene=livF] [locus\_tag=BN49\_RS02700] [protein=high-affinity branched-chain amino acid ABC transporter ATP-binding protein LivF] [protein\_id=WP\_004145133.1] [location=331466..332179] [gbkey=CDS]

MENAMLTFDNVSAHYGKIQALHNVSLHIKQGEIVTLIGANGAGKTTLLGTLCGDPRASSGRIVFDGKDIT

DWQTAKIMREAVAIVPEGRRVFSRMTVEENLAMGGFFADRDQFQTRIKWVYELFPRLHERRIQRAGTMSG

GEQQMLAIGRALMSQPRLLLLDEPSLGLAPIIIQQIFDTIEQLREQGMTIFLVEQNANQALKLADRGYVL

ENGHVVLEDTGDALLANEAVRSAYLGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004174006.1\_306 [locus\_tag=BN49\_RS02705] [protein=type II toxin-antitoxin system Phd/YefM family antitoxin] [protein\_id=WP\_004174006.1] [location=332343..332564] [gbkey=CDS]

MRTVNYSEARQNLADVLESAVTGVPVTITRRGHKSAVIISAEEFERYQAARMDDEFAAIMAVHGDEIREL

ADK

>lcl|NZ\_FO834906.1\_prot\_WP\_004185990.1\_307 [locus\_tag=BN49\_RS02710] [protein=type II toxin-antitoxin system death-on-curing family toxin] [protein\_id=WP\_004185990.1] [location=332561..332929] [gbkey=CDS]

MTLQIISAEEIIQFHDRLLRVTPGVAGMPDPGRAEAIMYRVLNKIEYEGVTDVCRLAAMHLLAISRGHIF

NDGNKRTALFITLLFLKRNGIILPANPDFVGMTVEAAAGQLTLEQIVARLRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002920796.1\_308 [gene=ugpB] [locus\_tag=BN49\_RS02715] [protein=sn-glycerol-3-phosphate ABC transporter substrate-binding protein UgpB] [protein\_id=WP\_002920796.1] [location=333202..334518] [gbkey=CDS]

MISLRHTALGLALSLAFAGQALAVTTIPFWHSMEGELGKEVDSLAQRFNAANPDYKIVPVYKGNYEQSLS

AGIAAFRTGNAPAILQVYEVGTATMMASKAIKPVYQVFSEAGIKFDESQFVPTVAGYYTDSKTGHLLSQP

FNSSTPVLYYNKDAFKKAGLDPDQPPKTWQDLAAYTAKLKAAGMKCGYASGWQGWIQIENFSAWHGLPVA

TKNNGFDGTDAVLEFNKPEQVKHIALLEEMNKKGDFSYFGRKDESTEKFYNGDCAITTASSGSLADIRQY

AKFNYGVGMMPYDADVKGAPQNAIIGGASLWVMQGKDKETYTGVAKFLDFLTKPENAAEWHQKTGYLPIT

TAAYDLTRQQGFYDKNPGADIATRQMLNKPPLPFTKGLRLGNMPQIRTIVDEELESVWTGKKTPQQALDS

AVQRGNQLLRRFEQATKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002920792.1\_309 [gene=ugpA] [locus\_tag=BN49\_RS02720] [protein=sn-glycerol-3-phosphate ABC transporter permease UgpA] [protein\_id=WP\_002920792.1] [location=334625..335512] [gbkey=CDS]

MSSSRPVFRSRWLPYVLVAPQLIITLIFFIWPAGEALWYSLQSVDPFGLSSQFVGLDNFVALFHDPYYLD

SFWTTIKFSALVTVSGLLISLFFAALVDYVVRGSRFYQTLMLLPYAVAPAVAAVLWIFLFNPGRGLITHF

LGELGYDWNHAQNSGQAMFLVVFASVWKQISYNFLFFFAALQSIPRSLVEAAAIDGAGPIRRFFKLALPL

IAPVSFFLLVVNLVYAFFDTFPVIDAATAGGPVQATTTLIYKIYREGFAGLDLSASAAQSVVLMFLVIIL

TVVQFRYVESKVRYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004145129.1\_310 [gene=ugpE] [locus\_tag=BN49\_RS02725] [protein=sn-glycerol-3-phosphate ABC transporter permease UgpE] [protein\_id=WP\_004145129.1] [location=335509..336354] [gbkey=CDS]

MIENRRGLTIFSHTMLILGIAVILFPLYVAFVAATLDNKSVFETPMTLIPGGHLLENMKTIWVNGVGVNS

APFWLMMLNSFIMAFAITVGKIVVSMLSAFAIVWFRFPLRNLFFWMIFITLMLPVEVRIFPTVEVIANLN

MLDSYAGLTLPLMASATATFLFRQFFMTLPDELIEAARIDGASPMRFFRDIVLPLSKTNLAALFVITFIY

GWNQYLWPLLIIQDVNLGTAVAGIKGMIATGEGTTQWNQVMAAMLLTLIPPVVIVLAMQRAFVRGLVDSE

K

>lcl|NZ\_FO834906.1\_prot\_WP\_004150074.1\_311 [locus\_tag=BN49\_RS02730] [protein=sn-glycerol-3-phosphate import ATP-binding protein UgpC] [protein\_id=WP\_004150074.1] [location=336356..337426] [gbkey=CDS]

MAGLKLQAVSKSWDGKTQVIQPLTLDVADGEFIVMVGPSGCGKSTLLRMVAGLERVTSGDIWIDRKRVTE

MEPKDRGIAMVFQNYALYPHMSVEENMAWGLKIRGMGKGLIAERVQEAARILELDGLLKRRPRELSGGQR

QRVAMGRAIVRDPAVFLFDEPLSNLDAKLRVQMRLELQQLHRRLKTTSLYVTHDQVEAMTLAQRVMVMNK

GVAEQIGTPVEVYEKPASRFVASFIGSPAMNLLEGRISDDGGRFELAGGMQLPTNHEHRRHAGRKMTLGI

RPEHFILSSQAQGGIPLLMDTLEILGADNLAHGRWGEQKLVVRLPHQQRPAAGSTLWLHLPLEHLHLFDG

ETGQRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531888.1\_312 [gene=ugpQ] [locus\_tag=BN49\_RS02735] [protein=glycerophosphodiester phosphodiesterase] [protein\_id=WP\_016531888.1] [location=337423..338163] [gbkey=CDS]

MSNWPYPRIVAHRGGGKLAPENTLAAIDVGARYGHTMIEFDAKLSKDGQIFLLHDDNLERTSNGWGVAGE

LAWDDLLKVDAGSWFSREFKGEPLPLLSQVAERCRRHGMMANIEIKPTTGLGPQTGRVVALAARDLWQGM

TAPLLSSFEIDALEAAQEAAPELPRGLLLDEWRDDWRELTTRLGCVSIHLNHKLLDAARVASLKQAGLHI

LVYTVNKPQRAAELLRWGVDCICTDAVDVIGPNFQP

>lcl|NZ\_FO834906.1\_prot\_WP\_004150073.1\_313 [locus\_tag=BN49\_RS02740] [protein=DUF2756 family protein] [protein\_id=WP\_004150073.1] [location=complement(338187..338507)] [gbkey=CDS]

MKAILFLAALMPLGVLAQPININNNPNQPGYVVPSQQRMQNEMKIQQQQQQSMLKQDLNNQTRSQQQHLQ

NQLQTNQQRAAQGGNLNAPQQVRPNNNGGMLRQTNP

>lcl|NZ\_FO834906.1\_prot\_WP\_004150072.1\_314 [gene=ggt] [locus\_tag=BN49\_RS02745] [protein=gamma-glutamyltransferase] [protein\_id=WP\_004150072.1] [location=338631..340376] [gbkey=CDS]

MIKTTIWRQVVIAALLAGGSFTVAANPPPPPPVSYGVEEDVFHPVRARQGMVASVDALATRVGVDILRQG

GNAVDAAVAVGYALAVTHPQAGNIGGGGFMMLRTKDGKTTAIDFREMAPEQATRDMFLDDQGNPDSKKSL

TSHLASGTPGSVAGFSLALEKYGTMPLNKVIRPAIKLAEEGFIVNDALADDLKTYGSEVIPQHENSKAIF

WKNGEPLKKGDRLVQKNLGKSLELIAEHGPDAFYKGAIADQIADEMKKHGGLITKADLAGYKAVERTPVS

GEYRGYEVYSMPPPSSGGIHIVQILNILENFDMQKYGFGSADAMQVMAEAEKHAYADRSEYLGDPDFVNV

PWQALTSKAYAKAIAAEIDVNKAKPSSQIRPGKLAPYESNQTTHFSVVDKDGNAVAVTYTLNTTFGTGIV

AGDSGILLNNQMDDFSAKPGVPNVYGLVGGDANAVEPKKRPLSSMSPTIVVKDGKTWLVTGSPGGSRIIT

TVLQMVVNTIDFGMNVAEATNAPRFHHQWLPDELRVEKGFSPDTLKLLEAKGQKVALKEAMGSTQSIMVG

PDGMLYGASDPRSPDDLTAGY

>lcl|NZ\_FO834906.1\_prot\_WP\_025861230.1\_315 [gene=yhhY] [locus\_tag=BN49\_RS02750] [protein=N-acetyltransferase] [protein\_id=WP\_025861230.1] [location=complement(340466..340942)] [gbkey=CDS]

MIRHAEPRDAEPLRMLMAHPEVYHDTLQIPYPSMEAWQEKLQPRPHTFHLVATLDEQVAGHLSLHVEPRP

RRSHVATFGMAVAAGHQGCGIGSALMREMIDLCDNWLRVERIELTVFADNAPAIAVYKKYGFEIEGTGRR

YALRNGEYVDAYYMARIK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531890.1\_316 [locus\_tag=BN49\_RS02755] [protein=polymer-forming cytoskeletal protein] [protein\_id=WP\_016531890.1] [location=complement(341181..341834)] [gbkey=CDS]

MDKQYLAINGALFFWLLALIAWSVDASALARLAAACALIAFLLHSQRNKINAMFIKKNKTEPQISEAATP

PAINPEPEAVASKKHETTVIASGVHFVGNIVASGHVYIHGQVTGNIEAKENLIKVMREGQVEGNVSCREL

IIDGKVQGQCHGDSITIEEHGHLEGTLAYRALAIKKGGVFSGRAELLAAAENKSHILGLVADAPSKADAE

PVRPQSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531891.1\_317 [locus\_tag=BN49\_RS02760] [protein=oxidoreductase] [protein\_id=WP\_016531891.1] [location=342099..343136] [gbkey=CDS]

MTLHCAFIGFGKSTTRYHLPYVLHRKDRWQVAHIYRRRAKPEEQAPQYSHIHFTSDLDEVLNDPLVKLVV

VCTHADSHFEYAKKALEAGKNVLVEKPFTPTLEEAKTLFALANSKGLTVTPYQNRRFDSCFLTTKKVIES

GKLGELVEIESHFDNYRPLAETNPGGPQNGEFYGLGVHTLDQIISLFGRPDHVSYDLRSLRNKANPDDTF

EAQLFYGDMKAIVKTSHLVQIDYPKFIVHGHKGSFVKYGIDQQETSLKANIMPGEPGFGADDSVGELVYV

NEAGEMVREAVPLESGDYGRVYDALYDTLVNSQPNYVKETDVLTNMEILQRGFEQPSPATITLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_002920779.1\_318 [locus\_tag=BN49\_RS02765] [protein=pirin family protein] [protein\_id=WP\_002920779.1] [location=343258..343953] [gbkey=CDS]

MIYLRKANERGHANHGWLDSWHTFSFANYYDPNFMGFSALRVINDDVIDAGQGFGTHPHKDMEILTYVLE

GAVEHQDSMGNKEQVPAGEFQIMSAGTGVRHSEYNPSKTDRLRLYQIWIIPEETGITPRYEQRRFDAAQG

KQLVLSPDARDGSLKVYQDMELYRWALLKDEQSVHQIAAERRVWIQVVKGEVTINGTKATTSDGLAIWDE

QAISVHADSDSEILLFDLPPV

>lcl|NZ\_FO834906.1\_prot\_WP\_002920777.1\_319 [gene=gntR] [locus\_tag=BN49\_RS02770] [protein=gluconate operon transcriptional repressor GntR] [protein\_id=WP\_002920777.1] [location=344067..345062] [gbkey=CDS]

MKKKRPVLQDVADLVGVTKMTVSRYLRNPEQVSEALRGKIAVALDELGYIPNRAPDILSNATSRAIGVLL

PSLTNQVFSEVLRGIESVTDAFGYQTMLAHYGYKPEMEEKRLESMLSWNIDGLILTERTHTPRTLKMIEV

AGIPVVELMDSRSPCLDIAVGFDNFEAARQMTAAIIARGHRHVAYLGARLDERTIIKQKGYEQAMLDAGM

TPYSVMVEQSSSYSSGIELMRQARREYPQLDGIFCTNDDLAVGAAFECQRLGLKIPDDMAIAGFHGHDIG

QVMEPRLASVLTPRERMGRIGAERLLARIRGEAITPKMLDLGFTLSPGGSI

>lcl|NZ\_FO834906.1\_prot\_WP\_002920775.1\_320 [gene=gntK] [locus\_tag=BN49\_RS02775] [protein=gluconokinase] [protein\_id=WP\_002920775.1] [location=345243..345773] [gbkey=CDS]

MSTTNHDHHVYVLMGVSGSGKSAVASEVAHQLHAAFLDGDFLHPRSNITKMASGEPLNDDDRTPWLQALN

DAAFAMQRTNKVSLIVCSALKKSYRDILRKGNPNLSFIYLKGDFDVIESRLKARKGHFFKTQMLVTQFET

LQEPGADESDVLIVDIDQPLEGVVASTIEVINKGSH

>lcl|NZ\_FO834906.1\_prot\_WP\_002920773.1\_321 [gene=gntU] [locus\_tag=BN49\_RS02780] [protein=gluconate transporter] [protein\_id=WP\_002920773.1] [location=345773..347113] [gbkey=CDS]

MSTLTLVLTAVGSVLLLLFLVMKARMHAFVALMVVSIGAGLFSGMPLDKIAATMEKGMGGTLGFLAIVVA

LGAMFGKILHETGAVDQIAVKMLKSFGHNRAHYAIGLAGLICALPLFFEVAIVLLISVAFSMARHTGTNL

VKLVIPLFAGVAAAAAFLLPGPAPMLLASQMHADFGWMILIGLCAAIPGMIIAGPLWGNFISRYVELHIP

DDVTEPHLGEGKMPSFGFSLALILLPLVLVGLKTIAARFVPVGSTAYEWFEFIGHPFTAILVACLVAIYG

LAVRQGMAKDRVMEICGHALQPAGIILLVIGAGGVFKQVLVDSGVGPALGEALTGMGLPIAITCFVLAAA

VRIIQGSATVACLTAVGLVMPVIEQLNYSGAQMAALSICIAGGSIVVSHVNDAGFWLFGKFTGASEAQTL

KTWTMMETILGTTGAIVGMIAFQLLS

>lcl|NZ\_FO834906.1\_prot\_WP\_020325126.1\_322 [locus\_tag=BN49\_RS02785] [protein=hypothetical protein] [protein\_id=WP\_020325126.1] [location=complement(347110..347472)] [gbkey=CDS]

MIAEQSEKQLILHIVHRRWSSSKAQRLSGKSPGEWNIFRRYFIDPDYGLSVKSGAFPLAKKKRQTQSQQG

LTRDTSIVVALIRANSWQGKEGKRAAYCKEARVSSVTLAFYFPRAGDERA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920570.1\_323 [gene=asd] [locus\_tag=BN49\_RS02790] [protein=aspartate-semialdehyde dehydrogenase] [protein\_id=WP\_002920570.1] [location=347576..348682] [gbkey=CDS]

MKNVGFIGWRGMVGSVLMQRMVEERDFDAIRPVFFSTSQLGQPAPSFGGSTGGTLQDAFDLDALKALDII

VTCQGGDYTNEIYPKLRASGWQGYWIDAASSLRMKDDAIIILDPVNQDVITAGLNNGVKTFVGGNCTVSL

MLMSLGGLFAQDLVEWVSVATYQAASGGGARHMRELLSQMGQLHNHVAAELADPASAILDIERKVTSLTR

SGELPVDNFGVPLAGSLIPWIDKQLDNGQSREEWKGQAETNKILATSSVIPVDGLCVRVGALRCHSQAFT

IKLKKDVSIPTVEELLAAHNPWAKVVPNDREITMRELTPAAVTGTLTTPVGRLRKLNMGPEYLSAFTVGD

QLLWGAAEPLRRMLRQLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150069.1\_324 [gene=glgB] [locus\_tag=BN49\_RS02795] [protein=1,4-alpha-glucan branching enzyme] [protein\_id=WP\_004150069.1] [location=348920..351106] [gbkey=CDS]

MSNHIDRDVINALIAGHFADPFSVLGMHRTDAGLEVRALLPDATDVWVIEPKTGRKVGKLECLDSRGFFS

GVLPRRKNAFRYQLAVTWHGQQNLIDDPYRFGPLLQDLDVWLLSEGTHLRPYETLGAHAATMDGVTGTRF

SVWAPNARRVSVVGQFNYWDGRRHPMRFRKESGIWELFVPGAHNGQLYKFELIDAHGNLRVKADPYAFES

QMRPESASLICDLPPKVEQPADRRAANQFDAPISIYEVHLGSWRRHTDNNFWLSYRELADQLVPYAKWMG

FTHLELLPVNEHPFDGSWGYQPTGLYAPTRRFGTRDDFRYFINAAHAAGLNVILDWVPGHFPADDFALAS

FDGTSLYEHSDPREGYHQDWNTLIYNYGRREVSNYLVGNALYWIERFGIDALRVDAVASMIYRDYSRKAG

EWIPNEYGGRENLEAIEFLRNTNRILGEQTPGAVTMAEESTDFAGVTRPPAGGGLGFWFKWNLGWMHDTL

DYMKLDPVHRRYHHDKMTFGMLYNYTENFVLPLSHDEVVHGKKSILDRMPGDAWQKFANLRAYYGWLFAF

PGKKLLFMGNEFAQGREWNHDVSLDWHLLEGGDNWHHGVQRLVRDLNHTYRHHKALHELDFDPYGFEWLV

VDDHERSVFVFVRRDRAGNEIIVASNFTPVPRHDYRFGINQPGRWREALNTDSMHYHGSNQGNGGVVESD

AIASHGREHSLSLTLPPLATIWLVREAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004174015.1\_325 [gene=glgX] [locus\_tag=BN49\_RS02800] [protein=glycogen debranching protein GlgX] [protein\_id=WP\_004174015.1] [location=351103..353079] [gbkey=CDS]

MTSLAAGKPAPLGASYDGKGVNFALFSAHAERVELCVFDEQGNEQRFDLPARSGDIWHGWLAAAGPGLRY

GYRVHGPWDPAQGHRFNPAKLLIDPSAHRVEGDLPDDERLHGGMWQPDRRDSAAVAPKSQVVDLRYDWRG

DKPPRTPWGETVIYEAHVKGLTLLNPQLPEAIRGTYKALGHPAMIAYFKSLGISALELLPVAQFASEPRL

QRMGLSNYWGYNPLAWFALDPRYASDPDRALDEFRDAVKALHAAGIEVILDIVLNHSAEIDLEGPTVSLR

GIDNRSYYWVREDGDYHNWTGCGNTLNLSHPGVVEWARQCLRFWVDECHVDGFRFDLASVMGRTPEFRQD

APLFEAIRRDSVLSQVKLIAEPWDIGPGGYQVGNFPPLFAEWNDHFRDSARRFWLQQNVSLGDFAQRFAA

SSDLFARDGKPPSATVNLVTAHDGFTLRDCVCFNQKHNEANGEENRDGTNNNYSNNHGIEGLEANFAVIE

RRRASAHALLTTLLLAQGTPMLLAGDEQGHSQHGNNNAYCQDNALTWLDWRQANPGLTAFTAALIHLRRR

IPALTRNRWWQEGDGNVRWLNRNAQPLTAAEWQQGAACMQIQLSDRWLLTLNATAEVVDMVLPEGEWRAV

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>lcl|NZ\_FO834906.1\_prot\_WP\_002920566.1\_326 [gene=glgC] [locus\_tag=BN49\_RS02805] [protein=glucose-1-phosphate adenylyltransferase] [protein\_id=WP\_002920566.1] [location=353161..354456] [gbkey=CDS]

MVRLEKNDPLMLARQLPIKSVALILAGGRGTRLKDLTIKRAKPAVHFGGKFRIIDFALSNCINSGIRRIG

VITQYQSHTLVQHIQRGWSFFSEEMNEFVDLLPAQQRVHGENWYRGTADAVTQNLDIISRYKAEYVVILA

GDHIYKQDYSRMLIDHVEKGARCTVACMPVPIEEASAFGVMAVDENEKIIEFVEKPANPPAMPTDPTKSL

ASMGIYVFDAAYLYELLEEDDRNENSSHDFGKDIIPKITEAGMAYAHPFPLSCVQSDPNAEPYWRDVGTL

EAYWKANLDLASVTPELDMYDQNWPIRTHMESLPPAKFVQDRSGSHGMTLNSLVSGGCIISGSVVVQSVL

FPRVRVNSFCNIDSAVLLPDVWVGRSCRLRRCVIDRACVIPEGMVIGENAEEDARRFYRSEEGIVLVTRD

MLRKLGHKQER

>lcl|NZ\_FO834906.1\_prot\_WP\_002920564.1\_327 [gene=glgA] [locus\_tag=BN49\_RS02810] [protein=glycogen synthase GlgA] [protein\_id=WP\_002920564.1] [location=354456..355889] [gbkey=CDS]

MQVLHVCSEMFPLLKTGGLADVIGALPAAQIAEGIDTRVLLPAFPDIRRGVVDAQVVTRRDTFAGRITLL

YGHFNGVGIYLIDAPHLYDRPGSPYHDTNQHAYPDNVLRFALLGWVGSEMASGLDPFWRPDVVHAHDWHA

GLTPAYLAARGRPAKSVFTVHNLAYQGMFYSWHMNDIELPWSFYNMHGLEFNGQISFLKAGLYYADHITA

VSPTYAREITEPQYAYGMEGLLRQRHHEGRLSGILNGVDDGIWSPQNDLLLPMRYDRDTLEEKAENKRQL

QIAMGLKVDDKAPLFAVVSRLTSQKGLDLVLEALPGLLEQGGQLALLGAGDPVLQEGFLAAAAEHPGKVG

VQIGYHEAFSHRIMGGADVILVPSRFEPCGLTQLYGLKYGTLPLVRRTGGLADTVADSSLENLADGLATG

FVFEDSNALSLLRAIRRAFVLWSRPSLWRYVQRQAMNMDFSWQVAANSYRELYQRLM

>lcl|NZ\_FO834906.1\_prot\_WP\_002920561.1\_328 [gene=glgP] [locus\_tag=BN49\_RS02815] [protein=glycogen phosphorylase] [protein\_id=WP\_002920561.1] [location=355907..358354] [gbkey=CDS]

MNVPFSYASPTLSVEALKHSIAYKLMFIIGKDPAIANKHEWLNATLFAVRDRMVERWLRSNRAQLSQEVR

QVYYLSMEFLIGRTLSNALLSLGIYDDVSSALAEMGLDLEELIDEENDPGLGNGGLGRLAACFLDSLAAL

GLPGRGYGIRYDYGMFKQNIVDGRQKESPDYWLEYGNPWEFERHNTRYKVRFGGRIQQEGKKTRWIETEE

IIAEAYDQIIPGFDTDATNTLRLWSAQASSEINLGKFNQGDYFAAVEDKNHSENVSRVLYPDDSTYSGRE

LRLRQEYFLVSATVQDILSRHYMLHKTYDNLADKIAIHLNDTHPVLSIPELMRLLIDEHKFSWDEAFEVT

CQVFSYTNHTLMSEALETWPVDMLGKILPRHLQIIFEINDYFLKTLQEQYPNDTDLLSRTSIIDESNGRR

VRMAWLAVVVSHKVNGVSELHSRLMVESLFAEFAKIFPMRFINVTNGVTPRRWLALANPPLSKVLDEHIG

RTWRTDLSQLDELKQHIDYPMVNQAVRQAKFENKQRLASYIAQQLNVVVNPKALFDVQIKRIHEYKRQLM

NVLHVITRYNRIKADPQAEWVPRVNIFAGKAASAYYMAKHIIHLINDVAAVINNDPQIGDKLKVVFIPNY

SVSLAQLIIPAADLSEQISLAGTEASGTSNMKFALNGALTIGTLDGANVEMQEHVGEENIFIFGNTAEEV

EELRRSGYKPREYYEQDEELHQALTQIGTGVFSPAEPGRYRDLLDSLINFGDHYQVLADYRSYVDCQDRV

DELYQNPEEWAYKAMLNIANMGYFSSDRTIQEYAKYIWHIDPVRL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529833.1\_329 [locus\_tag=BN49\_RS02820] [protein=type II toxin-antitoxin system RelE/ParE family toxin] [protein\_id=WP\_016529833.1] [location=358530..358877] [gbkey=CDS]

MWDVETTDTFDTWFELQSRALKEDMLATMLILSEFAPQLGRPYVDTVKDSTFQNMKELRVQHHGLPIRAF

FAFDPLRKAIVLCAGDKDGMNEKRFYKEMITLADREFSQHLTKER

>lcl|NZ\_FO834906.1\_prot\_WP\_016529832.1\_330 [locus\_tag=BN49\_RS02825] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016529832.1] [location=358877..359176] [gbkey=CDS]

MATLKELMAKQSPESQQRIAAKAAEIRQSVALNLLREELQMSQTEMAAAMGVKQPTIAKMEQTDNAPRLS

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>lcl|NZ\_FO834906.1\_prot\_WP\_002920554.1\_331 [gene=glpD] [locus\_tag=BN49\_RS02830] [protein=glycerol-3-phosphate dehydrogenase] [protein\_id=WP\_002920554.1] [location=complement(359239..360747)] [gbkey=CDS]

METKDLIVIGGGINGAGIAADAAGRGLSVLMLEARDLACATSSASSKLIHGGLRYLEHYEFRLVSEALAE

REVLLKMAPHIAFPMRFRLPHRPHLRPAWMIRIGLFMYDHLGKRTSLPGSTGLRFGAESVLKPEIVRGFE

YSDCWVDDARLVLANAQMVVRKGGEVRTRTRAISAKRENGLWVVEAEDIDSGEKFTWKARGLVNATGPWV

KQFFDEGMHLRSPYGIRLIKGSHIVVPRVHTQKQAYILQNEDKRIVFVIPWMDEFSIIGTTDVEYKGDPK

AVAIDDKEINYLLNVYNAHFKKTLSRDDIVWTYSGVRPLCDDESDSPQAITRDYTLDIHDENGQAPLLSV

FGGKLTTYRKLAEHALEKLTPYYKGIGPAWTKTAVLPGGDIGGDRDDYAAKLRRRFPFISESLARHYART

YGSNSEWILKEASALSDLGEDFGHEFYEAELKYLVEHEWVRSLDDAIWRRTKQGMWLTAEQQARISEWLA

QHAGKSELSLAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002920552.1\_332 [gene=glpE] [locus\_tag=BN49\_RS02835] [protein=thiosulfate sulfurtransferase GlpE] [protein\_id=WP\_002920552.1] [location=360952..361281] [gbkey=CDS]

MEQFECINVEEAHQKLHQQTAVLVDIRDPQSYAMGHTPGAFHLTNDTLGAFMRDNDFDTAVMVMCYHGNS

SKGAAQYLLQQGFDKVYSVDGGFDAWHRHFPAEVARGTF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151408.1\_333 [gene=glpG] [locus\_tag=BN49\_RS02840] [protein=rhomboid family intramembrane serine protease GlpG] [protein\_id=WP\_004151408.1] [location=361332..362162] [gbkey=CDS]

MLMITSFANPRVAQAFVDYMATQGIILTIQQHTQSDVWLADESQAGRVRAELARFLENPADPRYLAASWQ

SGQTNSGLRYQRFPFFATLRHNAGPFTWAILLICIAVFILQNLLGDQPVMIWLAWPYDPSLQFEAWRYFS

HAFMHFSLMHILFNLLWWWYLGGAVEKRIGSGKLVVITVISALLSGFVQHQFSGPWFGGLSGVVYALMGY

VWLRGERDPQSGIYLQRGLILFSLVWLIAGWFDVFGMAIANGAHVAGLATGLAMAFVDTLHGRKRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920548.1\_334 [locus\_tag=BN49\_RS02845] [protein=DeoR/GlpR family transcriptional regulator] [protein\_id=WP\_002920548.1] [location=362212..362970] [gbkey=CDS]

MKQTQRHDAIIELVKKQGYVSTEELVEQFAVSPQTIRRDLNDLAEQKMILRHHGGAALPSSSVNTSWHDR

KATQTAEKERIARRVASEIPDGATLFIDIGTTPEAVAHALLDHNDLRIVTNNLNVANTLMVKEDFRIILA

GGELRSRDGGIIGEATLDFISQFRLDFGILGISGVDSDGSLLEFDYHEVRTKRAIIENSRHVMLVVDHTK

FGRNAMVNMGSISMVDAVYTDVLPPAGVLKVITDNNLQLELC

>lcl|NZ\_FO834906.1\_prot\_WP\_016529568.1\_335 [gene=malT] [locus\_tag=BN49\_RS02850] [protein=HTH-type transcriptional regulator MalT] [protein\_id=WP\_016529568.1] [location=complement(362986..365691)] [gbkey=CDS]

MLIPSKLSRPVRLEHTVVRERLLAKLSGANNYRLVLITSPAGYGKTTLISQWAAGKNDLGWFSLDEGDNQ

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AMRFFLRHQPENMTLVVLSRNLPQLGIANLRVRDQLLEIGSQQLAFTHQEAKQFFDCRLTSPIEADDSSR

LCDDVAGWATALQLIALSARQNNSSAQHSARRLAGINASHLSDYLVDEVLNNVDARTRNFLLKSSLLRSM

NDALIVRVTGEENGQMQLEEIERQGLFLQRMDDSGEWFRYHPLFGSFLRQRCQWELAVELPEIHRAAAES

WMAQGFPSEAIHHALAAGDAKMLRDILLNHAWGMFNHSELGLLEQSLAALPWSNLLENPRLILLQAWLMQ

SQHRYSEVNTLLARAEQEMSVEMDTAMHGDFNALRAQVAINDGDQDEAERLSMVALEELPLANYYSRIVA

TSVHGEVLHCKGKLTKSLAVMQQTEQMARRHDVWHYALWSIIQQSEILFAQGFLQAAWESQEKAFQLVRE

QHLEQLPMHEFLLRIRSQLLWAWARLDEAEACARQGMDVLSTYQPQQQLQCLALMVQCSLARGDLDNARS

HLNRLENLLGNGHYHSDWVSNADKVRVIYWQMTGDKTAAANWLRQTPKPEFANNHFLQSQWRNIARAQIL

LGDFEPAEMVLEELNENARSLRLMSDLNRNLLLLNQLYWQSGRKSEAQKALLEALTLANRTGFINHFVIE

GEAMAQQLRQLIQLNTLPELEQHRAQRILRDINQHHRHKFAHFDEGFVERLLNHPEVPELIRTSPLTQRE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151407.1\_336 [gene=malP] [locus\_tag=BN49\_RS02855] [protein=maltodextrin phosphorylase] [protein\_id=WP\_004151407.1] [location=366316..368706] [gbkey=CDS]

MSQTTFNKAQFQAALTRQWQHFGLQSASEMTQRQWWRAVSGALAELLAAQPVAKPAQGQRHVNYISMEFL

IGRLTGNNLLNLGWYEGVSDALKGYDVNLTDLLEEETDPALGNGGLGRLAACFLDSMATVGQSATGYGLN

YQYGLFRQSFDDGQQMEAPDDWGRSSYPWFRHNEALDVQVGIGGKVSKNGEWQPAFVITGEAWDLPVLGY

RNNVAQPLRLWQAKHAHPFNLTKFNDGDFLRAEQQGIDAEKLTKVLYPNDNHQAGKKLRLMQQYFQCACS

VADILRRHHLAGRKLAELADYEVIQLNDTHPTIAIPELLRVLIDEHQLSWDDAWAITSKTFAYTNHTLMP

EALECWDEKLVKALLPRHMQIIKEINDRFKQLVDKTWPGDKQVWAKLAVVHDKQVRMANMCVVGGFAVNG

VAALHSDLVVKDLFPEYNQLWPNKFHNVTNGITPRRWIKQCNPALASLLDETLKKEWANDLDQLINLEKY

ADDAAFRQTYRDIKQANKVHLAEFVKQRTGIEINPQAIFDIQIKRLHEYKRQHLNLLHILALYKEIRENP

QSDRVPRVFLFGAKAAPGYYLAKNIIFAINKVAEAINNDPKVGDKLKVVFLPDYCVSAAEKLIPAADISE

QISTAGKEASGTGNMKLALNGALTVGTLDGANVEIAEQVGEENIFIFGHTVEEVKALKAKGYDPLKWRKK

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>lcl|NZ\_FO834906.1\_prot\_WP\_002920543.1\_337 [gene=malQ] [locus\_tag=BN49\_RS02860] [protein=4-alpha-glucanotransferase] [protein\_id=WP\_002920543.1] [location=368717..370810] [gbkey=CDS]

MESKRLDNAALAAGISPSYINAHGKPQSIAAVTKQRLLDAMHRSTAATKVAVNPLPNVKIFTHGKKMSLP

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GKKLWGTCVQLYTLRSEKNWGIGDFGDLRAMLPEIARRGGSFIGLNPIHALYPANPESASPYSPSSRRWL

NVIYIDVNAVEDFQRSEEAQAWWQSPATQQALQAARETDDVDYTAVTTLKMTALRMAWKQFSRREDEQMT

AFREFVLREGESLYWQAAFDALHAWQVQQDPLRWGWPAWPKAFQDIDSPEVKAFCVEHEDDVSFYLWLQW

LAWSQFAACWETSQRDGMPIGLYRDLAVGVAEGGSETWCDRELYCLKASVGAPPDILGPLGQNWGLPPMD

PHIIAARAYEPFIDLLRANMQNCGALRIDHVMSVLRLWWIPYGETADHGAYVQYPVDDLLSLLALESQRH

RCMVIGEDLGTVPVEIVSKLRNSGVYSYKVLYFESDAEKTFRAPALYPEQSMAVATTHDLPTLRGYWESG

DLTLGKALGLYPDEVVLRGLYQDRELAKQGLLDALHKYGCLPKRAGHKASLMSMTGILNRGMQRYIADSN

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>lcl|NZ\_FO834906.1\_prot\_WP\_002920542.1\_338 [gene=gntT] [locus\_tag=BN49\_RS02865] [protein=gluconate transporter] [protein\_id=WP\_002920542.1] [location=complement(370913..372229)] [gbkey=CDS]

MPLVIVAIGVALLLLLMIRFKMNGFIALVLVALAVGLMQGMPLDKVIVSIKNGVGGTLGSLALIMGFGAM

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VPMAAALSVTHGFLPPHPGPTAIATIFHADMGKTLLYGTILAIPTVILAGPVFARFLKGIDKPIPEGLHN

PKVFTEEEMPGFGVSVWTSLVPVILMAMRAVAEMILPKGHAFLPIAEFFGDPVMATLIAVLIALFTFGLN

RGRSMEQINDTLTSSIKIIAMMLLIIGGGGAFKQVLVDSGMDKYIASIMHESNMSPLFMAWSIAAVLRIA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002920540.1\_339 [gene=nfuA] [locus\_tag=BN49\_RS02870] [protein=Fe-S biogenesis protein NfuA] [protein\_id=WP\_002920540.1] [location=complement(372566..373141)] [gbkey=CDS]

MIRISDAAQAHFAKLLANQEEGTQIRVFVINPGTPNAECGVSYCPPDAVEDTDTALKFEQLTAYVDELSA

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AILQFGGGCNGCSMVDVTLKEGIEKQLLNEFPELKGVRDLTEHQRGEHSYY

>lcl|NZ\_FO834906.1\_prot\_WP\_004185961.1\_340 [gene=gntX] [locus\_tag=BN49\_RS02875] [protein=DNA utilization protein GntX] [protein\_id=WP\_004185961.1] [location=complement(373200..373874)] [gbkey=CDS]

MLTAHSLCWLCQMPLAVARWGICSRCSRALLACPPLCPQCGLPAAASRHPCGRCLQKPPPWHRLVAVNDY

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WRGCVWHREGLTRQRAGAVQHSLNARQRRQNLKNAFQLEFAVQGLHIALVDDVVTTGSTVAEISRLLLRN

GAATVQVWCLCRTL

>lcl|NZ\_FO834906.1\_prot\_WP\_004174021.1\_341 [gene=bioH] [locus\_tag=BN49\_RS02880] [protein=pimeloyl-ACP methyl ester esterase BioH] [protein\_id=WP\_004174021.1] [location=373913..374686] [gbkey=CDS]

MNDIWWQTIGEGDCHLVLLHGWGLNAQVWDCITPQLASHFTLHLVDLPGYGRSGGFGAMSLEAMAQRVLE

QAPPQAVWLGWSLGGLVASQVAIMRPERVQALVTVASSPCFAARDDWPGIKPEVLAGFQQQLSDDFQRTV

ERFLALQTMGTESARQDARALKQAVLSLPMPSAEALNGGLEILRTVDLRQALVRLPMPFLRLYGRLDGLV

PRKIVPLLDDLWPESESILFDKAAHAPFVSHPAAFCEPLLALKTRLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002920510.1\_342 [locus\_tag=BN49\_RS02885] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_002920510.1] [location=374807..375076] [gbkey=CDS]

MKLVTGMVASLVIGTLSFGAFAAKEIQKEDVAKMNLTKVGSITTSRTTSPMDARRDLSKKADELGGKYFV

VIAGQKNEKTVHANADVYK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920509.1\_343 [gene=feoC] [locus\_tag=BN49\_RS02890] [protein=[Fe-S]-dependent transcriptional repressor FeoC] [protein\_id=WP\_002920509.1] [location=complement(375165..375404)] [gbkey=CDS]

MASLMEVRDMLALQGRMEAKQLSARLQTPQPLIDAMLERMEAMGKVVRISETSEGCLSGSCKSCPEGKAA

CRQEWWALR

>lcl|NZ\_FO834906.1\_prot\_WP\_014906839.1\_344 [gene=feoB] [locus\_tag=BN49\_RS02895] [protein=Fe(2+) transporter permease subunit FeoB] [protein\_id=WP\_014906839.1] [location=complement(375414..377732)] [gbkey=CDS]

MQKLTVGLIGNPNSGKTTLFNQLTGARQRVGNWAGVTVERKEGIFATTDHQVTLVDLPGTYSLTTISSQT

SLDEQIACHYILSGDADMLINVVDASNLERNLYLTLQLLELGIPCVVALNMLDIAEKQQVRIDIDALAAR

LGCPVIPLVSTRGRGIEALKIALDRHQANSDLELVHYPQPLLREADLLAQQMSAQIPPRQRRWLGLQMLE

GDIYSRAYAGDAADKLDIALANLSDEIDDPALHIADARYQTIAAICDAVSNTLTAEPSRFTAAMDKVILN

RFLGLPIFLFVMYLMFLLAINIGGALQPIFDAGSVAIFVHGIQWLGYTLHFPDWLTVFLAQGIGGGINTV

LPLVPQIGMMYLFLSFLEDSGYMARAAFVMDRLMQALGLPGKSFVPLIVGFGCNVPSVMGARTLDAPRER

LMTIMMAPFMSCGARLAIFAVFAAAFFGQNGALAVFSLYVLGIVMAILTGLMLKHTIMRGEASPFVMELP

VYHVPHIKSLIIQTWQRLKGFVLRAGKVIVIVSIFLSALNSFSLSGKVVDNINDSALASVSRVITPVFKP

IGVHEDNWQATVGLFTGAMAKEVVVGTLNTLYTAEDIQNEEFNPQTFSLGEELLAAVDETWQGLKDTFSL

SVLANPIEASKGDGEMATGAMGVMGSKFGSAAAAYSYLIFVLLYIPCISVMGAIARESSRGWMTFSILWG

LNIAYSLSTLYYQTVSFSDHPRYSLVCILAVVLFNVVLFGLLRRARSRVDVSLLATRKTPASCCSSPAGD

CH

>lcl|NZ\_FO834906.1\_prot\_WP\_002920506.1\_345 [gene=feoA] [locus\_tag=BN49\_RS02900] [protein=ferrous iron transporter A] [protein\_id=WP\_002920506.1] [location=complement(377761..377988)] [gbkey=CDS]

MQFTPDSAWKITGFSRDISPAYRQKLLSLGMLPGSSFHVVRVAPLGDPVHIETRRVSLVLRKKDLALIEL

EAVAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004150056.1\_346 [locus\_tag=BN49\_RS02905] [protein=RNA-binding transcriptional accessory protein] [protein\_id=WP\_004150056.1] [location=complement(378401..380731)] [gbkey=CDS]

MMNDSLCRIIAGELQARAEQVEAAVRLLDEGNTVPFIARYRKEVTGGLDDTQLRNLETRLGYLRELEDRR

QAILKSIAEQGKLTDALEKAINTTLSKTELEDLYLPYKPKRRTRGQIAIEAGLEPLADLLWNEPAHDPEA

EAAKYIDADKGVADSKAALDGARYILMERFAEDAALLAKVRDYLWKNAHLVSTVVSGKEEEGAKFRDYFD

HHEPIATVPSHRALAMFRGRNEGVLQLSLNADPQFDEPPKESHGEQIIIDHLGLRLNNAPADSWRKGVVS

WTWRIKVLMHLETELMGTVRERAEDEAINVFARNLHDLLMAAPAGLRATMGLDPGLRTGVKVAVVDATGK

LVATDTIYPHTGQAAKAAVAVAALCEKYNVELVAIGNGTASRETERFFLDVQKQFPKVTAQKVIVSEAGA

SVYSASELAAQEFPDLDVSLRGAVSIARRLQDPLAELVKIDPKSIGVGQYQHDVSQTQLARKLDAVVEDC

VNAVGVDLNTASVPLLTRVAGLTRMMAQNIVAWRDENGQFQNRQQLLKVSRLGPKAFEQCAGFLRINHGD

NPLDASTVHPEAYPVVERILAATQQALKDLMGNSSALRHLKAVDFTDEKFGVPTVTDIIKELEKPGRDPR

PEFKTAKFADGVETMNDLLPGMILEGAVTNVTNFGAFVDIGVHQDGLVHISSLSDRFVEDPHTVVKAGDI

VKVKVMEVDLPRKRIALTMRLDEQPGDSNARRGGGQERPQGNRPAAKAAKPRGREAQPAGNSAMMDALAA

AMGKKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002920503.1\_347 [gene=greB] [locus\_tag=BN49\_RS02910] [protein=transcription elongation factor GreB] [protein\_id=WP\_002920503.1] [location=complement(380832..381305)] [gbkey=CDS]

MKTPLITREGYEKLKQEMDYLWRQERPEVTKKVTWAASLGDRSENADYQYNKKRLREIDRRVRYLTKCLE

QLKIVDYSPQQEGKVFFGAWVEIENDEGDIKRFRIVGYDEIFGRKDYISIDSPMARALLKKEVGDLAIVN

TPAGEASWYVNEIEYVK

>lcl|NZ\_FO834906.1\_prot\_WP\_001157751.1\_348 [gene=ompR] [locus\_tag=BN49\_RS02915] [protein=two-component system response regulator OmpR] [protein\_id=WP\_001157751.1] [location=381533..382252] [gbkey=CDS]

MQENYKILVVDDDMRLRALLERYLTEQGFQVRSVANAEQMDRLLTRESFHLMVLDLMLPGEDGLSICRRL

RSQSNPMPIIMVTAKGEEVDRIVGLEIGADDYIPKPFNPRELLARIRAVLRRQANELPGAPSQEEAVIAF

GKFKLNLGTREMFREDEPMPLTSGEFAVLKALVSHPREPLSRDKLMNLARGREYSAMERSIDVQISRLRR

MVEEDPAHPRYIQTVWGLGYVFVPDGSKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920333.1\_349 [gene=envZ] [locus\_tag=BN49\_RS02920] [protein=two-component system sensor histidine kinase EnvZ] [protein\_id=WP\_002920333.1] [location=382249..383604] [gbkey=CDS]

MKRVRFSPRSSFARTLLLIVTLLFVSLVTTYLVVLNFAILPSLQQFNKVLAYEVRMLMTDKLQLEDGTQL

VVPPAFRREIYRELGISLYSNEAAEDAGLRWAQHYEFLSQQMAHQLGGPTEVRVEVNKSSPVVWLKTWLS

PNIWVRVPLTEIHQGDFSPLFRYTLAIMLLAIGGAWLFIRIQNRPLVDLEHAALQVGRGIIPPPLREYGA

SEVRSVTRAFNHMAAGVKQLADDRTLLMAGVSHDLRTPLTRIRLATEMMGEQDGYLAESINKDIEECNAI

IEQFIDYLRTGQEMPMELADLNAVLGEVIAAESGYEREIATALQAGEIPVRMHPLSIKRALANMVVNAAR

YGNGWIKVSSGSEASRAWFQVEDDGPGIKPEQREHLFQPFVRGDSARSTSGTGLGLAIVQRIIDNHNGRL

EIGSSERGGLLIRAWLPVHRMLAPMKPARES

>lcl|NZ\_FO834906.1\_prot\_WP\_004210368.1\_350 [gene=pckA] [locus\_tag=BN49\_RS02925] [protein=phosphoenolpyruvate carboxykinase (ATP)] [protein\_id=WP\_004210368.1] [location=complement(383682..385304)] [gbkey=CDS]

MRVNHGLTPQDLKAYGINDVQDIVHNPSYDMLFQEELDPNLEGYERGVLTTLGAIAVDTGIFTGRSPKDK

YLVRDDTTRDTVWWSDKGKGKNDNKPLSQETWQHLKGLVTQQLSGKRLFIVDAFCGANADTRLSVRFITE

VAWQAHFVKNMFIRPSDEELAEFVPDFIVMNGAKCTNPQWKEQGLNSENFVAFNLTERIQLIGGTWYGGE

MKKGMFSIMNYLLPLKGIASMHCSANVGEKGDVAIFFGLSGTGKTTLSTDPKRRLIGDDEHGWDDDGVFN

FEGGCYAKTIKLSEAAEPDIYHAIRRNALLENVVVRADGTVDFDDGSKTENTRVSYPIDHIDNIVKPVSK

AGHATKVIFLTADAFGVLPPVSRLTADQTQYHFLSGFTAKLAGTERGVTEPTPTFSACFGAAFLSLHPTQ

YAEVLVKRMQAAGAQAYLVNTGWNGTGKRISIKDTRAIIDAILNGSLDNAETFTLPMFNLQIPTALPGVD

THILDPRSTYGSPEQWQEKADQLAKLFIENFEKYTDTPAGAALVAAGPQR

>lcl|NZ\_FO834906.1\_prot\_WP\_171819464.1\_351 [gene=hslO] [locus\_tag=BN49\_RS02935] [protein=Hsp33 family molecular chaperone HslO] [protein\_id=WP\_171819464.1] [location=complement(385665..386549)] [gbkey=CDS]

MIMTQHDQLHRYLFENYAVRGELVTVSETLEQILANHTYPQPVKTVLAELLVATSLLTATLKFAGDITVQ

LQGDGPLQLAVINGNNQQQLRGVARVQGEIADDADLKTMVGNGYLVITISPEEGERYQGVVGLEGDTLAA

CLEDYFQRSEQLPTRLIIRTGDHEGQPMAGGMLLQVMPAQDAQTADFEHLTTLTETIKAEELFTLPANDV

LWRLYHEEEVTVYDPQSVEFKCTCSRERCAGALKTLPDEEIDSILADEGEIDMHCDYCGNHYIFNAMDIA

EIRNNASPADPQVH

>lcl|NZ\_FO834906.1\_prot\_WP\_002920326.1\_352 [gene=hslR] [locus\_tag=BN49\_RS02940] [protein=ribosome-associated heat shock protein Hsp15] [protein\_id=WP\_002920326.1] [location=complement(386568..386969)] [gbkey=CDS]

MKEKPTETVRLDKWLWAARFYKTRALAREMIEGGKVHYNGQRSKPGKIVELDAMLTLRQGNDERTVRIIG

ITEQRRPASEAVNLYEETAESIEKREKMALARKMNALTMPHPDRRPDKKERRDLMRFKHGESE

>lcl|NZ\_FO834906.1\_prot\_353 [gene=yrfG] [locus\_tag=BN49\_RS02945] [protein=GMP/IMP nucleotidase] [pseudo=true] [location=complement(386966..387650)] [gbkey=CDS]

MHFDIAWQEVDTVLLDMDGTLLDLAFDNYFWQTLVPETWGGRPRPQFAGGERRHAPGVSRRAAYAKLVLS

GLLERAPGFGYLCDDQRTRSARHAARGYRAVP\*CAQGLR\*ATHSVDQCPSPQSGGEAQTHRPGRAP\*FIT

FHPHIWLSERGSASVARRGGGNWP\*GAQNAVCRRQRGDTGCREGVWHSLLPGYYQS\*LRTGGKAVSAPSG

AE\*LPTTDPFAYPEGEAM

>lcl|NZ\_FO834906.1\_prot\_WP\_016530730.1\_354 [locus\_tag=BN49\_RS02950] [protein=intracellular growth attenuator family protein] [protein\_id=WP\_016530730.1] [location=complement(387711..389837)] [gbkey=CDS]

MGTFLIFLTALLICVLLIGWWYRAHARRRRLPLLHAFSDATTRQLPADERQAIEKYVAELSHAQQVPASG

ATSAPVALALNEQSDTVYAVTRAITRYGITTDAPNKWRYFLDSVEVHLPPFWEQHINDENSVELIPTDSL

PLVITLNGHSLSDYRQEAQSYALERASATQASIRGEESEQVELRQIRRETPEEHALNRPDGLREAILIVA

SFLFFYFSLIGPAVFTPWLVAAGLLLLAAGLWGIYAPPRRAALREIHCLRGVPKRWGLFGENDQEQINNI

SLGIIDLIYPRHWQPWIAQDLGQQTDIDIYLNRHVARQGRYLSLHDEVKNFPLQYWLRSAIIAAGALVVV

IMLWASVPLNMPFKFTLSWLKGAQTIEATTVSQLEKAHVRIGDTLRLTGTGMCNIRTPGSWSAKEDSPFL

PFDCSQIVWNDAPPLPLPESDIVSKATALMQSVQRQLHPETDDDSRVSPALRSAIQKSGMVLLDDFGDIV

QKTNDLCSAKDDCLRLKNALVNLGNTRNWETLTKRATAGKLDGVNVLLRPVSAESLENLVTTSTAPFVIR

ETSRAAQALNSPAPGGFLIASDEGSVLVNQPWPAVSLYDYPAHEQWGELRRLAGMLMHTPFHAEGIVTNL

FTDANGTQHINLHRIPDRSGLWRYLGITLLLSMVGCMAYHAVQALRRYQRHRQRMEEIQKYYESCLNPVL

LPSSDSQD

>lcl|NZ\_FO834906.1\_prot\_WP\_002920321.1\_355 [gene=nudE] [locus\_tag=BN49\_RS02955] [protein=ADP compounds hydrolase NudE] [protein\_id=WP\_002920321.1] [location=390158..390718] [gbkey=CDS]

MSKSLQKPTILNVETVARSRLFNVESVDLEFSNGVRRVYERMRPSTREAVMIVPIVDDHIILIREYAVGT

ESYELGFSKGLIDPGETVDEAANRELKEEVGYGANKLTFLKKLSMAPSYFSSKMNIMVAEDLYPESLPGD

EPEPLPQVRWPLAQLMSLLDEEDFNEARNVSALFLVREWLQAQGRL

>lcl|NZ\_FO834906.1\_prot\_WP\_004185951.1\_356 [gene=mrcA] [locus\_tag=BN49\_RS02960] [protein=peptidoglycan glycosyltransferase/peptidoglycan DD-transpeptidase MrcA] [protein\_id=WP\_004185951.1] [location=complement(390772..393330)] [gbkey=CDS]

MKFVKYLLILAVCCVLLGAGSIFGLYKYIEPQLPDVATLKDVRLQIPMQVYSADGELIAQYGEKRRIPVT

LQQIPPELVKAFIATEDSRFYEHHGVDPVGIFRAASVAMFSGHASQGASTITQQLARNFFLSPEKTLMRK

IKEAFLAIRIEQLLNKDEILELYLNKIYLGYRAYGVGAAAQVYFGKPIDQLTLSEMAVIAGLPKAPSTFN

PLYSMDRATARRNVVLSRMLSEGYITQAQYDEARSEPIDASYHAPKIAFSAPYLSEMVRQEMVNRYGEQA

YEDGYRVYTTITRKNQQAAQQAVRNNVLDYDMRHGYRGPASVLWKVGETPWETKKIVDSLKRQSGYGPLF

PAVVTSANAQEAVALLANGDSVSLTMEGVRWARRFISDTQQGATPRKVNDVVQAGQQIWVRKVGDSWWLS

QLPDVNSALVSINPQNGAIIALVGGFDFNQSKFNRATQALRQVGSNIKPFLYTAAMDKGLTLASMLNDVP

ISRWDAGAGSDWRPKNSPPQYAGPIRLRQGLGQSKNVVMVRAMRAMGVDYAAEYLQRFGFPAQNIVHTES

LALGSASFTPLQVARGYSVMANGGFLVNPFFISKIENDQGGVLFEERPKIACPQCDLPVIYGDTPKSNVL

ENKDVEDVATSAEPQNGNVPPQPQLEQANQSLVAQSGAQEYAPHVINTPLAFLIKSALNSNIFGEPGWMG

TGWRAGRDLQRHDIGGKTGTTNSSKDAWFSGYGPGVVTSVWIGFDDHRRDLGRTTASGAIKDQISGYEGG

AKSAQPAWDSFMKSVLEGVPEEPLTPPPGIVTVNIDRSTGQLANGGNSRAEYFIEGTQPTQQAVREVGTT

LTDGGGETHELF

>lcl|NZ\_FO834906.1\_prot\_WP\_046042236.1\_357 [locus\_tag=BN49\_RS02965] [protein=hypothetical protein] [protein\_id=WP\_046042236.1] [location=393449..394249] [gbkey=CDS]

MAFRNWRLGMHIQQDSIAIVALLHERSHWALRRWWRIPLPPGLVRQGMVADVSALGSRLAAWRRELPAQH

QVSIAFPAVRTLQKRLPYPQFALREREQATWVASAMSQQLAMPASALCIDYAPSSRDDGWQVTAAQRLDI

NVLRELAGRLRLRVAAIVPDASALGAFFPWMTAADQGLAWRDEKHWLWATREAWGSDACADVGSLSQLAG

QLQVLLRLCIDAGDEASRFDVWQVIHRRQPPLPADGDRYAIALGLALGGGRHDACR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042238.1\_358 [locus\_tag=BN49\_RS02970] [protein=pilus assembly protein PilN] [protein\_id=WP\_046042238.1] [location=394233..394766] [gbkey=CDS]

MTHVVNLLPWRDLRRRQRLRYVLLLTIGIVLLGGMGLLVSRTARLQRDFLATLHTTADAQLLASLKQREQ

AMREAWQQHQRQRQQYQRRSAIAAWQPRLQALAADLPAQAWLTRLEYQGVLLTLDGLALNLKALTSVEAA

LTRVAGFAPAKAGGTQRDAEGRWQFSFTLTGARADAD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151403.1\_359 [locus\_tag=BN49\_RS02975] [protein=hypothetical protein] [protein\_id=WP\_004151403.1] [location=394756..395184] [gbkey=CDS]

MRINLRGAWTGLPILLAMGLSGGGVALWRDLRPPQAAVTRDAALQTQWRRIMALRIPGEENPGARIDTQS

FSPIAIPLSGAKLIAWRPQGSGGEMELTLSWSTVPALFSWLARCGMNPRSFSLGREAQTLRLRLLLEAED

ER

>lcl|NZ\_FO834906.1\_prot\_WP\_002920279.1\_360 [locus\_tag=BN49\_RS02980] [protein=HofP DNA utilization family protein] [protein\_id=WP\_002920279.1] [location=395174..395557] [gbkey=CDS]

MSGKRWIFLWLPLSLLAAERDPFQPVEDPCRTAQLSQWRYGGAVGDEAGWTGFLQDGNGKWRRVRMDEQL

PTGWRVSRLTAGELDIVTSSGCEPPAWRWQREGKQHDAMDKPAASAAAAGGGPRRPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004174030.1\_361 [gene=hofQ] [locus\_tag=BN49\_RS02985] [protein=DNA uptake porin HofQ] [protein\_id=WP\_004174030.1] [location=395490..396734] [gbkey=CDS]

MMRWISLLLLLLPLAVAPAARNDKPVSLVIDDAPVAQVLQALAEMNHKNLVVAPDVSGTLSLRLQKVPWS

QALRAVADSAGLSLQQQGTVIYAHTQAWQKANQAQREAEQEKRLQNLPLQAESVTLHFADAEELAKSGGK

LLSARGHLMADKRTNRLLIRDDARHLPALKAWAQEMDLPVGQVELAAHIVSMSETSLRELGVKWRLAEAG

SPPGSGQITTLSSDVSVNDASTRAGFNIGKINGRLLELELSALERKQQVEIIASPRLLASHMQPASIKQG

SEIPYQVSSGESGATSVEFKEAVLGMEVTPTVLQQGRVRLKLRISENTPGQVLKQENGEALAIDKQEIET

LVEVRSGETLALGGIFSQKNKTARDSVPLLGDIPVLGRLFRRDGKDNERRELVVFITPRILAVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002920267.1\_362 [gene=aroK] [locus\_tag=BN49\_RS02990] [protein=shikimate kinase AroK] [protein\_id=WP\_002920267.1] [location=397005..397526] [gbkey=CDS]

MAEKRNIFLVGPMGAGKSTIGRQLAQQLNMEFYDSDQEIEKRTGADVGWVFDVEGEEGFRDREEKIINEL

TEKQGIVLATGGGSVKSRETRNRLSARGVVVYLETTIEKQLARTQRDKKRPLLQVDAPPREVLEALADER

NPLYEEIADVTIRTDDQSAKVVANQIIHMLESN

>lcl|NZ\_FO834906.1\_prot\_WP\_004150047.1\_363 [gene=aroB] [locus\_tag=BN49\_RS02995] [protein=3-dehydroquinate synthase] [protein\_id=WP\_004150047.1] [location=397582..398676] [gbkey=CDS]

MERLTVTLGERSYPITIAAGLFNDPASFLPLKSGDQAMLVTNETLAPLYLDTVRSALEQSGVNVDSVILP

DGEQYKSLAVMDTVFTALLQKPHGRDTTLVALGGGVIGDLTGFAAASYQRGVRFIQVPTTLLSQVDSSVG

GKTAVNHPLGKNMIGAFWQPVSVVVDLNCLKTLPKRELASGLAEVIKYGVILDGEFFSWLENNIDALLAL

DDTAMAYCIRRCCELKAEVVAADERETGLRALLNLGHTFGHAIEAEMGYGNWLHGEAVAAGMVMAARTSE

RLGQFRAQDTQRIIELLKRAGLPVRGPQEMSAQAYLPHMMRDKKVLAGEMRLVLPLAIGSSELRGGVPHD

VVLGAIADTQQAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529309.1\_364 [gene=damX] [locus\_tag=BN49\_RS03000] [protein=cell division protein DamX] [protein\_id=WP\_016529309.1] [location=398761..400047] [gbkey=CDS]

MDDFKPEDDMKADRNDRRAGRSRQSSERDADPHINFDDVDLDADEGRPTRAGKARREREEEEFEEELDAQ

DEEMLEEQPVERRPRKRKKAPAKPASRQYIMMGVGILVLLLLIVGIGSALKSPSSSSQQTASGEKSINLS

DDQSASMPAAGQDQTAAANSTSQQDVTVPPIAANPTQGQAAVAPQGQQRIEVQGDLNNALTQQQGQLDGA

VANSTLPTEPATVAPIRNGANGTAAPRQATERQTAATPRPAERKHTVIEAKPQSKPQAVAKTPVESKPVQ

QKHVESTATTAPAKTSVSESKPVATAQSKPTTTTAAPAATAAAAAPAAKSGKTAGDVSSMKTAPSGHYTL

QLSSSSNYDNLNNWAKKEKLDKYVVYETSRNGQPWYVLVSGIYASKDEAKRAVTSLPADVQAKNPWAKPL

HQVQADLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920260.1\_365 [gene=dam] [locus\_tag=BN49\_RS03005] [protein=adenine-specific DNA-methyltransferase] [protein\_id=WP\_002920260.1] [location=400126..400953] [gbkey=CDS]

MKKNRAFLKWAGGKFPLLDDIKKHLPEGECLIEPFVGAGSVFLNTDFSRYILADINSDLIGLYNIVKLRT

DEYVAAAREMFTPENNVAERYYLYRDEFNQSQDPLRRAVLFLYLNRHGYNGLCRYNLRGEFNVPFGRYKK

PYFPEAELYHFAEKAQNAEFYCESYEECMQRADSRTVVYCDPPYAPLTATANFTAYHTNSFNLEQQVLLA

QKAESLMKKRIPVLISNHRTPLTQEWYKNAAETHIVKVRRSISSNGGTRKKVDELLALYRPPKTK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920259.1\_366 [gene=rpe] [locus\_tag=BN49\_RS03010] [protein=ribulose-phosphate 3-epimerase] [protein\_id=WP\_002920259.1] [location=400971..401648] [gbkey=CDS]

MKQYLIAPSILSADFARLGEDTAKALAAGADVVHFDVMDNHYVPNLTIGPMVLKSLRNYGITAPIDVHLM

VKPVDRIIPDFAEAGASIITFHPEASEHVDRSLQLIKEHGCKAGLVFNPATPLSYLDYVMDKLDVILLMS

VNPGFGGQSFIPQTLDKLREVRQRIDASGYDIRLEVDGGVKASNIGEIAAAGADMFVAGSAIFGQPDYKQ

VIDQMRSELAKVSHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004188345.1\_367 [gene=gph] [locus\_tag=BN49\_RS03015] [protein=phosphoglycolate phosphatase] [protein\_id=WP\_004188345.1] [location=401641..402402] [gbkey=CDS]

MDKLQAIRGIAFDLDGTLVDSAPGLTSAVDNALYALELPVAGEERVITWIGNGADVLMERALTWARQERA

TLRAAMGKPSVDDHDIPQDEQLRILRKLFDRYYAEAAEEGSFLFPAVADTLGALHAKGLPLALVTNKPTP

FVAPLLDALDIAKYFTVVIGGDDVQNKKPHPEPLLLVAEKLSLAPAELLFVGDSRNDIQAAKAAGCCSVG

LTYGYNYGEPLALSEPDYLFDQFNELLPALGLPHSETQELKHD

>lcl|NZ\_FO834906.1\_prot\_WP\_002920253.1\_368 [gene=trpS] [locus\_tag=BN49\_RS03020] [protein=tryptophan--tRNA ligase] [protein\_id=WP\_002920253.1] [location=402395..403399] [gbkey=CDS]

MTKPIVFSGAQPSGELTIGNYMGALRQWVNMQDDYHCIYCIVDQHAITVRQDPQQLRKATLDTLALYLAC

GIDPQKSTIFVQSHVPEHAQLGWALNCYTYFGELSRMTQFKDKSARYAENINAGLFDYPVLMAADILLYQ

TNQVPVGEDQKQHLELSRDIAQRFNAIYGDIFKVPEPFIPKSGARVMSLLEPTKKMSKSDDNRNNVIGLL

EDPKSVVKKIKRAVTDSDEPPVVRYDLKEKAGVSNLLDILSAVTGKTIPELEQHFEGKMYGHLKGEVAEA

VSGMLIDLQERYHRFRNDEAFLNQVMKDGAEKASARASQTLKAVYEAIGFVAKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002920252.1\_369 [gene=cysG] [locus\_tag=BN49\_RS03025] [protein=siroheme synthase CysG] [protein\_id=WP\_002920252.1] [location=complement(403472..404845)] [gbkey=CDS]

MDHLPIFCQLRQRDCLLVGGGDVAERKARLLLDAGANVTVNALDFTPQFQVWADSQMLTLVQGEFIPSLL

DNCWLAIAATDDETVNQQVSEAAEARRIFCNVVDAPRQASFIMPSIIDRSPLMVAVSSGGTSPVLARLLR

EKLESILPLHLGQLARYAGHLRARVKQQFATVGERRRFWEKLFVNDRLAQSLANDDRQAVADTTEQLLTE

PLEHRGEVVLVGAGPGDAGLLTLKGLQQIQQADVVVYDRLVSDDIMNLVRRDADRVFVGKRSGYHCVPQE

EINQILLREAQKGRRVVRLKGGDPFIFGRGGEELETLCEAGIPFSVVPGITAASGCSAYSGIPLTHRDFA

QGVRLVTGHLKTGGELDWANLAVEKQTLVFYMGLNQAPAIREKLIAHGMAEDMPAAIVENGTAVTQKVVS

GTLGQLDILAQQMASPALIIVGRVVGLRDKLNWFSNH

>lcl|NZ\_FO834906.1\_prot\_WP\_002920249.1\_370 [gene=nirD] [locus\_tag=BN49\_RS03030] [protein=nitrite reductase small subunit NirD] [protein\_id=WP\_002920249.1] [location=complement(404998..405324)] [gbkey=CDS]

MSQWVNICSIDDILPATGVCALLGQQQVAIFRPYHDDRVFAISNIDPFFNASVLSRGIIAEHDGALWVAS

PLKKQRFRLSDGLCMEDASHSIARFDARVKDGHVQLKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920243.1\_371 [gene=nirB] [locus\_tag=BN49\_RS03035] [protein=nitrite reductase large subunit NirB] [protein\_id=WP\_002920243.1] [location=complement(405321..407864)] [gbkey=CDS]

MSKVRIAIIGNGMVGHRFIEELLDKAPAGQFDITVFCEEPRIAYDRVHLSSYFSHHTAEELSLVREGFYE

KHGVKVLVGERAITINRQEKVIHSSAGRTVFYDKLIMATGSYPWIPPIKGAETQDCFVYRTIEDLNAIES

CARRSKRGAVVGGGLLGLEAAGALKNLGVETHVIEFAPMLMAEQLDQMGGEQLRRKIESMGVKVHTSKNT

KEIVQQGTEARKTMHFADGSELQVDFIVFSTGIRPRDKLATQCGLAVAQRGGIMVNDSCQTSDPDIYAIG

ECASWNNRVYGLVAPGYKMAQVAVDHLLGSENSFTGADLSAKLKLLGVDVGGIGDAHGRTPGARSYVYLD

ESKEVYKRLIVSADNKTLLGAVLVGDTSDYGNLLQLVLNAIELPENPDSLILPAHAGSGKPSIGVDKLPD

SAQICSCFDVSKGDLIAAINKGCHTVAALKAETKAGTGCGGCIPLVTQVLNAELAKQGIEVNNNLCEHFA

YSRQELFHLIRVEGIKTFDELLEKHGQGYGCEVCKPTVGSLLASCWNEYILKPQHTPLQDSNDNFLANIQ

KDGTYSVIPRSAGGEITPEGLVAVGRIAREFNLYTKITGSQRIGLFGAQKDDLPEIWRQLIEAGFETGHA

YAKALRMAKTCVGSTWCRYGVGDSVGFGVELENRYKGIRTPHKMKFGVSGCTRECAEAQGKDVGIIATEK

GWNLYVCGNGGMKPRHADLLAADLDRDTLIKYLDRFMMFYIRTADKLTRTAPWLDNMEGGIDYLRSVIID

DKLGLNDHLEEELARLRAAFACEWTETVNNPAAQTRFKHFINSDQRDPNVQVVPERDQHRPATPYERIPV

TLVEEKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531177.1\_372 [locus\_tag=BN49\_RS03045] [protein=cytosine deaminase] [protein\_id=WP\_016531177.1] [location=408103..409425] [gbkey=CDS]

MTAAPLWLIQNVRLADRDGLWQIAIDKGRFGEITPMGEAHDESYEVLNARGGLAIPPFIEPHIHLDTTQT

AGEPNWNQSGTLFEGIERWAERKALLSHEDVKARAWKTLKWQIANGVQFVRTHVDVFDPTLTALKAMLEV

KQEVAPWVELQIVAFPQEGILSYLNGEALLEEALKLGADVVGAIPHFEFTREYGVESLHIAFRLAQQYDR

PLDIHCDEIDDEQSRFVETVAALALKAGIGPRVTASHTTAMHSYNGAYTSRLFRLLKLSGINFVANPLVN

IHLQGRFDDYPKRRGITRVKELLAAGINVCFGHDDVFDPWYPLGTGNMLQVLHMGLHVCQLMGYQQINDG

LQLITDNSARTFGLEDYGIVSGNPANLIILPAENGFEAVRCQVPVRWSIRQGRVIATTQPAQSWIQTDRG

GEELSFMRNSPLADAKGPKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920240.1\_373 [gene=tsgA] [locus\_tag=BN49\_RS03050] [protein=MFS transporter TsgA] [protein\_id=WP\_002920240.1] [location=complement(409422..410609)] [gbkey=CDS]

MTNSNRIKLTWISFFSYALTGALVIVTGMVMGNIADYFHLPVSSMSNTFTFLNAGILISIFLNAWLMEIV

PLKTQLRFGFILMVLAVAGLMLSHSLALFSASMFVLGLVSGITMSIGTFLITHMYEGRQRGARLLFTDSF

FSMAGMIFPMVAAVLLARSIEWYWVYACIGLVYVAIFVLTFGCDFPVLGKKAQSENSQPVVKEKWGIGVL

FLSVAALCYILGQLGFISWVPEYAKSLGMSLGDAGKLVSDFWMSYMIGMWSFSFILRFFDLQRILTVLAG

LATVLMYLFINGSPEHMPWFILTLGFFSSAIYTSIITLGSQQTRVASPKLVNFILTCGTIGTMLTFVVTG

PIVAASGPLAALHTANGLYAVVFVMCFILGFVSRHRQNNAQAASH

>lcl|NZ\_FO834906.1\_prot\_WP\_002920238.1\_374 [gene=ppiA] [locus\_tag=BN49\_RS03055] [protein=peptidylprolyl isomerase A] [protein\_id=WP\_002920238.1] [location=410886..411455] [gbkey=CDS]

MLKSTLAAMAAVFAISAFSPAMAAKGDPHVLLTTSAGNIELELNSQKAPISVDNFLKYVNSGFYNNTTFH

RVIPGFMVQGGGFNEQMQQKQPNPPIKNEADNGLRNTRGTIAMARTADQDSATSQFFINVADNAFLDHGQ

RDFGYAVFGKVVKGMDVADKISQVQTHNVGPYQNVPTKPVVILSAKVLP

>lcl|NZ\_FO834906.1\_prot\_WP\_002920231.1\_375 [locus\_tag=BN49\_RS03060] [protein=YhfG family protein] [protein\_id=WP\_002920231.1] [location=411562..411729] [gbkey=CDS]

MRPLTDKQKSRLWEQTRNTNFQASRRLEGVTVPLVTLTAEEALARLATLRREYER

>lcl|NZ\_FO834906.1\_prot\_WP\_002920230.1\_376 [locus\_tag=BN49\_RS03065] [protein=putative adenosine monophosphate-protein transferase Fic] [protein\_id=WP\_002920230.1] [location=411719..412321] [gbkey=CDS]

MSDKFGDERDPYLYPALNVLRNRLGIRQAKNLQQAAFEMTALRAATLPLGPRVRGLPYLCAIHHQLYQDL

FDWAGRLREVNLYLGDTPFCHFARIEEEGNALMQALEQEDYLSGLPRDTFIERLSWFYGEINVLHPFRLG

NGLTQRIFFEQLAIHAGYLLNWRDVDPAGWSAACQQSAMGDLAPLVAIFRKVVSEARESE

>lcl|NZ\_FO834906.1\_prot\_WP\_002920229.1\_377 [gene=pabA] [locus\_tag=BN49\_RS03070] [protein=aminodeoxychorismate synthase component 2] [protein\_id=WP\_002920229.1] [location=412354..412917] [gbkey=CDS]

MILLIDNYDSFTWNLYQYFCELGAEVLVRRNDALTLEEIAALAPEKIVISPGPCTPDEAGISLAVIRHYA

GKTPLLGVCLGHQAIAQAFGATIVRAAQVMHGKTSLIEHNGEGVFQGLNNPLTVTRYHSLVIDPPTLPSE

FNVTARSASGEIMGIRHREWDLEGVQFHPESILSEQGHQLLANFLKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004174049.1\_378 [locus\_tag=BN49\_RS03075] [protein=aspartate aminotransferase family protein] [protein\_id=WP\_004174049.1] [location=413008..414228] [gbkey=CDS]

MATEQPAITRATFDEVILPIYAPAEFIPVKGKGSRVWDQQGKEYIDFAGGIAVTALGHCHPALVAALHQQ

GETLWHTSNVFTNEPALRLGRKLVEATFAERVVFMNSGTEANETAFKLARHYAVTRHSPYKTKIIAFHNA

FHGRSLFTVSVGGQPKYSDGFGPKPADIVHVPFNDLQAVKAVMDDHTCAVVVEPIQGEGGVTAATPAFLQ

GLRELCDQHQALLVFDEVQCGMGRTGSLFAYMHYGVTPDILTSAKALGGGFPVSAMLTTHEIASAFHAGS

HGSTYGGNPLACAVANAAFDLINTPAVLDGVSAKRELFVKHLQRLDAEFDLFSDIRGMGLLIGAELKPQH

KGRARDFLYAAADAGVMVLNAGPDVMRFVPSLIIDEQDITEGMARFAQAVAKVING

>lcl|NZ\_FO834906.1\_prot\_WP\_016531180.1\_379 [locus\_tag=BN49\_RS03080] [protein=YccS/YhfK family putative transporter] [protein\_id=WP\_016531180.1] [location=complement(414218..416296)] [gbkey=CDS]

MWRRLIYHPEVNYALRQTLVLCLPVAIGLLLGHLQQGLLFSLVPACCNIAGLDTPHKRFFKRLIIGGCLF

AGCSLVVQLLLAQAIPLPFILSGLALLLGVTAEISSLHARLLPASLIAAIFTLSLAGNMPIWEPLLIYAF

GTLWYGVFNWFWFWLWREQPLWESLSLLYRELADYCEAKYSLLTQHTDPSTALPPLLTRQQKVVDLITQC

YQQMHMLAANQRNDHKRLLRAFQMGLDLQEHISVSLHQPEEVQKLVERSHAEAVIRWNAQTVAARLRVLA

DDMLYHRFPKRFQMDKQIEALEKIARQHPDNPVGHFCAWHFSRIARVLHTQRPLYARDLMADKERRLPLL

PALKNYLSLKSPALRNAARISVMLSVASLMGNALHLPKPYWILMTVLFVTQNGYGATRVRIVHRAAGTLA

GLTIAGLTLHFHVPESYTLSGMLLITLLSYLIIRKHYGWAMVGFTVTAVYTLQLLTLNGEQFIIARLIDT

LIGCLIAFGGMVWLWPQWQSGLLKKNAHDALEADQQAIRLILSADPKAPALAYQRMRVNQAHNALYNSLN

QAMQEPGFNTHYLEDMKLWVTHSQFIVEHINAMTTLAREHTMLTPDLAQRYLESCEIALQRCQQRLDSDG

PGSAGDANIMESPESEAPIGPLSTLEQHLQRILGHLNTMHTISSVAWRQRPHHGIWLRKISR

>lcl|NZ\_FO834906.1\_prot\_WP\_000242758.1\_380 [gene=crp] [locus\_tag=BN49\_RS03085] [protein=cAMP-activated global transcriptional regulator CRP] [protein\_id=WP\_000242758.1] [location=complement(416348..416980)] [gbkey=CDS]

MVLGKPQTDPTLEWFLSHCHIHKYPSKSTLIHQGEKAETLYYIVKGSVAVLIKDEEGKEMILSYLNQGDF

IGELGLFEEGQERSAWVRAKTACEVAEISYKKFRQLIQVNPDILMRLSSQMARRLQVTSEKVGNLAFLDV

TGRIAQTLLNLAKQPDAMTHPDGMQIKITRQEIGQIVGCSRETVGRILKMLEDQNLISAHGKTIVVYGTR

>lcl|NZ\_FO834906.1\_prot\_WP\_002920158.1\_381 [locus\_tag=BN49\_RS03090] [protein=OsmC family protein] [protein\_id=WP\_002920158.1] [location=417287..417691] [gbkey=CDS]

MQARVKWVEGLTFIGESASGHQILMDGNSGDKAPSPMEMVLMAAGGCSAIDVVSILQKGRHDVTNCEVKL

TSERREEAPRLFTHINLHFIVTGKALKDAAVSRAVDLSAEKYCSVALMLEKAVNITHSYEVIEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042248.1\_382 [locus\_tag=BN49\_RS03095] [protein=phosphoribulokinase] [protein\_id=WP\_046042248.1] [location=complement(417746..418615)] [gbkey=CDS]

MSAKHPVIAVTGSSGAGTTTTSLAFRKIFAQLNLHAAEVEGDSFHRYTRPEMDMAIRKARDQGKHISYFG

PEANDFGLLEQTFVDYGRHGKGQSRKYLHTYDEAVPWNQVPGTFTPWQPLPEPTDVLFYEGLHGGVVTPQ

HDVASHVDLLVGVVPIVNLEWIQKLIRDTSERGHSREAVMDSVVRSMEDYINFITPQFSRTHINFQRVPT

VDTSNPFAAKAIPSLDESFVVLHFRNLQNIDFPWLLAMLQGSFISHMNTLVVPGGKMGLAMELIMTPLVE

RLMEGRKIG

>lcl|NZ\_FO834906.1\_prot\_WP\_002920151.1\_383 [locus\_tag=BN49\_RS03100] [protein=YheU family protein] [protein\_id=WP\_002920151.1] [location=complement(418652..418870)] [gbkey=CDS]

MIIPWQDLDPETLDNLIESFVLREGTDYGEHERSLADKVADVKQQLKRGEAVLVWSELHETVNIMPRALF

NG

>lcl|NZ\_FO834906.1\_prot\_WP\_024264627.1\_384 [locus\_tag=BN49\_RS03105] [protein=hydrolase] [protein\_id=WP\_024264627.1] [location=complement(418867..419865)] [gbkey=CDS]

MTPPENDSREFHPMRGVGNRHLQTMLPRLIRRKLRFTPHWQRLELPDGDFVDLAWSEDPHQARHKPRLVV

FHGLEGSLHSPYAHGLIHAAMQRGWLGVVMHFRGCSGEPNRNHRIYHSGETEDGTWFLHWLKREFGPAPT

AAVGYSLGGNMLGCLLAEEGDRCPLDAAVIVSAPFMLEACSYHMDKGFSRVYQRYLLNLLKANASRKLKA

YPGSLPVDLRQLKGMRRIREFDDMITAKIHGFADALDYYRQCSAMPRLSDITKPTLIIHAKDDPFMDHHS

IPPQEQLPANVEYQLTEQGGHVGFVSGTLRKPEMWLERRIPDWLNRWLEVPV

>lcl|NZ\_FO834906.1\_prot\_WP\_016532008.1\_385 [locus\_tag=BN49\_RS03115] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016532008.1] [location=complement(420093..421997)] [gbkey=CDS]

MIVFSSLQIRRGVRVLLDNATATINPGQKVGLVGKNGCGKSTLLSLLKNEISADGGSMTFPGNWQLAWVN

QETPALPQPAIDYVIDGDREYRQLEAALQLANERNDGHAIATVHGKLDAIDAWTIRSRAASLLHGLGFSN

EQLERPVSDFSGGWRMRLNLAQALICRSDLLLLDEPTNHLDLDAVIWLEKWLKGYTGTLILISHDRDFLD

PIVDKIIHIEQQTMFEYTGNYSSFEVQRATRLAQQQAMYESQQQRVAHLQSYIDRFRAKATKAKQAQSRI

KMLERMELIAPAHVDNPFHFSFRQPESLPNPLLKMEKVSAGYGERIILDSIKLNLVPGSRIGLLGRNGAG

KSTLIKLLAGELQPVSGEIGLAKGIKLGYFAQHQLEFLRADESPLQHLARLAPQELEQKLRDYLGGFGFQ

GDKVSEETRRFSGGEKARLVLALIVWQRPNLLLLDEPTNHLDLDMRQALTEALIDFEGALVVVSHDRHLI

RSTTDDLYLVHDGKVEPFDGDLEDYQQWLSDSQKQESQSGEAPKESGNSAQARKDQKRREAELRSQTQPL

RKEIARLEKEMDKLNAQLASAEEKLGDSELYDASRKAELTECLQQQASAKSGLEECEMAWLEAQEQLERM

LQEG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151401.1\_386 [gene=kefG] [locus\_tag=BN49\_RS03120] [protein=glutathione-regulated potassium-efflux system ancillary protein KefG] [protein\_id=WP\_004151401.1] [location=422171..422734] [gbkey=CDS]

MMSQTAKVLLLYAHPESQDSVANRVLLEPALQLPNVTVHDLYAHYPDFFIDIAYEQDLLRQHEVIVFQHP

LYTWSCPALLKEWLDRVLSRGFASGAGGNELAGKYWRSVITTGEPESAYRRDANRYPMNDILRPFELTAG

MCRMHWMSPIIVYWARRQQPEELRSRALAYRDWLANPIAAGGVHGGI

>lcl|NZ\_FO834906.1\_prot\_WP\_004150031.1\_387 [gene=kefB] [locus\_tag=BN49\_RS03125] [protein=glutathione-regulated potassium-efflux system protein KefB] [protein\_id=WP\_004150031.1] [location=422721..424526] [gbkey=CDS]

MAGSDLLLAGVLFLFAAVIAVPLASRLGIGAVLGYLLAGIAIGPWGLGFISDVDEILHFSELGVVFLMFI

IGLELNPAKLWRLRSSIFGVGAAQVMLSAAILGGLLMTTGFSWQAAVVGGIGLAMSSTAMALQLMREKGM

SRSEAGQLGFSVLLFQDLAVIPALALVPLLAGSADEHVNWLTVGMKVLAFAGMLIGGRYLLRPVFRFIAS

SGVREVFTAATLLLVLGSALFMEALGLSMALGTFIAGVLLAESEYRHELEIAIDPFKGLLLGLFFISVGM

ALNLGVLYTHLLWVAVSVAVLVAVKMLVLYLLARLYGLRSSERMQFAGVLSQGGEFAFVLFSLPASQRLF

QHDQMALLLVAVTLSMMTTPLLMKGIDKLLSRRLNPADDTGEAPWVEDDKPQVIIVGFGRFGQVIGRLLM

ANKMRITVLERDISAVNLMRNYGYKVYFGDATQLELLRSAGAEEAQSIVITCNEPEDTMRLVEMCQQHFP

HLHILARARGRVEAHELLQAGVTQFSRETFSSALELGRKALITLGMHPHQAQRAQLHFRRLDMRMLRELM

PVHTDTVQISRVREARRELEEIFQREMQKESRQLDGWDEFE

>lcl|NZ\_FO834906.1\_prot\_WP\_002920143.1\_388 [locus\_tag=BN49\_RS03130] [protein=YheV family putative metal-binding protein] [protein\_id=WP\_002920143.1] [location=424538..424738] [gbkey=CDS]

MAVRKRFIAGAKCPACQAQDSLAMWRENNVDVVECVKCGHQMREADKEAREHVRKEEQVIGIFHPD

>lcl|NZ\_FO834906.1\_prot\_WP\_002920140.1\_389 [gene=slyD] [locus\_tag=BN49\_RS03135] [protein=peptidylprolyl isomerase] [protein\_id=WP\_002920140.1] [location=424832..425419] [gbkey=CDS]

MKVAKDLVVSLAYQVRTEDGVLVDESPVSAPLDYLHGHGSLISGLENALDGHEVGDKFDVAVGANDAYGQ

YDENLVQRVPKDVFMGVDELQVGMRFLAETDQGPVPVEITEVEDDHVVVDGNHMLAGQNLKFNVEVVAIR

EATAEELEHGHVHGAHGHDHDHDHGHDGCCGGHGHDHGHDHGKGGCGGHGGCGCH

>lcl|NZ\_FO834906.1\_prot\_WP\_002920136.1\_390 [locus\_tag=BN49\_RS03140] [protein=SlyX family protein] [protein\_id=WP\_002920136.1] [location=complement(425478..425696)] [gbkey=CDS]

MHDSTLETRLAELESRLAFQEITIEDLNKTVTAHEIEMAKMREHMRLMIEKLKATQPSHIASQAEETPPP

HY

>lcl|NZ\_FO834906.1\_prot\_WP\_004150030.1\_391 [gene=fkpA] [locus\_tag=BN49\_RS03145] [protein=FKBP-type peptidyl-prolyl cis-trans isomerase] [protein\_id=WP\_004150030.1] [location=425919..426749] [gbkey=CDS]

MKSLFKVTLLATTMAVALNAPLTFAADTATKAAPAAESKSAFKNDDQKSAYALGASLGRYMENSLKEQEK

LGIKLDKSQLIAGVQDAFADKSKLSDQEIEQTLQAFETRVKTAAQQKMEKDATENEAKGKAFRDNFAKEK

GVKTSKTGLLYKVEKEGAGDAPKDSDTVVVNYKGTLIDGKEFDNSYTRGEPLSFRLDGVIPGWTEGLKNI

KKGGKIKLVIPPDLAYGKTGVPGIPANSTLVFDVELLDIKPAPKADAQPEAAGDAKAADAKADAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002920130.1\_392 [locus\_tag=BN49\_RS03150] [protein=transcriptional regulator] [protein\_id=WP\_002920130.1] [location=426918..427640] [gbkey=CDS]

MSRSLLTNETSELDLLDQRPFDQTDFDILKSYEAVVDGLAMLIGSHCEIVLHSLQDLKCSAIRIANGEHT

GRQIGSPITDLALRMLHDMTGADSSVSKCYFTRAKSGVLMKSVTIAIRNRDHRVIGLLCINMNLDVPFSQ

IMSTFIPPETPEVNSPVNFASSVDDLVAQTLEFTIEEVNADRSVSNNAKNRQIVLNLYEKGIFDIKDAIN

QVADRLNISKHTVYLYIRQFKSGDFQGLDK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528954.1\_393 [gene=tusD] [locus\_tag=BN49\_RS03155] [protein=sulfurtransferase complex subunit TusD] [protein\_id=WP\_016528954.1] [location=427640..428026] [gbkey=CDS]

MRFALTVTGPAYGTQQASSAWQFAQAVLQEGHELACVFFYREGVLNANQLTAPASDEFDLVRGWQSLHDE

HGVALHICVAAALRRGVTDEREAQQLALPGHNLQPGFSLSGLGALAEAALTCDRMVQF

>lcl|NZ\_FO834906.1\_prot\_WP\_004174061.1\_394 [gene=tusC] [locus\_tag=BN49\_RS03160] [protein=sulfurtransferase complex subunit TusC] [protein\_id=WP\_004174061.1] [location=428026..428385] [gbkey=CDS]

MKRVAFVFSSAPHGSAAGREGLDALLATSALTDDIGVFFVGDGVFQLLPEQRPGAVLARDYIATFKLLSL

YDIDQCWLCADSARERGLDPATPWVVDVECLAPDALRARLHEFDVILRF

>lcl|NZ\_FO834906.1\_prot\_WP\_002920119.1\_395 [gene=tusB] [locus\_tag=BN49\_RS03165] [protein=sulfurtransferase complex subunit TusB] [protein\_id=WP\_002920119.1] [location=428393..428680] [gbkey=CDS]

MLHTLSVSPWHADIAAMLRLMEHGDDLVLLSDGVTAAIADGRFLEILQSAPITLYVLQDDVDARGLAGQI

ADSVGRVSYTDFVRLTVKHAGQLAW

>lcl|NZ\_FO834906.1\_prot\_WP\_002920115.1\_396 [gene=rpsL] [locus\_tag=BN49\_RS03170] [protein=30S ribosomal protein S12] [protein\_id=WP\_002920115.1] [location=428805..429179] [gbkey=CDS]

MATINQLVRKPRARKVAKSNVPALEACPQKRGVCTRVYTTTPKKPNSALRKVCRVRLTNGFEVTSYIGGE

GHNLQEHSVILIRGGRVKDLPGVRYHTVRGALDCSGVKDRKQARSKYGVKRPKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002920113.1\_397 [gene=rpsG] [locus\_tag=BN49\_RS03175] [protein=30S ribosomal protein S7] [protein\_id=WP\_002920113.1] [location=429276..429746] [gbkey=CDS]

MPRRRVIGQRKILPDPKFGSELLAKFVNILMVDGKKSTAETIVYSALETLAQRSGKSELEAFEVALENVR

PTVEVKSRRVGGSTYQVPVEVRPVRRNALAMRWIVEAARKRGDKSMALRLANELTDAADNKGTAVKKRED

VHRMAEANKAFAHYRW

>lcl|NZ\_FO834906.1\_prot\_WP\_002920103.1\_398 [gene=fusA] [locus\_tag=BN49\_RS03180] [protein=elongation factor G] [protein\_id=WP\_002920103.1] [location=429843..431957] [gbkey=CDS]

MARTTPIARYRNIGISAHIDAGKTTTTERILFYTGVNHKIGEVHDGAATMDWMEQEQERGITITSAATTA

FWSGMAKQYEPHRVNIIDTPGHVDFTIEVERSMRVLDGAVMVYCAVGGVQPQSETVWRQANKYKVPRIAF

VNKMDRMGANFLKVVGQIKTRLGANPVPLQLAIGAEEGFTGVVDLVKMKAINWNDADQGVTFEYEDIPAD

MQDLADEWHQNLIESAAEASEELMEKYLGGEELTEEEIKKALRQRVLNNEIILVTCGSAFKNKGVQAMLD

AVIDYLPSPVDVPAINGILDDGKDTPAERHASDDEPFSALAFKIATDPFVGNLTFFRVYSGVVNSGDTVL

NSVKAARERFGRIVQMHANKREEIKEVRAGDIAAAIGLKDVTTGDTLCDPDAPIILERMEFPEPVISIAV

EPKTKADQEKMGLALGRLAKEDPSFRVWTDEESNQTIIAGMGELHLDIIVDRMKREFNVEANVGKPQVAY

REAIRAKVTDIEGKHAKQSGGRGQYGHVVIDMYPLEPGSNPKGYEFINDIKGGVIPGEYIPAVDKGIQEQ

LKAGPLAGYPVVDMGIRLHFGSYHDVDSSELAFKLAASIAFKEGFKKAKPVLLEPIMKVEVETPEENTGD

VIGDLSRRRGMLRGQESEVTGVKIHAEVPLSEMFGYATQLRSLTKGRASYTMEFLKYDDAPNNVAQAVIE

ARGK

>lcl|NZ\_FO834906.1\_prot\_399 [gene=tuf] [locus\_tag=BN49\_RS30830] [protein=elongation factor Tu] [pseudo=true] [location=432027..433212] [gbkey=CDS]

MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGSARAFDQIDNAPEEKARGITINTSHVEY

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VDDEELLELVEMEVRELLSQYDFPGDDSPIVRGSALKALEGDA\*WEAKIIYLAGHLDTSPPHPERAIDKP

FLLPIEDVFSISGRGTVGTGSCRARYHQSR\*RS\*NRWYQRNRENHLYWR\*NVPQTAGRRPCW\*ERRCSAA

WYQT\*RNRTWSGTG\*AGHHQPAHQVRI\*SVHPVQRRRRPSHSVLQRLPSAVLLPYY\*RDWHHRTAGRRRD

GNAGRQHQNGCYPDPPDRDGRRSAFRNP\*RRPYRWRGRCS\*SSGL

>lcl|NZ\_FO834906.1\_prot\_WP\_004152415.1\_400 [gene=bfd] [locus\_tag=BN49\_RS03190] [protein=bacterioferritin-associated ferredoxin] [protein\_id=WP\_004152415.1] [location=433393..433587] [gbkey=CDS]

MYVCLCNGVSDKKIRQVVRQFQPQSFQQLRKFVPVGNQCGKCVRAAREVMEDELTTMPEFKEIA

>lcl|NZ\_FO834906.1\_prot\_WP\_002919971.1\_401 [gene=bfr] [locus\_tag=BN49\_RS03195] [protein=bacterioferritin] [protein\_id=WP\_002919971.1] [location=433661..434137] [gbkey=CDS]

MKGDVKIISYLNKLLGNELVAINQYFLHARMFKNWGLMRLNDIEYHESIDEMKHADKYIERILFLEGIPN

LQDLGKLGIGEDVEEMLRSDLRLELEGAQNLREAIAYADSVHDYVSRDMMIEILADEEGHIDWLETELDL

IGKIGLQNYLQSQIKVSD

>lcl|NZ\_FO834906.1\_prot\_WP\_042941280.1\_402 [locus\_tag=BN49\_RS03200] [protein=A24 family peptidase] [protein\_id=WP\_042941280.1] [location=complement(434121..434606)] [gbkey=CDS]

MLAALPFLLCYSGLTVALCHQDLRHGLLPDRYTCPLLWSGLLFYLCLAPHQLHDAVRGAIAGYLSLAAIY

WLYRGIRGYEGLGYGDIKYLAALGAWHGWRLLPQLVLVASLLAGIAWAGAGLYASCGGRSKWRRSNPLPF

GPFLAAAGFWCGWQTLASLTL

>lcl|NZ\_FO834906.1\_prot\_WP\_001181005.1\_403 [gene=rpsJ] [locus\_tag=BN49\_RS03205] [protein=30S ribosomal protein S10] [protein\_id=WP\_001181005.1] [location=434990..435301] [gbkey=CDS]

MQNQRIRIRLKAFDHRLIDQSTAEIVETAKRTGAQVRGPIPLPTRKERFTVLISPHVNKDARDQYEIRTH

KRLVDIVEPTEKTVDALMRLDLAAGVDVQISLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002919796.1\_404 [gene=rplC] [locus\_tag=BN49\_RS03210] [protein=50S ribosomal protein L3] [protein\_id=WP\_002919796.1] [location=435334..435963] [gbkey=CDS]

MIGLVGKKVGMTRIFTEDGVSIPVTVIEVEANRVTQVKDLANDGYRAIQVTTGAKKANRVTKPEAGHFAK

AGVEAGRGLWEFRLADGEEFTVGQNISVELFADVKKVDVTGTSKGKGFAGTVKRWNFRTQDATHGNSLSH

RVPGSIGQNQTPGKVFKGKKMAGQLGNERVTVQSLDVVRVDAERNLLLVKGAVPGATGSDLIVKPAVKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002919794.1\_405 [gene=rplD] [locus\_tag=BN49\_RS03215] [protein=50S ribosomal protein L4] [protein\_id=WP\_002919794.1] [location=435974..436579] [gbkey=CDS]

MELVLKDAQSALTVSETTFGRDFNEALVHQVVVAYAAGARQGTRAQKTRAEITGSGKKPWRQKGTGRARS

GSIKSPIWRSGGVTFAARPQDHSQKVNKKMYRGALKSILSELVRQDRLIVVEKFSVEAPKTKLLAQKLKD

MALEDVLIITGELDENLFLAARNLHKVDVRDANGIDPVSLIAFDKVVMTADAVKQVEEMLA

>lcl|NZ\_FO834906.1\_prot\_WP\_000617546.1\_406 [gene=rplW] [locus\_tag=BN49\_RS03220] [protein=50S ribosomal protein L23] [protein\_id=WP\_000617546.1] [location=436576..436878] [gbkey=CDS]

MIREERLLKVLRAPHVSEKASTAMEKTNTIVLKVAKDATKAEIKAAVQKLFEVEVEVVNTLVVKGKVKRH

GQRIGRRSDWKKAYVTLKEGQNLDFVGGAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919786.1\_407 [gene=rplB] [locus\_tag=BN49\_RS03225] [protein=50S ribosomal protein L2] [protein\_id=WP\_002919786.1] [location=436896..437717] [gbkey=CDS]

MAVVKCKPTSPGRRHVVKVVNPELHKGKPFAPLLEKNSKSGGRNNNGRITTRHIGGGHKQAYRIVDFKRN

KDGIPAVVERLEYDPNRSANIALVLYKDGERRYILAPKGLKAGDQIQSGVDAAIKAGNTLPMRNIPVGST

VHNVEMKPGKGGQLARSAGTYVQIVARDGAYVTLRLRSGEMRKVEADCRATLGEVGNAEHMLRVLGKAGA

ARWRGVRPTVRGTAMNPVDHPHGGGEGRNFGKHPVSPWGLQTKGKKTRSNKRTDKFIVRRRSK

>lcl|NZ\_FO834906.1\_prot\_WP\_001138115.1\_408 [gene=rpsS] [locus\_tag=BN49\_RS03230] [protein=30S ribosomal protein S19] [protein\_id=WP\_001138115.1] [location=437734..438012] [gbkey=CDS]

MPRSLKKGPFIDLHLLKKVEKAVESGDKKPLRTWSRRSTIFPNMIGLTIAVHNGRQHVPVFVSDEMVGHK

LGEFAPTRTYRGHAADKKAKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002919773.1\_409 [gene=rplV] [locus\_tag=BN49\_RS03235] [protein=50S ribosomal protein L22] [protein\_id=WP\_002919773.1] [location=438027..438359] [gbkey=CDS]

METLAQHRHARSSAQKVRLVADLIRGKKVSQALDILTYTNKKAAVLVKKVLESAIANAEHNDGADIDDLK

VAKIFVDEGPSMKRIMPRAKGRADRILKRTSHITVVVSDR

>lcl|NZ\_FO834906.1\_prot\_WP\_002919766.1\_410 [gene=rpsC] [locus\_tag=BN49\_RS03240] [protein=30S ribosomal protein S3] [protein\_id=WP\_002919766.1] [location=438377..439075] [gbkey=CDS]

MGQKVHPNGIRLGIVKPWNSTWFANTKEFADNLDSDFKVRQFLTKELAKASVSRIVIERPAKSIRVTIHT

ARPGIVIGKKGEDVEKLRKVVADIAGVPAQINIAEVRKPELDAKLVADSITSQLERRVMFRRAMKRAVQN

AMRLGAKGIKVEVSGRLGGAEIARTEWYREGRVPLHTLRADIDYNTSEAHTTYGVIGVKVWIFKGEILGG

MAAVEQPEPAAQPKKQQRKGRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002919759.1\_411 [gene=rplP] [locus\_tag=BN49\_RS03245] [protein=50S ribosomal protein L16] [protein\_id=WP\_002919759.1] [location=439088..439498] [gbkey=CDS]

MLQPKRTKFRKVHKGRNRGLAQGTDVSFGTFGLKAVGRGRLTARQIEAARRAMTRAVKRQGKIWIRVFPD

KPITEKPLEVRMGKGKGNVEYWVALIQPGKVLYEMDGVPEELAREAFGLAAAKLPIKTTFVTKTVM

>lcl|NZ\_FO834906.1\_prot\_WP\_002919754.1\_412 [gene=rpmC] [locus\_tag=BN49\_RS03250] [protein=50S ribosomal protein L29] [protein\_id=WP\_002919754.1] [location=439498..439689] [gbkey=CDS]

MKAKELREKSVEELNAELLNLLREQFNLRMQAASGQLQQTHLLKQVRRDVARVKTLLTQKAGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002919751.1\_413 [gene=rpsQ] [locus\_tag=BN49\_RS03255] [protein=30S ribosomal protein S17] [protein\_id=WP\_002919751.1] [location=439689..439943] [gbkey=CDS]

MTDKIRTLQGRVVSDKMEKSIVVAIERMVKHPVYGKFIKRTTKLHVHDENNECGIGDKVEIRECRPLSKT

KSWTLVRVVEKAVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002919748.1\_414 [gene=rplN] [locus\_tag=BN49\_RS03260] [protein=50S ribosomal protein L14] [protein\_id=WP\_002919748.1] [location=440109..440480] [gbkey=CDS]

MIQEQTMLNVADNSGARRVMCIKVLGGSHRRYAGVGDIIKITIKEAIPRGKVKKGDVLKAVVVRTKKGVR

RPDGSVIRFDGNACVILNNNSEQPIGTRIFGPVTRELRTEKFMKIISLAPEVL

>lcl|NZ\_FO834906.1\_prot\_WP\_000729185.1\_415 [gene=rplX] [locus\_tag=BN49\_RS03265] [protein=50S ribosomal protein L24] [protein\_id=WP\_000729185.1] [location=440491..440805] [gbkey=CDS]

MAAKIRRDDEVIVLTGKDKGKRGKVKNVLSSGKVIVEGINLVKKHQKPVPALNQPGGIVEKEAAIQVSNV

AIFNAATGKADRVGFRFEDGKKVRFFKSNSETIK

>lcl|NZ\_FO834906.1\_prot\_WP\_001096200.1\_416 [gene=rplE] [locus\_tag=BN49\_RS03270] [protein=50S ribosomal protein L5] [protein\_id=WP\_001096200.1] [location=440820..441359] [gbkey=CDS]

MAKLHDYYKDEVVKKLMTEFNYNSVMQVPRVEKITLNMGVGEAIADKKLLDNAAADLAAISGQKPLITKA

RKSVAGFKIRQGYPIGCKVTLRGERMWEFFERLITIAVPRIRDFRGLSAKSFDGRGNYSMGVREQIIFPE

IDYDKVDRVRGLDITITTTAKSDEEGRALLAAFDFPFRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002919667.1\_417 [gene=rpsN] [locus\_tag=BN49\_RS03275] [protein=30S ribosomal protein S14] [protein\_id=WP\_002919667.1] [location=441374..441679] [gbkey=CDS]

MAKQSMKAREVKRVALADKFFAKRAELKAIISDVNATDEDRWNAVLKLQTLPRDSSPSRQRNRCRQTGRP

HGFLRKFGLSRIKVREAAMRGEIPGLKKASW

>lcl|NZ\_FO834906.1\_prot\_WP\_002919665.1\_418 [gene=rpsH] [locus\_tag=BN49\_RS03280] [protein=30S ribosomal protein S8] [protein\_id=WP\_002919665.1] [location=441713..442105] [gbkey=CDS]

MSMQDPIADMLTRIRNGQAANKAAVTMPSSKLKVAIANVLKEEGFIEDFKVEGDTKPELELTLKYFQGKA

VVESIQRVSRPGLRIYKKKDELPKVMAGLGIAVVSTSKGVMTDRAARQAGLGGEIICYVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002919662.1\_419 [gene=rplF] [locus\_tag=BN49\_RS03285] [protein=50S ribosomal protein L6] [protein\_id=WP\_002919662.1] [location=442118..442651] [gbkey=CDS]

MSRVAKAPVVVPAGVDVKINGQVITIKGKNGELTRTLNDAVEVKHADNALTFGPRDGYADGWAQAGTARA

LLNSMVIGVTEGFTKKLQLVGVGYRAAVKGNVVNLALGFSHPVDHQLPAGITAECPTQTEIVLKGADKQV

IGQVAADLRAYRRPEPYKGKGVRYADEVVRTKEAKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_000358960.1\_420 [gene=rplR] [locus\_tag=BN49\_RS03290] [protein=50S ribosomal protein L18] [protein\_id=WP\_000358960.1] [location=442661..443014] [gbkey=CDS]

MDKKSARIRRATRARRKLQELGATRLVVHRTPRHIYAQVIAPNGSEVLVAASTVEKAIAEQLKYTGNKDA

AAAVGKAVAERALEKGIKDVSFDRSGFQYHGRVQALADAAREAGLQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002919545.1\_421 [gene=rpsE] [locus\_tag=BN49\_RS03295] [protein=30S ribosomal protein S5] [protein\_id=WP\_002919545.1] [location=443029..443532] [gbkey=CDS]

MAHIEKQAGELQEKLIAVNRVSKTVKGGRIFSFTALTVVGDGNGRVGFGYGKAREVPAAIQKAMEKARRN

MINVALNHGTLQHPVKGTHTGSRVFMQPASEGTGIIAGGAMRAVLEVAGVRNVLAKAYGSTNPINVVRAT

IDGLENMKSPDMVAAKRGKSVEEILGK

>lcl|NZ\_FO834906.1\_prot\_WP\_001140434.1\_422 [gene=rpmD] [locus\_tag=BN49\_RS03300] [protein=50S ribosomal protein L30] [protein\_id=WP\_001140434.1] [location=443536..443715] [gbkey=CDS]

MAKTIKITQTRSAIGRLPKHKATLLGLGLRRIGHTVEREDTPAVRGMVNAVSFMVKVEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919516.1\_423 [gene=rplO] [locus\_tag=BN49\_RS03305] [protein=50S ribosomal protein L15] [protein\_id=WP\_002919516.1] [location=443719..444153] [gbkey=CDS]

MRLNTLSPAEGSKKAGKRLGRGIGSGLGKTGGRGHKGQKSRSGGGVRRGFEGGQMPLYRRLPKFGFTSRK

AMITAEIRLSDLAHVEGDVVDLNALKAANIIGVQIEFAKVILSGEVTRPVTVRGLRVTKGARAAIEAAGG

KIEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919515.1\_424 [gene=secY] [locus\_tag=BN49\_RS03310] [protein=preprotein translocase subunit SecY] [protein\_id=WP\_002919515.1] [location=444161..445492] [gbkey=CDS]

MAKQPGLDFQSAKGGLGELKRRLLFVVGALIVFRIGSFIPIPGIDAAVLAKLLEQQRGTIIEMFNMFSGG

ALSRASIFALGIMPYISASIIVQLLTVVYQPLAELKKEGESGRRKISQYTRYGTLVLAIFQSIGIATGLP

NMPGMQGLVINPGFAFYFTAVVSLVTGTMFLMWLGEQITERGIGNGISIIIFAGIVAGLPPAIAHTIEQA

RQGDLHFLLLLLVAVLVFAVTFFVVFVERGQRRIVVNYAKRQQGRRVYAAQSTHLPLKVNMAGVIPAIFA

SSIILFPATITSWFGGGTGWNWLTTISLYLQPGQPLYVLLYASAIIFFCFFYTALVFNPRETADNLKKSG

AFVPGIRPGEQTAKYIDKVMTRLTLVGALYITFICLIPEFMRDAMKVPFYFGGTSLLIVVVVIMDFMAQV

QTLMMSSQYESALKKANLKGYGR

>lcl|NZ\_FO834906.1\_prot\_WP\_000868187.1\_425 [gene=rpmJ] [locus\_tag=BN49\_RS28570] [protein=50S ribosomal protein L36] [protein\_id=WP\_000868187.1] [location=445526..445642] [gbkey=CDS]

MKVRASVKKLCRNCKIVKRDGVIRVICSAEPKHKQRQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002919259.1\_426 [gene=rpsM] [locus\_tag=BN49\_RS03315] [protein=30S ribosomal protein S13] [protein\_id=WP\_002919259.1] [location=445789..446145] [gbkey=CDS]

MARIAGINIPDHKHTVIALTAIFGIGKTRSKAICAETGIAENVKISELSEEQIDILREAVGKFVVEGDLR

REITLSIKRLMDLGCYRGLRHRRGLPVRGQRTKTNARTRKGPRKPIKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002919257.1\_427 [gene=rpsK] [locus\_tag=BN49\_RS03320] [protein=30S ribosomal protein S11] [protein\_id=WP\_002919257.1] [location=446162..446551] [gbkey=CDS]

MAKAPIRARKRVRKQVSDGVAHIHASFNNTIVTITDRQGNALGWATAGGSGFRGSRKSTPFAAQVAAERC

AEAVKEYGIKNLEVMVKGPGPGRESTIRALNAAGFRITNITDVTPIPHNGCRPPKKRRV

>lcl|NZ\_FO834906.1\_prot\_WP\_002919224.1\_428 [gene=rpsD] [locus\_tag=BN49\_RS03325] [protein=30S ribosomal protein S4] [protein\_id=WP\_002919224.1] [location=446585..447205] [gbkey=CDS]

MARYLGPKLKLSRREGTDLFLKSGVRAIDTKCKIEQAPGQHGARKPRLSDYGVQLREKQKVRRMYGVLER

QFRNYYKEAARLKGNTGENLLALLEGRLDNVVYRMGFGATRAEARQLVSHKAIMVNGRVVNIASYQVKAN

DVVSIREKAKKQSRVKAALELAEQREKPTWLEVDAGKMEGTFKRQPERSDLSADINEHLIVELYSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002919219.1\_429 [gene=rpoA] [locus\_tag=BN49\_RS03330] [protein=DNA-directed RNA polymerase subunit alpha] [protein\_id=WP\_002919219.1] [location=447231..448220] [gbkey=CDS]

MQGSVTEFLKPRLVDIEQVSSTHAKVTLEPLERGFGHTLGNALRRILLSSMPGCAVTEVEIDGVLHEYST

KEGVQEDILEILLNLKGLAVRVQGKDEVILTLNKSGIGPVTAADITHDGDVEIVKPQHVICHLTDENAAI

SMRIKVQRGRGYVPASARIHSEEDERPIGRLLVDACYSPVERIAYNVEAARVEQRTDLDKLVIEMETNGT

IDPEEAIRRAATILAEQLEAFVDLRDVRQPEVKEEKPEFDPILLRPVDDLELTVRSANCLKAEAIHYIGD

LVQRTEVELLKTPNLGKKSLTEIKDVLASRGLSLGMRLENWPPASIADE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919206.1\_430 [gene=rplQ] [locus\_tag=BN49\_RS03335] [protein=50S ribosomal protein L17] [protein\_id=WP\_002919206.1] [location=448261..448647] [gbkey=CDS]

MRHRKSGRQLNRNSSHRQAMFRNMAGSLVRHEIIKTTLPKAKELRRVVEPLITLAKTDSVANRRLAFART

RDNEIVAKLFNELGPRFASRAGGYTRILKCGFRAGDNAPMAYIELVDRAEPKAEAAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919204.1\_431 [locus\_tag=BN49\_RS03340] [protein=DUF1992 domain-containing protein] [protein\_id=WP\_002919204.1] [location=448756..449124] [gbkey=CDS]

MWLLDQWAERHILDAQTKGEFDNLPGSGEPLTLDDDSHVPAELRAGYRLLKNAGCLPPELEQRKEALALA

DLLNGVRQDDPRHAELSKRLALLELKLRQAGLNTDFLRGEYADALLQKINQE

>lcl|NZ\_FO834906.1\_prot\_WP\_004185894.1\_432 [gene=zntR] [locus\_tag=BN49\_RS03345] [protein=Zn(2+)-responsive transcriptional regulator] [protein\_id=WP\_004185894.1] [location=449127..449552] [gbkey=CDS]

MYRIGELAKLADVTPDTIRYYEKQQMMDHDIRTEGGFRLYSDNDLQRLRFIRYARQLGFTLEAIRELLSI

RIDPEHHTCQESKGIVQARLSEVEARIKELQTMRRSLQRLNDACCGTAHSSVYCSILEALEQGASNGNGG

R

>lcl|NZ\_FO834906.1\_prot\_WP\_016530588.1\_433 [locus\_tag=BN49\_RS28575] [protein=alternative ribosome-rescue factor A] [protein\_id=WP\_016530588.1] [location=449610..449888] [gbkey=CDS]

MSRYQHTKGQIKDNAIEALLHDPLFRQRVEKNKKGKGSYQRKDKHAGRVDREASGKQANRFFTTGLLLSL

LIKNGCSVLSADREFRSAELLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004145325.1\_434 [gene=mscL] [locus\_tag=BN49\_RS03350] [protein=large-conductance mechanosensitive channel protein MscL] [protein\_id=WP\_004145325.1] [location=complement(449824..450237)] [gbkey=CDS]

MSFLKEFREFAMRGNVVDLAVGVIIGAAFGKIVSSLVADIIMPPLGLLIGGIDFKQFAVTLRDAQGDVPA

VVMHYGVFIQNVFDFIIVAFAIFMAIKLMNKLNRKKEEAPAAPPAPSKEEVLLSEIRDLLKEQNNRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002919153.1\_435 [gene=trkA] [locus\_tag=BN49\_RS03355] [protein=Trk system potassium transporter TrkA] [protein\_id=WP\_002919153.1] [location=complement(450378..451754)] [gbkey=CDS]

MKIIILGAGQVGGTLAENLVGENNDITLVDTNGDRLRSLQDKFDLRVVQGHGSHPRVLREAGADDADMLV

AVTSSDETNMVACQVAYSLFNTPNRIARIRAPDYVRDAEKLFNSEAVPIDHLIAPEQLVIDNIHRLIEYP

GALQVVNFAEGKVSLAVVKAYYGGPLVGNALSTMREHMPHIDTRVAAIFRHDRPIRPQGSTIVEAGDEVF

FIAASQHIRAVMSELQRLEKPYKRIMLVGGGNIGAGLAHKLEKDYSVKLIERNQQRAAELAEKLQHTIVF

YGDASDQELLAEEHIDQVDLFIAVTNDDEANIMSAMLAKRMGAKKVMVLIQRRAYVDLVQGSVIDIAISP

QQATISALLSHVRKADIVGVSSLRRGVAEAIEAVAHGDESTSRVVGRSIDEIKLPPGTIIGAVVRGNDVM

IANNNLRIEQGDHVIMFLTDKKFISDVERLFQPSPFFL

>lcl|NZ\_FO834906.1\_prot\_436 [gene=rsmB] [locus\_tag=BN49\_RS03360] [protein=16S rRNA (cytosine(967)-C(5))-methyltransferase RsmB] [pseudo=true] [location=complement(451768..453063)] [gbkey=CDS]

MKKNINLRSLAAQAIEQVVEKGQSLSNVLPPLQQKVSDKDKALLQELCFGVLRTLSQLEWLISKLMARPM

TGKQRTVHFLIMVGLYQLLYTRIPPHAALAETVEGAVAIKRPQLKGLINGVLRQFQRQQEALLAEFAEHE

NRYLHPKWLLKRLQQAWPQQWQEIVEANNQRPPMWLRVNRNHHSRDEWLALLNETGLEGFTHPDYPDAVR

LATPAPVHALPGFAEGWVTVQDASAQGCMRYLQPENGERILDLCAAPGGKTTHILEVAPQAQVMAVDIDE

QRLSRVYDNLKRLGMKAEVKQGDGRFPEQWCGNEQFDRILLDAPCSATGVIRRHPDIKWLRRDRDIAELA

QLQAEILNAT\*THLKPGGTLVYATCSILPEENSQQIAAFLARTPDAELHATGTPASPGQQNLPGVEEGDG

FFYAKLIKRRN

>lcl|NZ\_FO834906.1\_prot\_WP\_004150007.1\_437 [gene=fmt] [locus\_tag=BN49\_RS03365] [protein=methionyl-tRNA formyltransferase] [protein\_id=WP\_004150007.1] [location=complement(453116..454063)] [gbkey=CDS]

MSQSLRIIFAGTPDFAARHLDALLSSEHQVVGVFTQPDRPAGRGKKLMPSPVKVLAEAHNLPVFQPSSLR

PQDNQRLVADLGADIMVVVAYGLILPKAVLEMPRLGCINVHGSLLPRWRGAAPIQRSLWAGDSETGVTIM

QMDVGLDTGDMLYKLSCPITAEDTSGSLYDKLAELGPQGLLATLAQLANGTARPEVQDESLVCHAEKLSK

EEARIDWSLSAAQLERCIRAFNPWPMSWLEIDGQPVKVWRASVIAEAAHAEPGTIVAATKQGIQVATGDG

ILSLESLQPAGKKAMSAQDLLNSRREWFIPGTRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150006.1\_438 [gene=def] [locus\_tag=BN49\_RS03370] [protein=peptide deformylase] [protein\_id=WP\_004150006.1] [location=complement(454078..454587)] [gbkey=CDS]

MAVLQVLHIPDERLRKVAEPVKEVNAEIQRIVDDMFDTMYAEEGIGLAATQVDIHQRIIVIDVSENREEQ

LVLINPEMLEKDGETGIEEGCLSIPEQRALVPRAEKVKIRALDRNGKPFELEADGLLAICIQHEMDHLVG

KLFIDYLSPLKQQRIRQKVEKLDRLRSRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530584.1\_439 [gene=dprA] [locus\_tag=BN49\_RS03375] [protein=DNA-protecting protein DprA] [protein\_id=WP\_016530584.1] [location=454716..455840] [gbkey=CDS]

MTPDEIWLRLMKVSSLYGDRMVEIAQRLCAAASVDREALHAVGMTAAQAKLFFRLDEHELDETRRWLEQP

DHHLLRGDDPRYPLRLKAIADYPGALLVSGGLALLHSAQLAVIGSRSHSWYGACWGKLFSETLAHKGITI

TSGLALGIDGVAHRGALAAEGKTIAVLGNGLSQVYPRRHATLARQIIDNGGTLVSEFPLVTPPLPAHFPR

RNRIISGLSLGVLVIEAALRSGSLVTVRCALEQGRDVFALPGPIGNPGSEGPHWLIKQGAVPVTSPEDIV

EYWHNELAWLTDTSDSINICVDQPSVALPFPELLANVGDEVTPVDVVAERAGQSVPVTVAQLLELELAGW

IAAVPGGYVRLRRASHVRRTHVFV

>lcl|NZ\_FO834906.1\_prot\_WP\_002919137.1\_440 [gene=smg] [locus\_tag=BN49\_RS03380] [protein=DUF494 family protein Smg] [protein\_id=WP\_002919137.1] [location=455812..456285] [gbkey=CDS]

MFDVLMYLFETYIHSEAEMRVDQDKLTRDLTDAGFEREDIYNALMWLEKLADYQEGLVEPMQLASDPLSL

RVYTEEECQRLDASCRGFLLFLEQIQVLNLETREMVIERVLALDTAEFELEDLKWVILMVLFNIPGCENA

YQQMEELLFEVNEGMLH

>lcl|NZ\_FO834906.1\_prot\_WP\_004145330.1\_441 [locus\_tag=BN49\_RS03385] [protein=topoisomerase DNA-binding C4 zinc finger domain-containing protein] [protein\_id=WP\_004145330.1] [location=456312..456854] [gbkey=CDS]

MTKSALFSVRKNEPCPQCGAELVIRSGKHGPFLGCSHYPDCDYIRPLKSQADGHIVKVLEGQECPSCGAV

MVLRQGRFGMFIGCSRYPECEHTELIDKPDETAIACPQCGQGHLVQRRSRFGKTFHSCDRYPDCQFVINF

KPVAGECPECHYPLLIEKKTAQGLRRFCASKQCGKPIPAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919132.1\_442 [gene=tsaC] [locus\_tag=BN49\_RS03390] [protein=L-threonylcarbamoyladenylate synthase type 1 TsaC] [protein\_id=WP\_002919132.1] [location=456859..457431] [gbkey=CDS]

MNNNLPSEAVAHAVAVLKNEHVIAYPTEAVFGVGCDPDSETAVMRLLELKQRPVEKGLILIAASFEQLKP

YIDDSRLSDSQREAIFSCWPGPVTFVFPARPETPRWLTGRFDSLAVRVTNHPLVIELCEAYGKPLVSTSA

NLTGQPPCRTTAEVHAQFGDSFPVVDGATGGRQNPSEIRDALTGELFRQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002919126.1\_443 [gene=aroE] [locus\_tag=BN49\_RS03395] [protein=shikimate dehydrogenase] [protein\_id=WP\_002919126.1] [location=457435..458253] [gbkey=CDS]

METYAVFGNPIAHSKSPAIHQLFARQLGITHPYGRVLAPLDDFVSSLNQFFAEGGKGANVTVPFKEEAFA

RADELTERAALAGAVNTLKRLEDGRLLGDNTDGIGLLSDLERLGFIKPRQRILLVGAGGASRGVLLPLLS

LGCAVTIVNRTYSRARELATLFAHTGSVSAREMDTLSGETFDLIVNATSSGIDGDVPAIPASIVNADVYC

YDMFYQKGPTPFLHWCQQYGAVHCADGLGMLVAQAAHAVLLWHGVLPAIAPVIETLQQELNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002919125.1\_444 [locus\_tag=BN49\_RS03400] [protein=DUF1488 domain-containing protein] [protein\_id=WP\_002919125.1] [location=458250..458507] [gbkey=CDS]

MNQAIQFPDRESWDAERQGVVFPALVNGMQLTCAISGQILQQRFGAEGPAQWLAAFQEHRWDLEEEAEAL

IRDGQEDAQGWIWLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002919123.1\_445 [locus\_tag=BN49\_RS03405] [protein=gamma carbonic anhydrase family protein] [protein\_id=WP\_002919123.1] [location=complement(458483..459037)] [gbkey=CDS]

MSAQLRPYKAFFPQIGLRVMIDASSVVIGDVRIADDVSVWPLVAIRGDVNYVSIGQRSNIQDGSVLHVTH

KSSYKPEGNPLIIGEDVTVGHKVMLHGCTIGNRVLVGMGSILLDGVVVGDDVMIGAGSLVPQNKQLESGY

LYFGNPVKQIRPLTEAEREGLKYSANNYVKWKNEYLDQDNQIQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002919103.1\_446 [locus\_tag=BN49\_RS03435] [protein=membrane protein] [protein\_id=WP\_002919103.1] [location=complement(465017..465238)] [gbkey=CDS]

MKKYLIVALLASLLAGCAHDSPCVPVYDSQGRLVHTNTCMKGTTEDNWETAGAIAGGAAAVAGLTLGIVA

LTR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529116.1\_447 [locus\_tag=BN49\_RS03440] [protein=efflux RND transporter permease subunit] [protein\_id=WP\_016529116.1] [location=complement(465531..468641)] [gbkey=CDS]

MSKFFIHRPVFAWVLAIIMMIAGGLAILQLPIAQYPTIAPPAVAISATYPGADAQTVQDTVTQVIEQNMN

GIDNLMYMSSTSDSAGSVTITLTFKSGTDPDIAQVQVQNKLQLATPLLPQEVQQQGISVEKSSSSFLLVA

GFISDNPTTTQDDISDYVASNVKDPISRLNGVGDVQLFGAQYAMRVWLDGNLLNKYNLTPVDVINALQVQ

NDQIAAGQLGGTPALKGQQLNASIIAQTRLKDPQEFGKVTLRVNADGSVVHLKDVARIELGGENYNVVAR

INGKPASGLGIKLATGANALDTATAIKAKLAELQPYFPQGMKVVYPYDTTPFVKISIHEVVKTLFEAIIL

VFLVMYLFLQNMRATLIPTIAVPVVLLGTFAVLSMFGYSINTLPMFGMVLAIGLLVDDAIVVVENVERVM

VEEKLSPKEATEKSMSQIQGALVGIAMVLSAVFVPMAFFGGSTGAIYRQFSITIVSAMALSVLVALVLTP

ALCATLLKPASAEHHEKKGFFGWFNARFDQSVNHYTNSVSGILRGTGRYLVIYLLIVVGMAVLFMRLPTS

FLPDEDQGVFLTMIQLPSGATQERTQKVLDTVTDYYLHNEKANVESVFTVNGFSFSGQGQNSGMAFVSLK

PWEARSGDKNSVESIIKRATVAFSQIKDAMVFPFNMPAIIELGTATGFDFELIDQGGLGHTALTQARNQL

LGMVKQHPDQLVRVRPNGLEDTPQFKLDVDQEKAQALGVSLSDINETISAALGGYYVNDFIDRGRVKKVY

VQADAHFRMLPSDINNMYVRSANGEMVPFSAFVTSRWIYGSPRLERYNGLPSMEILGEASPGKSTGEAMA

LMETLASKLPSGIGYDWTGMSYQERLSGNQAPALYAISLIVVFLCLAALYESWSIPFSVMLVVPLGVIGA

LLAATLRGLNNDVYFQVGLLTTIGLSAKNAILIVEFAKDLMEKEGKGIIEATLEASRMRLRPILMTSLAF

ILGVMPLVISHGAGSGAQNAVGTGVMGGMLTATLLAIFFVPVFFVVVRRRFTRHAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002919101.1\_448 [locus\_tag=BN49\_RS03445] [protein=efflux RND transporter periplasmic adaptor subunit] [protein\_id=WP\_002919101.1] [location=complement(468654..469793)] [gbkey=CDS]

MTTHARVTLLSGLIISALLLTGCDNSDNQQPHAQAPQVTVHVVNSAPLSVTTELPGRTSAFRVAEVRPQV

SGIILKRNFVEGSDVEAGQSLYQIDPATYQAAWNSAKGDEAKAEAAAAIAHLTVKRYVPLLGTKYISQQE

YDQAVATARQADADVIATKAAVETARINLAYTKVTSPISGRIGKSSVTEGALVTNGQSDALATVQQLDPI

YVDVTESSNDFMRLKQESLQRGGDTKSVELVMENGQAYPLKGSLQFSDVTVDESTGSITLRAIFPNPQHV

LLPGMFVRARIDEGVDPQAILVPQQGVTRTPRGDASVMLVNDKNQVETREVVATQAVGDKWLITSGLKPG

DKVIVSGLQKVRPGVTVKAEAERAAPAVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530888.1\_449 [gene=envR] [locus\_tag=BN49\_RS03450] [protein=acrEF/envCD operon transcriptional regulator] [protein\_id=WP\_016530888.1] [location=470171..470824] [gbkey=CDS]

MARKTREEAQRTRQLLIESAIQQFALRGVTNTTLTDIADAAGVTRGAVYWHFASKTELFNEMWQQQPPLR

DLIQPSQAIEYEQEPLNALRERFIAGLRYIAANPRQRALMQILYQRCEFSSDMLSEYEIRQRIGFNYSLI

GGILQCCVRNNILPAETNIEMILIVLHSAFSGLIKNWLLDPQRFDLYQQAPALVDNIMAVVCAARLSGGS

ALRLVNQ

>lcl|NZ\_FO834906.1\_prot\_WP\_000462905.1\_450 [gene=fis] [locus\_tag=BN49\_RS03455] [protein=DNA-binding transcriptional regulator Fis] [protein\_id=WP\_000462905.1] [location=complement(470909..471205)] [gbkey=CDS]

MFEQRVNSDVLTVSTVNSQDQVTQKPLRDSVKQALKNYFAQLNGQDVNDLYELVLAEVEQPLLDMVMQYT

RGNQTRAALMMGINRGTLRKKLKKYGMN

>lcl|NZ\_FO834906.1\_prot\_WP\_004144972.1\_451 [gene=dusB] [locus\_tag=BN49\_RS03460] [protein=tRNA dihydrouridine synthase DusB] [protein\_id=WP\_004144972.1] [location=complement(471230..472195)] [gbkey=CDS]

MRIGHHQLRNRLIAAPMAGITDRPFRTLCYEMGAGLTVSEMMSSNPQVWESDKSRLRMVHIDEPGIRTVQ

IAGSVPEEMAAAARINVESGAQIIDINMGCPAKKVNRKLAGSALLQYPDQVKSILTAVVNAVDVPVTLKI

RTGWEPEHRNCVEIAQLAEECGIQALTIHGRTRACLFNGDAEYDSIRAVKQKVSIPIIANGDITDPLKAR

AVLDYTGADALMIGRAAQGRPWIFREIQHYLDTGELLPPLPLAEVKRLLCAHVRELHDFYGQAKGYRIAR

KHVSWYLQEHAPDDQFRRTFNAIEDASEQLEALEAYFENFA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144971.1\_452 [gene=prmA] [locus\_tag=BN49\_RS03465] [protein=50S ribosomal protein L11 methyltransferase] [protein\_id=WP\_004144971.1] [location=complement(472553..473434)] [gbkey=CDS]

MPWIQLKLNTTGANAEDLSDALMEAGSVSITFQDTHDTPVFEPLPGETRLWGDTDVIGLFDAETDMKAVV

AQLEQHPLLGAGFAHKIEQLEDKDWEREWMDNFHPMRFGERLWICPSWRDVPDENAVNVMLDPGLAFGTG

THPTTSLCLQWLDGLDLNGKTVIDFGCGSGILAIAALKLGAAKAIGIDIDPQAIQASRDNAQRNGVSERL

ELYLPQDQPESMKADVVVANILAGPLRELAPLISVLPVSGGLLGLSGILASQAESVCEAYADLFTLDPVV

EKEEWCRITGRKN

>lcl|NZ\_FO834906.1\_prot\_WP\_004181435.1\_453 [gene=panF] [locus\_tag=BN49\_RS03470] [protein=sodium/pantothenate symporter] [protein\_id=WP\_004181435.1] [location=complement(473446..474897)] [gbkey=CDS]

MQFEVIIPLIAYLVVVFGLSLYAMRKRASGSFLNEYFLGSRSMGGFVLAMTLTATYISASSFIGGPGAAY

KYGLGWVLLAMIQLPAIWLSLGVLGKKFAILARRYNAVTLNDMLFARYQSRLLVWLASLSLLVAFVGAMT

VQFIGGARLLETAAGIPYDTGLLIFGVSIALYTAYGGFRASVLNDTMQGMVMLIGTIVLLVGVIHAAGGV

GHAVETLQSIDVKLVSPQGAEDILSPTFMASFWVLVCFGVIGLPHTAVRCISYKDSKAVHRGIIIGTIVV

AILMFGMHLAGALGRAVIPDLTVPDLVIPTLMVKVLPPFAAGIFLAAPMAAIMSTINAQLLQSSATIIKD

LYLNWRPDQATNEKRLKRMSAGITLLLGVLLLLAAWRPPEMIIWLNLLAFGGLEAVFLWPLVLGLYWERA

NAAGALSAMIVGGVLYAVLATLKVQFLGFHPIVPALLLSLLAFVAGNRFGRPAPQPPILTTDK

>lcl|NZ\_FO834906.1\_prot\_WP\_002918740.1\_454 [locus\_tag=BN49\_RS03475] [protein=YhdT family protein] [protein\_id=WP\_002918740.1] [location=complement(474887..475129)] [gbkey=CDS]

MDKRFVQAHKEARWALWLTLLYLAAWLAAAYLPGVAIGFTGLPHWFEMACLLVPLLFILLCWAMVKLIFR

DISLEDDDAV

>lcl|NZ\_FO834906.1\_prot\_WP\_002918738.1\_455 [gene=accC] [locus\_tag=BN49\_RS03480] [protein=acetyl-CoA carboxylase biotin carboxylase subunit] [protein\_id=WP\_002918738.1] [location=complement(475240..476589)] [gbkey=CDS]

MLDKIVIANRGEIALRILRACKELGIKTVAVHSTADRDLKHVLLADETVCIGPAPSVKSYLNIPAIISAA

EITGAVAIHPGYGFLSENANFAEQVERSGFIFIGPKADTIRLMGDKVSAITAMKKAGVPTVPGSDGPLGD

DMDANRAHAKRIGYPVIIKASGGGGGRGMRVVRSDAELAQSISMTKAEAKAAFNNDMVYMEKYLENPRHI

EIQVLADGQGNAIYLAERDCSMQRRHQKVVEEAPAPGITPELRRYIGERCAKACVDIGYRGAGTFEFLFE

NGEFYFIEMNTRIQVEHPVTEMITGVDLIKEQLRIAAGQPLSIKQDEVVVRGHAVECRINAEDPNTFLPS

PGKITRFHAPGGFGVRWESHIYAGYTVPPYYDSMIGKLICYGESRDVAIARMKNALQELIIDGIKTNVDL

QMRIMSDENFQHGGTNIHYLEKKLGLQEK

>lcl|NZ\_FO834906.1\_prot\_WP\_002918736.1\_456 [gene=accB] [locus\_tag=BN49\_RS03485] [protein=acetyl-CoA carboxylase biotin carboxyl carrier protein] [protein\_id=WP\_002918736.1] [location=complement(476600..477067)] [gbkey=CDS]

MDIRKIKKLIELVEESGISELEISEGEESVRISRSAPAASYPVMQQAYAAPMMQPQAPAAATAAPAAAAE

APAKAEISGHIVRSPMVGTFYRTPSPDAKAFVEVGQKVNVGDTLCIVEAMKMMNQIEADKAGVVKAILIE

SGQPVEFDEPLVVIE

>lcl|NZ\_FO834906.1\_prot\_WP\_004174104.1\_457 [gene=aroQ] [locus\_tag=BN49\_RS03490] [protein=type II 3-dehydroquinate dehydratase] [protein\_id=WP\_004174104.1] [location=complement(477090..477542)] [gbkey=CDS]

MAVKFHILLLNGPNINMLGTREPEKYGPLTLAEIVNRLTSEAAALNVSLDHLQSNAEHALIDRIHQAKDN

VDYILINPAAFTHTSVAIRDALLAVNIPFIEIHLSNVHAREPFRQHSYLSDVAAGVICGLGADGYSYALQ

TAVKRLSQSH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529298.1\_458 [gene=msrQ] [locus\_tag=BN49\_RS03495] [protein=protein-methionine-sulfoxide reductase heme-binding subunit MsrQ] [protein\_id=WP\_016529298.1] [location=complement(477766..478374)] [gbkey=CDS]

MRFTVKQIVWLKVLLHLAGFLPLVWLFWAGHQGYLSADPAKDIQHFTGRMALKFLLATLLVSPLARYAKQ

PLSIRVRRLLGLWCFAWATLHLSSYTLLELGINNLALLGSEIITRPYLTLGMISWAILLALAVTSTQAMQ

RKLGRRWQLLHNFVYLVAILAPIHYLWSVKIVSPQPVIYALLAAGLLTWRYKKFRQWWRSIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004211677.1\_459 [gene=msrP] [locus\_tag=BN49\_RS03500] [protein=protein-methionine-sulfoxide reductase catalytic subunit MsrP] [protein\_id=WP\_004211677.1] [location=complement(478374..479375)] [gbkey=CDS]

MKRKKLTEADVTAESVFMLKRRQVLKMLGISATALSLPAAAQADLLDWFKGNDRPPAPAGKALEFAKPAE

WQANLTLTPEDKVAGYNNFYEFGLDKADPAANAGSLRTDPWTLTIGGEVAKPLTLDHDDLTKRFPLEERI

YRMRCVEAWSMVVPWVGFPLHKLLALVEPTSSARYVAFKTLYAPDQMPGQKDRFIGGGLAYPYVEGLRLD

EAMHPLTLLTVGVYGKALPPQNGAPVRLTVPWKYGFKGIKSIVSIELTRERPPTTWNLAAPDEYGFFANV

NPHVDHPRWSQASERFIGAGGVLDVKRQPTLLFNGYADEVASLYRGMNLRENF

>lcl|NZ\_FO834906.1\_prot\_WP\_004144963.1\_460 [locus\_tag=BN49\_RS03505] [protein=hypothetical protein] [protein\_id=WP\_004144963.1] [location=479604..479795] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918686.1\_461 [gene=csrD] [locus\_tag=BN49\_RS03510] [protein=RNase E specificity factor CsrD] [protein\_id=WP\_002918686.1] [location=479875..481815] [gbkey=CDS]

MRLTTKFSAFITLLTSLTIFVTLIGASLSFYNGIENKVENRVQAVATMLDNRLITTSFDKLEPQLDELMT

PIEIVHIDFMLNGKPLYSHSRPDSYRPLGSHEQFREITVQSLKHPGITLHLVYVDPMVNYFRSLSITAPL

SISIGFMVVIIFFAVRWIRRQLAGQELLELRSTRILSGERGPQVRGSVYEWPASTSSALDMLLSELQFAS

DQRSRMDTLIRSYAAQDSKTGLNNRLFFDNQLATLLEDQEKVGAYGIVMMIRLPEFDLLRDNWGRAAAEE

HYFTLINLLSTFIMRYPGALLARYHRSDFAVLLPHRTLKEADSIAGLLLKAMDALPPTRILDRDDMMHIG

ICSFRSGQSAAQVMEHAEAATRNAVLQGSNSWSVYDDTLPEKGRGNVRWRTLIEQMLSRGGPRLYQKPAV

TRDGRVHHRELMSRMYDGKEEVIAAEYMPMVLQFGLAEEYDRLQVTRLLPFLGFWPEENLALQLSVESLI

RPRFQRWLRDALMQCEKSQRQRIIFELAEADVCQYIGRLQPVMRLVNALGVRVAVVQAGLTLVGTSWIKQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918653.1\_462 [gene=mreB] [locus\_tag=BN49\_RS03515] [protein=rod shape-determining protein MreB] [protein\_id=WP\_002918653.1] [location=482121..483164] [gbkey=CDS]

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AAIRPMKDGVIADFFVTEKMLQHFIKQVHSNSFMRPSPRVLVCVPVGATQVERRAIRESAQGAGAREVFL

IEEPMAAAIGAGLPVSEATGSMVVDIGGGTTEVAVISLNGVVYSSSVRIGGDRFDEAVINYVRRNYGSLI

GEATAERIKHEIGSAYPGDEVREIEVRGRNLAEGVPRGFTLNSNEILEALQEPLTGIVSAVMVALEQCPP

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>lcl|NZ\_FO834906.1\_prot\_WP\_004149974.1\_463 [gene=mreC] [locus\_tag=BN49\_RS03520] [protein=rod shape-determining protein MreC] [protein\_id=WP\_004149974.1] [location=483235..484227] [gbkey=CDS]

MKPIFSRGPSLQIRLILAVLVALGVIIADSRLGTFSQIRTYMDTAVSPFYFVSNGPRELLDSVSQTLATR

DQLELENRALRQELLLKNSDLLMLGQYKQENARLRELLGSPLRQDEQKMVTQVISTVNDPYSDQVVIDKG

SVNGVYEGQPVISDKGVVGQVVAVAKMTSRVLLICDATHALPIQVLRNDIRVIAAGNGCTDDLQLEHLPA

NTDIRVGDVLVTSGLGGRFPEGYPVGVVSSVKLDTQRAYTVIQARPTAGLQRLRYLLLLWGADRNGANPM

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918648.1\_464 [gene=mreD] [locus\_tag=BN49\_RS03525] [protein=rod shape-determining protein MreD] [protein\_id=WP\_002918648.1] [location=484227..484715] [gbkey=CDS]

MASYRSQGRWVIWLSFLIALLLQIMPWPADISVFRPNWVLLILLYWILALPHRVNVGTGFVMGAILDLIS

GSTLGVRALSLSIVAYLVALKYQLFRNLALWQQALVVMLLSLAVDIIVFWAEFLVINVSFRPEVFWSSVV

NGILWPWLFLLMRKVRQQFAVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002918646.1\_465 [locus\_tag=BN49\_RS03530] [protein=Maf-like protein] [protein\_id=WP\_002918646.1] [location=484723..485304] [gbkey=CDS]

MTTLYLASGSPRRQELLTQLGLAFERLVPGIEEQRQPQESAQHYVVRLAREKAQAGVAMATRDLPVLGAD

TIVILNGEVLEKPRDAEHAAAMLRLLSGHTHQVMTAVALADKQQTLDCLVVTEVTFRRLSEQDIADYVAS

GEPLDKAGAYGIQGLGGCFVRKINGSYHAVVGLPLVETYELLSNFNSLRKGKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002918644.1\_466 [gene=rng] [locus\_tag=BN49\_RS03535] [protein=ribonuclease G] [protein\_id=WP\_002918644.1] [location=485307..486776] [gbkey=CDS]

MTAELLVNVTPSETRVAYIDGGILQEIHIEREARRGIVGNIYKGRVSRVLPGMQAAFVDIGLDKAAFLHA

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VSQRIESEAERERLKKVVAEYCDEQGGFIIRTAAEGVHEQEMAADAAYLKRVWTKVMERKKRNQTRYQLY

GELALAQRVLRDFADAQLDRIRVDSRLTYEALLEFTAEYIPEMTSKLEHYSGRQPIFDLFDVENEIQRAL

ERKVELKSGGYLIIDQTEAMTTIDINTGAFVGHRNLDDTIFNTNIEATQAIARQLRLRNLGGIIIIDFID

MNNEDHRRRVLHSLEQALSKDRVKTSINGFSQLGLVEMTRKRTRESVEHVLCNECPTCHGRGTVKSVETV

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>lcl|NZ\_FO834906.1\_prot\_WP\_032105137.1\_467 [gene=yhdP] [locus\_tag=BN49\_RS03540] [protein=AsmA2 domain-containing protein YhdP] [protein\_id=WP\_032105137.1] [location=486814..490611] [gbkey=CDS]

MRRLPGILLLTVATLIVIVALLVSGLRLVLPQLDAWRPQLLEKISTLTGTPVDASQITASWQTFGPTLDA

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RQFDHFTLRDSHLSFLTLSGQRAELAVPQLTWLNGRNRHRAEGQLSLSSLTGQHGVMQVRMDLRDEDGLL

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GLQPFADKLAPSLGELWRTTQPGGKINLLALDIPLQATEKTRFQAQWSDLAWKQWKLLPGAEHFSGSLNG

SVEHGELRAHMAKALMPYAGVFRAPLEIAAGEATLSWVKNDKGFMLDGRDIDVQATGVRARGGFRYLQPQ

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VYVPLKNATFAFQPDWPALTGLNIDLNFINNGLWMRADKAMLGNVTASNLDAAIPDYAQEKLLIDADIKG

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LSGNFSFVNGDLNSQTLSATWFNQPLNLNFSTREGEKAFLVDVGMNANWQPSRTGLLPKAVSEALSGSVP

WDGKVAIELPYHGNASYKVDINGDLKNVSSRLPSPVSKPAGEPLPVKINVAGGLSSFDLTGSVGAKNHIN

SRWLLNHKLTLDRAILTTDSKGHSPLPDQPGIELNLPPMDGAQWLALFENGAANEVSSSVLFPPRIVLRT

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AGQLLRLLSVDALLRKLRFDFSDTFSEGFYFDSINSTAWIKDGVLHTDDTLVDGLEADIAMKGSVDLVRR

QLDLQAVVAPEISATVGVAAAFAVNPIVGAAVFAASKVLGPLWNKVSILRYRITGPIDQPQINEVLRQAR

SNKKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004144958.1\_468 [gene=tldD] [locus\_tag=BN49\_RS03545] [protein=metalloprotease TldD] [protein\_id=WP\_004144958.1] [location=490700..492145] [gbkey=CDS]

MSLNLVSEQLLSANGLNHQDLFAILGQLTERRLDYGDLYFQSSYHESWVLEDSIIKDGSYNIDQGVGVRA

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VDKVARAADQRVQEVSASLSGVYELILVAATDGTLAADVRPLVRLSVSVLVEEDGKRERGSSGGGGRFGY

DYFLASQEGDVRADAWAKEAVRMALVNLSAVAAPAGMLPVVLGAGWPGVLLHEAVGHGLEGDFNRRGTSV

FSGHMGELVASELCTVVDDGTIADRRGSVAIDDEGTPGQYNVLIENGILKGYMQDKLNARLMGVAPTGNG

RRESYAHLPMPRMTNTYMLAGQSTPQEIIESVDYGIFAPNFGGGQVDITSGKFVFSTSEAYLIEKGKVTK

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918641.1\_469 [gene=aaeR] [locus\_tag=BN49\_RS03550] [protein=HTH-type transcriptional activator AaeR] [protein\_id=WP\_002918641.1] [location=complement(492181..493110)] [gbkey=CDS]

MERLKRMSVFAKVVELGSFTAAARQLQMSVSSISQTVAKLEDELQVKLLNRSTRSLGLTEAGKIYYQGCR

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VVIRVGALQDSSLFSRRLGSMPMVLCAAKSYLAQAGNPEKPADLAGHAWLEYSVRPDNEFVIIAPEGIST

RLTPQGRFVTNDPMTLVRWLTAGVGIAYVPLMWAIEEINRGELEILLPSYQSDPRPVYALYTEKDKLPLK

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918640.1\_470 [locus\_tag=BN49\_RS03555] [protein=p-hydroxybenzoic acid efflux pump operon protein AaeX] [protein\_id=WP\_002918640.1] [location=493242..493445] [gbkey=CDS]

MSLFPVIVIFGLSFPPIFFELLLSLAIFWLVHRLLVPTGIYDFVWHPALFNTALYCCLFYLISRLFV

>lcl|NZ\_FO834906.1\_prot\_WP\_002918639.1\_471 [gene=aaeA] [locus\_tag=BN49\_RS03560] [protein=p-hydroxybenzoic acid efflux pump subunit AaeA] [protein\_id=WP\_002918639.1] [location=493453..494385] [gbkey=CDS]

MKTLTRNILRTAITVILVILAFVAIFRAWVYYTASPWTRDARFSADIVAIAPDVSGLISQVNVKDNQLVK

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AVASRDLARLDLERTVIRAPADGWVTNLNVYTGEFITRGSTAVALVKENTFYVMAYLEETKLEGVRPGYR

AEITPLGSSKTIKGTVDSIAAGVTNASSSSDSKGMASVDSNLEWVRLAQRVPVRIRLDHQQGNLWPSGTT

ATVVITGQEDRDTSQANFFQKLAMRLREFG

>lcl|NZ\_FO834906.1\_prot\_WP\_002918632.1\_472 [gene=aaeB] [locus\_tag=BN49\_RS03565] [protein=p-hydroxybenzoic acid efflux pump subunit AaeB] [protein\_id=WP\_002918632.1] [location=494391..496358] [gbkey=CDS]

MGTYTIAPRHLRFAIKLACAVVLALFVGFHFQLETPRWAVLTAAIVAAGPAFAAGGEPYSGAIRYRGMLR

IAGTFIGCIAALVIIILMIRAPLLMMLVCCLWAGFCTWVSSLVKVENSYAWGLAGYTALIIIITIHTNPM

LAPQFAVERCSEIVIGIVSAIVADLLFSPRSIKKEIDLELDNLLIAQYKLMQLCVAHGEKEEVDQAWGAL

VRRTTALEGMRSNLIMESSRWAKANQRLKAINTLSLTLITQACETYLIQNSRPEMVTDDYRELFAEPVET

VQDVHQQLKRMRRFLTWKGEHNTPVTIYSWVGAATRYLLLKRGVVGNTKISRIEDGVLRGETVVKVESAE

RHHAMVNFWRTSVSCILGTLFWLWTGWTSGSGAMVMIAVVTALAMRLPNPRMVAIDFLYGTLAALPLGTL

YFLVIMPATQQSMLLLCISLAAMAFFIGIEVQKRRLGSLGALASTINILVLDNPMQFQFSQFLDSALGQI

VGCFLALMVILIVRDNSRARTGRVLLNQFVSAAVSSLTTNSARRKENHLPALYQQLFLLLNKFPGDVARF

RLALTLIIAHQRLRDAPVPVNDDLSAFHRQLRRTADHVISAGSDDKRRRYFTQLLAELDVYQEKLRVWEA

SPQVTEPVRRLVEMLHKYQHVLTSS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529685.1\_473 [locus\_tag=BN49\_RS03570] [protein=barstar family protein] [protein\_id=WP\_016529685.1] [location=496438..496713] [gbkey=CDS]

MTTYTFDFDEIAEQQDFYREFSRTFELAQDKVNNLDSLWDAVTGGLLPLPLDIEFIHLNDKQRRCFGALI

LLFDEAEEELEGELRFNARQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918627.1\_474 [gene=yhcN-B] [locus\_tag=BN49\_RS03575] [protein=DUF1471 family stress response protein YhcN-B] [protein\_id=WP\_002918627.1] [location=complement(496764..497030)] [gbkey=CDS]

MKRAMIIASLGLASLLSFGASAAVQQVNAEQAQNLQSMGTISVSQVGSAPMDMRQELAAKAEKEGASSYR

IIEARTGDSWHATAELYK

>lcl|NZ\_FO834906.1\_prot\_WP\_002918626.1\_475 [gene=yhcN] [locus\_tag=BN49\_RS03580] [protein=peroxide/acid stress response protein YhcN] [protein\_id=WP\_002918626.1] [location=complement(497129..497392)] [gbkey=CDS]

MKIKTTVAAISILSVVSFGAFAADIINSEQAQGREAIGTVSVGAVASSPMDMHEMLNKKAQEEGASSYRI

IEARTGDHWHATAELYK

>lcl|NZ\_FO834906.1\_prot\_WP\_002918625.1\_476 [gene=argR] [locus\_tag=BN49\_RS03585] [protein=transcriptional regulator ArgR] [protein\_id=WP\_002918625.1] [location=complement(497768..498238)] [gbkey=CDS]

MRSSAKQEELVKAFKALLKEEKFSSQGEIVQALQEEGFENINQSKVSRMLTKFGAVRTRNAKMEMVYCLP

AELGVPTTSSPLKNLVLDIDYNDAVVVIHTSPGAAQLIARLLDSLGKAEGILGSIAGDDTIFTTPARGFT

VKDLHDAILVLFEQEL

>lcl|NZ\_FO834906.1\_prot\_WP\_002918570.1\_477 [gene=mdh] [locus\_tag=BN49\_RS03590] [protein=malate dehydrogenase] [protein\_id=WP\_002918570.1] [location=498653..499591] [gbkey=CDS]

MKVAVLGAAGGIGQALALLLKTQLPSGSELSLYDIAPVTPGVAVDLSHIPTDVKIKGFSGEDATPALEGA

DVVLISAGVARKPGMDRSDLFNVNAGIVKNLVQQIAKTCPQACIGIITNPVNTTVAIAAEVLKKAGVYDK

NKLFGVTTLDIIRSNTFVAELKGKSATEVEVPVIGGHSGVTILPLLSQIPGVSFSDQEIADLTKRIQNAG

TEVVEAKAGGGSATLSMGQAAARFGLSLVRAMQGEKGVVECAYVEGDGHYARFFSQPLLLGKNGVEERQS

IGKLSAFEQQALEGMLDTLKKDIALGEDFVNK

>lcl|NZ\_FO834906.1\_prot\_WP\_009309620.1\_478 [locus\_tag=BN49\_RS03595] [protein=GntR family transcriptional regulator] [protein\_id=WP\_009309620.1] [location=499722..500351] [gbkey=CDS]

MKKIERKQTRDQIAQMIRYQILSGAMKAGDELTQESIAEQLGLSRMPVREALQSLEQEGFLVRLPNRHMQ

VSTLAVEDVSHIFRVIAVMAAELFALVPANQGEVLRARAQELARPGENTRELAFHQLLISYLDNRYLAKA

YQQFLDGYISYVILYLKENGQESALILSELANAIGNGEGGKIAQTTQRYFLMLAEIMRQHMKDWESAEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181429.1\_479 [locus\_tag=BN49\_RS03600] [protein=GntR family transcriptional regulator] [protein\_id=WP\_004181429.1] [location=500338..501003] [gbkey=CDS]

MQKPKLGKIKLLSAKEQVAAVLRKAILSRDLVEGQEITLEGIARLVGVSSMPVREAFQILAADGLIQVRP

NKGAVVLGINEQTIREHYEIRAVLESEAVAKASRPGTDISRIAQVHYAAEKALADNNSAEYSDLNQAFHM

EIWSAAGNEKMKMLLCNMWNGLSMGHKVTEEEYAVISIREHKAILQALEQHNEALARQRMHEHIIRSMEN

MLTRYLPDTTT

>lcl|NZ\_FO834906.1\_prot\_WP\_004181428.1\_480 [locus\_tag=BN49\_RS03605] [protein=SLC13 family permease] [protein\_id=WP\_004181428.1] [location=501215..502483] [gbkey=CDS]

MEPITITLCLLVFAIIMFVWEKVPLAVTSMVVCVALVLTGVLDLKQAFAGFIDSNVILFVAMFIVGGALF

ETGMANKVGGVITHFAKTEKQLIFIIMVVVGVMSGFLSNTGTAAVLIPVVIGVAAKSGFTRSRLLMPLVF

AAALGGNLSLIGAPGNLIAQSALQNIGSGFGFFEYAKVGLPMLVCGILYFLTIGYKFLPNNSNSSEVGSI

GEQRDYSHVPRWKQILSLVVLIATILGMIFEKQTGISLTVAGCIGALVLVITGVLTEKQAYKAIDSQTIF

IFGGTLALAKALEMTGAGKLVADQVIGLLGNNSSPFMLLVVVFALSVVMTNFMSNTATVALLVPVSLSIA

AGMGADPRAVLMATVIGSSCAYATPIGMPANMMVLSAGGYKFVDYAKSGIPLIIVSTIVSLILLPILFPF

HP

>lcl|NZ\_FO834906.1\_prot\_WP\_004181427.1\_481 [gene=ttdA] [locus\_tag=BN49\_RS03610] [protein=L(+)-tartrate dehydratase subunit alpha] [protein\_id=WP\_004181427.1] [location=502516..503415] [gbkey=CDS]

MSKSEQISRMTDIMARFVGYTGKVLPDDVTAKLQDLHKKETSQLADVIFTTMIENQRLAKELDRPSCQDT

GVIQFLVECGANFPLIGELEALLRESVIKATIDSPLRHNSVETFDEYNTGKNVGKGTPTVFWEIVPNSDQ

CSIYTYMAGGGCSLPGKAMVLMPGAGYEGVTRFVLDVMTSYGLNACPPLLVGVGVATSVETAALLSKKAL

MRPIGSHNDNERAALLEKMLEDGINKIGLGPQGMSGNTSVMGVNIENTARHPSTIGVAVNVGCWSHRKGH

IVFDKDLNYTITSHTGVAF

>lcl|NZ\_FO834906.1\_prot\_WP\_004188410.1\_482 [gene=ttdB] [locus\_tag=BN49\_RS03615] [protein=L(+)-tartrate dehydratase subunit beta] [protein\_id=WP\_004188410.1] [location=503415..504032] [gbkey=CDS]

MTKKILTTPIKDEDLADIKAGDIIYLNGHIVTCRDVAHRRLIEGGRELPVNVAGGAILHAGPIVRPIKGT

EDKFEMVSVGPTTSMRMEKFEKEFIAKTGVKLIVGKGGMGKGTEEGCMEHKALHCVFPAGCAVVAAVCVE

EIEDAQWRDLGMPETLWVCRVKEFGPLIVSIDTHGNNLFEQNKVIFNQRKEIVADEICKHVSFIK

>lcl|NZ\_FO834906.1\_prot\_WP\_014906863.1\_483 [locus\_tag=BN49\_RS03620] [protein=oxaloacetate decarboxylase subunit gamma] [protein\_id=WP\_014906863.1] [location=504174..504425] [gbkey=CDS]

MTDNAILLGEGFTLMFLGMGFVLVFLLLLIFAIRGMSLAVNRLFPEPSAAPAAAPAAVAPADDFARLKPA

IVAAIHHHRRLHP

>lcl|NZ\_FO834906.1\_prot\_484 [gene=oadA] [locus\_tag=BN49\_RS03625] [protein=sodium-extruding oxaloacetate decarboxylase subunit alpha] [pseudo=true] [partial=3'] [location=504441..>506225] [gbkey=CDS]

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TLSYTTSPAHTLQTWLDLTEQLLETGVDSVAIKDMSGILTPHAAFELVSEIKKRYDVTLHLHCHATTGMA

EMALLKAIEAGVDGVDTAISSMSATYGHPATEALVATLAGTQYDTGLDIHRLENIAAYFREVRKKYHAFE

GQLKGTDSRILVSQVPGGMLTNLEGQLKQQSAAHRLDDVLAEIPRVREDLGFIPLVTPTSQIVGTQAVLN

VLGGERYKTIAKETAGILKGEYGRTPAPVNAALQARVLDGADPVTCRPADLLKPELAALEADVRRQAQEK

GITLAENAIDDVLTVALFPQIGLKFLENRHNQAASEPEPQPEAAQPQAKAEKRAASGVYTEEVEGKA\*VV

KVNVSDDVSQMPAAAPAPAPAPAPASAPAAAAPAGAGTPVTAPLAGTIWKVLASEGQTVAEGEVLLILEA

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>lcl|NZ\_FO834906.1\_prot\_WP\_046044004.1\_485 [locus\_tag=BN49\_RS03630] [protein=sodium ion-translocating decarboxylase subunit beta] [protein\_id=WP\_046044004.1] [location=506247..507443] [gbkey=CDS]

MESLNALIQGMGLMHLGAGQAAMLLVSLLLLWLAIAKKFEPLLLLPIGFGGLLSNIPEAGLALTALESLL

AHHDPAQLAVIAAKLHCAPDVHAIKAALALALPSVQGQMESLAVDMGYSAGVLAIFYKVAIGSGIAPLVI

FMGVGAMTDFGPLLANPRTLLLGAAAQFGIFATVLGALTLNYFGIISFTLPQAAAIGIIGGADGPTAIYL

SGKLAPELLGAIAVAAYSYMALVPLIQPPIMKALTTDKERKIRMVQLRTVSKREKILFPAVLLLLVALLL

PDAAPLLGMFCFGNLMRESGVVERLSDTVQNALINIVTIFLGLSVGAKLVADKFLQPQTLGILVLGVIAF

CVGTAAGVLMAKLMNVFSRHKINPLIGSAGVIGSAIAAGVMLKYVLAM

>lcl|NZ\_FO834906.1\_prot\_WP\_004181422.1\_486 [locus\_tag=BN49\_RS03635] [protein=hypothetical protein] [protein\_id=WP\_004181422.1] [location=507503..508213] [gbkey=CDS]

MNEGIACCPENRTSTREAVVDAMLASGDELAQLQPALNLLSPPLNATPGEALLASCYEAGADHNADEATR

AVSALPAAVVRSATPSLQRSGLLCMAAGALSARQLPLTHNRLCDVAGQFARAIPEGDEEAGSGFYTVRSV

SLPVYRRLRRDNHSHSVCLQQALLHLLAWKSESPWARQQAQRLLWQGGVLGEKGEFALLTLDDELRERQI

VWPALRSLLAVTGFLVRFPAGPVFSD

>lcl|NZ\_FO834906.1\_prot\_WP\_002918568.1\_487 [gene=degS] [locus\_tag=BN49\_RS03640] [protein=outer membrane-stress sensor serine endopeptidase DegS] [protein\_id=WP\_002918568.1] [location=complement(508239..509297)] [gbkey=CDS]

MPGKLLRSVLIGLLVGGLLLALMPSLRQWQLAPTTQNDTADDSPASYNAAVRRAAPAVVNVYNRALNSTS

HNQLTLGSGVIMDQRGYILTNKHVINDADQIIVALQDGRVFEALLVGSDSLTDLAVLKINATGGLPVIPI

NPKRTPHIGDVVLAIGNPYNLGQTITQGIISATGRIGLNPTGRQNFLQTDASINHGNSGGALVNSLGELM

GINTLSFDKSNDGETPEGIGFAIPFQLATKIMDKLIRDGRVIRGYIGISGREIAPLHAQGGGIDQIQGIV

VNDVAPDGPAAQAGIRANDVIISVNDKPAVSALETMDQVAEIRPGSEIPVVIMRDDKKITLHIAVQEYPA

TN

>lcl|NZ\_FO834906.1\_prot\_WP\_004174125.1\_488 [gene=degQ] [locus\_tag=BN49\_RS03645] [protein=serine endoprotease DegQ] [protein\_id=WP\_004174125.1] [location=complement(509385..510752)] [gbkey=CDS]

MKKQTLLLSALALSIGLSLSVLPPAAASLPTQVPGQGALPSLAPMLEKVLPAVVSVQVEGTASPTLNMPE

ELKKYFGDNAPQEQAQPFEGLGSGVIIDAAKGYVLTNNHVINQAQKISVQLNDGREFDAKLVGSDEQSDI

ALLQLIKPDHLTQIAIADSDKLRVGDFAVAVGNPFGLGQTATSGIISALGRSGLNLEGLENFIQTDASIN

RGNSGGALLNLNGELIGINTAILAPGGGSIGIGFAIPSNMAKTLADQLIQFGEIKRGLLGIKGMEMSADI

AKAMNLNVQRGAFVSEVLPNSGSAKAGIKSGDVIVSLNGKPLNSFAELRSRIATTEPGTKVKLGLLRDGK

PVDVEVTLDKSTSSTASAELIIPALQGASFSDGQMKDGTKGVVIDNVDKGSAAAQVGLHKDDIIIGLNRQ

RIHSIAELRKALEGKPPVIALNVIRGNESIYLLLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002918565.1\_489 [locus\_tag=BN49\_RS03650] [protein=Z-ring associated protein ZapG] [protein\_id=WP\_002918565.1] [location=complement(510926..511324)] [gbkey=CDS]

MTWEYALIGLVVGIIIGAVAMRFGNRKLRQQQALQYELEKNKAELEEYREELVSHFARSAELLDNMAHDY

RQLYQHMAKSSNNLLPDSMADANPFRNRLEESEASNDQAPVQMPRDYSEGASGLLRGGAKRD

>lcl|NZ\_FO834906.1\_prot\_WP\_004144945.1\_490 [locus\_tag=BN49\_RS03655] [protein=cell division protein ZapE] [protein\_id=WP\_004144945.1] [location=511515..512642] [gbkey=CDS]

MQSLSPTSRYLLALKEGSHQPDDVQQEAVSRLDTIYQELQTQPAPVASGGGLRAKFGKLLGKREPAAGTA

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LCFDEFFVSDITDAMLLGGLMKALFARGITLVATSNIPPDELYRNGLQRARFLPAIDAIKQHCDIMNVDA

GIDYRLRTLTQAHLWLSPLNNDTREQMDKLWLALAGAPRAAGPTLEINHRELPTLGVENQTLAASFATLC

VDARSQHDYIALSRLFHTVMLFDVPVMTAQLESEARRFIALVDEFYERHVKLVVSAAVPLYDIYQGERLK

FEFQRCLSRLQEMQSEEYLKRPHMP

>lcl|NZ\_FO834906.1\_prot\_WP\_002918559.1\_491 [gene=rplM] [locus\_tag=BN49\_RS03660] [protein=50S ribosomal protein L13] [protein\_id=WP\_002918559.1] [location=512908..513336] [gbkey=CDS]

MKTFTAKPETVKRDWYVVDATGKTLGRLATELARRLRGKHKAEYTPHVDTGDYIIVLNAEKVAVTGNKRE

DKMYYHHTGHIGGIKEATFEEMIARRPERVIEIAVKGMLPKGPLGRAMYRKLKVYAGNEHNHAAQQPQVL

DI

>lcl|NZ\_FO834906.1\_prot\_WP\_000829818.1\_492 [gene=rpsI] [locus\_tag=BN49\_RS03665] [protein=30S ribosomal protein S9] [protein\_id=WP\_000829818.1] [location=513352..513744] [gbkey=CDS]

MAENQYYGTGRRKSSAARVFIKPGNGKIVINQRSLEQYFGRETARMVVRQPLELVDMVEKLDLYITVKGG

GISGQAGAIRHGITRALMEYDESLRSELRKAGFVTRDARQVERKKVGLRKARRRPQFSKR

>lcl|NZ\_FO834906.1\_prot\_WP\_135801240.1\_493 [locus\_tag=BN49\_RS30695] [protein=hypothetical protein] [protein\_id=WP\_135801240.1] [location=513802..514086] [gbkey=CDS]

MDKTAVIHKHSAGSRHFFSISRIPSPQRLQNLVNYHPIFCPNAGDCSFFVLFVNEGDIALMGFLHLAGHE

WPAAVQNSEYTWRFSWLSLPTNVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002918467.1\_494 [gene=sspA] [locus\_tag=BN49\_RS03670] [protein=stringent starvation protein A] [protein\_id=WP\_002918467.1] [location=514056..514694] [gbkey=CDS]

MAVAANKRSVMTLFSGPTDIYSHQVRIVLAEKGVSFEIEHVEKDNPPQDLIDLNPNQSVPTLVDRELTLW

ESRIIMEYLDERFPHPPLMPVYPVARGESRLYMQRIEKDWYSLMNTIQSGTAAQADAARKQLREELLAIA

PVFTQKPYFLSDEFSLVDCYLAPLLWRLPVLGVELVGAGAKELKGYMTRVFERDSFLASLTEAEREMRLG

RG

>lcl|NZ\_FO834906.1\_prot\_WP\_002918465.1\_495 [gene=sspB] [locus\_tag=BN49\_RS03675] [protein=ClpXP protease specificity-enhancing factor] [protein\_id=WP\_002918465.1] [location=514698..515192] [gbkey=CDS]

MDVSQLTPRRPYLLRAFYDWLLDNQLTPHLVVDVTLPGVLVPMEYARDGQIVLNIAPRAVGNLELANDEV

RFNARFGGVPRNVSVPLAAVLAIYARENGAGTMFEPEAAYDEDVSSLNDDDVAPESESETVMSVIDGDKP

DNHDDDPDDTPPPRGGRPALRVVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004188425.1\_496 [locus\_tag=BN49\_RS03680] [protein=N-acetylmannosamine-6-phosphate 2-epimerase] [protein\_id=WP\_004188425.1] [location=515317..516021] [gbkey=CDS]

MSLLAQLDQRIRHHGGLIVSCQPVPGSPLDNPAIVAAMALAAEQAGAVALRIEGLANLQAVRPLVTVPVI

GLIKRDLPDSPVRITPWLEDIDALAQGGADIIAIDGTQRQRPASVSALLAEIHQLGKVAMADCSSLDDAL

ECWQLGAEIVGTTLSGYTAEETPDEPDLALVQCLSVAGCRVIAEGRYNTPAQAAEAMRCGAWAVTVGSAI

TRLEHICGWYNTALKAAVCPANEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002918461.1\_497 [locus\_tag=BN49\_RS03685] [protein=glutamate synthase small subunit] [protein\_id=WP\_002918461.1] [location=complement(516076..517494)] [gbkey=CDS]

MSQNVYQFIDLQRVDPPKKPLKIRKIEFVEIYEPFSEGQAKAQADRCLSCGNPYCEWKCPVHNYIPNWLK

LANEGRIFEAAELSHQTNTLPEVCGRVCPQDRLCEGSCTLNDEFGAVTIGNIERYINDKAFEMGWRPDLS

DVKPTGKTVAIIGAGPAGLACADVLTRNGVKAVVFDRHPEIGGLLTFGIPAFKLEKEVMTRRREIFTGMG

IEFKLNTEVGRDVQLDDLLKEYDAVFLGVGTYQSMRGGLDNEDAPGVYDALPFLIANTKQIMGFGETADE

PYVSMEGKRVVVLGGGDTAMDCVRTSVRQNAAHVICAYRRDEENMPGSKREVKNAREEGVEFQFNVQPLG

VEVNANGKVCGVKMARTEMGQPDAKGRRRAEIVPGSEHVVPADAVVMAFGFRPHSMEWLAKHSVELDSQG

RIIAPEGSENAFQTSNPKIFAGGDIVRGSDLVVTAIAEGRKAADGILNYLEV

>lcl|NZ\_FO834906.1\_prot\_WP\_002918458.1\_498 [gene=gltB] [locus\_tag=BN49\_RS03690] [protein=glutamate synthase large subunit] [protein\_id=WP\_002918458.1] [location=complement(517504..521964)] [gbkey=CDS]

MLYDKSLERDNCGFGLIAHIEGEPSHKVVRTAIHALARMQHRGAILADGKTGDGCGLLLQKPDRFFRIVA

EERGWRLAKNYAVGMLFLNKDPELAKAARRIVEEELQLETLSIVGWRDVPTNEGVLGEIALSSLPRIEQI

FVNAPAGWRPRDMERRLFIARRRIEKRLQEDKDFYVCSLSNLVNIYKGLCMPADLPRFYLDLADLRLESA

ICLFHQRFSTNTVPRWPLAQPFRYLAHNGEINTITGNRQWARARTYKFQTPLIPDLHDAAPFVNETGSDS

SSMDNMLELLLAGGMDIVRAMRLLVPPAWQNNPDMDPELRSFFDFNSMHMEPWDGPAGIVMSDGRYAACN

LDRNGLRPARYVITKDKLITCASEVGIWDYQPDEVVEKGRVGPGELMVIDTRAGRILHSAETDDDLKSRH

PYKEWMEKNVRRLVPFEDLPDEEVGSRQLDDDTLASYQKQFNYSAEELDSVLRVLGENGQEAVGSMGDDT

PFAVLSSQPRIIYDYFRQQFAQVTNPPIDPLREAHVMSLATSIGREMNVFCEAEGQAHRLSFKSPILLYS

DFKQLTTMEEEHYRADVLDITFNPAEASLSETVKALCDKAEQMVRDGTVLLVLSDRNIAKDRLPVPAPMA

VGAIQTRLVDKSLRCDANIIVETASARDPHHFAVLLGFGATAIYPYLAYETLAKLVDSKAIDKPYRAVML

NYRNGINKGLYKIMSKMGISTIASYRCSKLFEAVGLHRDVSELCFQGVVSRIGGASFDDFQQDLLNLSKR

AWLARKPLAQGGLLKYVHGGEYHAYNPDVVRTLQQAVQSGEYSDYQQYAKLVNERPAATLRDLLALNPGE

DAISIDEVEPAKELFKRFDTAAMSIGALSPEAHESLAEAMNSIGGFSNSGEGGEDPARYGTNKVSRIKQV

ASGRFGVTPAYLVNADVIQIKVAQGAKPGEGGQLPGDKVTPYIAKLRYSVPGVTLISPPPHHDIYSIEDL

AQLIFDLKQVNPKAMISVKLVSEPGVGTIATGVAKAYADLITIAGYDGGTGASPLSSVKYAGCPWELGLV

ETQQALVANGLRHKIRLQVDGGLKTGLDIIKAAILGAESFGFGTGPMVALGCKYLRICHLNNCATGVATQ

DDKLRKNHYHGLPFKVTNYFEFIARETRELMAQLGVKRLVDLIGRTDLLKELDGFTAKQQKLDLGKLLET

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LAGDPIVAHFSGTAGQSFGVWNAGGVELHLTGDANDYVGKGMAGGLLAIRPPVGSAFRSHEASIIGNTCL

YGATGGRLYAAGRAGERFAVRNSGAITVVEGIGDNGCEYMTGGIVCVLGKTGVNFGAGMTGGFAYVLDED

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LGHRSRSAAELRVQAQ

>lcl|NZ\_FO834906.1\_prot\_499 [locus\_tag=BN49\_RS03695] [protein=TIGR01212 family radical SAM protein] [pseudo=true] [partial=3'] [location=522638..>523552] [gbkey=CDS]

MQLQKLVNMFGGDLMRRYGEKVHKLTLHGGFSCPNRDGTLGRGGCTFCNVASFADEAQQHRSIAEQLAHQ

AQLVNRAKRYLAYFQAYTSTFAEVQVLRSMYRQAVSAANIVGLCVGTRPDCVPQAVLDLLSEYHQQGYEV

WLELGLQTAHDKTLHRINRGHDFACYQRTARLARERGLKVCAHLIVGLPGESQGHCLQTLEQVVATGVDG

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TGMVELDRYLNQQGAQGSALGRSWV

>lcl|NZ\_FO834906.1\_prot\_WP\_002918453.1\_500 [locus\_tag=BN49\_RS03700] [protein=MFS transporter] [protein\_id=WP\_002918453.1] [location=complement(523621..524904)] [gbkey=CDS]

MGKNIRWIIVLLLFLVYMINYLDRVALSITVPMIEKDLALNAEQFGIIFGSFFFGYAVFNFIGGLAVDKF

GATLVMGLAVGLWSLFCGLTAVATGFYSMLVLRVLFGMAEGPICASANKMINGWFPKKQAATAVGFLSAG

SPLGGAVAGPIVGYLALAFGWRPAFMIIFAIGIVWMIAWFFIAANSPEKHKKVSQEELKLINKMKEEEVA

LETIENQTAHSLGYYLKQPIILVTAFAFFCYNYILFFFLSWFPSYLVQQHHLDIKQMSLTTMIPWIVGFV

GLALGGYISDKIFKLTGRLLLSRKIVLVVCLLMAAICVGLAGTVSSVVPAVLLMSVSIFFLYVTGAIYWA

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TMKASQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918451.1\_501 [locus\_tag=BN49\_RS03705] [protein=Zn-dependent oxidoreductase] [protein\_id=WP\_002918451.1] [location=complement(524990..526006)] [gbkey=CDS]

MRSVVVKEPGQLNIESRPVPVPGAHEVRVKIAFAGICGSDVHIYHGHNPFAKYPRVIGHEFYGIIDAVGE

QVSPARIGERVAVDPVVSCGHCYPCSVGRPNVCTQLQVIGVHRDGGFSDYACVPAKNAWRIPEAISDRQA

TMVEPFTIAANITAQLQPTAQDIALVYGAGPMGLTIIQALKGVYGVKQVIVVDRIAERLQMARENGADLT

LDNTDQPLAEQLAQRQLAPTLVIDAACHPAILQEAILLASPAARIGILGFSGEASTLTQQSITSKEISIF

SSRLNSGRFPLVIDWMEKGLIRPEALITHCMPLEQVKEAMEIFANDRKTCCKVLLQLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004188429.1\_502 [gene=uxuA] [locus\_tag=BN49\_RS03715] [protein=mannonate dehydratase] [protein\_id=WP\_004188429.1] [location=526303..527367] [gbkey=CDS]

MQMTMRWFGPEEDKISLEHIRQVPGVEGVVGALYDVAVGEVWPVDKIERLVDQAHAAGLKMEVIESVNIH

DDIKIGLPTRDRYIANYQQTIRNLARFGVKVICYNFMPVFDWMKTDMNYVLPDGSLTMAFEKKDIDKRLE

DVVKEVLENSNGFALPGWEPERLAEVQTLFAKYSAVDDQKLRENLVYFLQAVIPVCEEVGVKMAIHPDDP

PYSIFGLPRVVKNRDDLDWICRAVDSPANGITLCTGSIAEDPDNDVYAILAEFTRRKRIHFAHVRNIKLM

QDKDFYECAHPSEYGSLDMYKVMQALYDNGFDGYIRPDHGRFIWGETGRPGYGLFDRALGVTYLKGLWEA

LSKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002918444.1\_503 [gene=arcB] [locus\_tag=BN49\_RS03720] [protein=aerobic respiration two-component sensor histidine kinase ArcB] [protein\_id=WP\_002918444.1] [location=527514..529853] [gbkey=CDS]

MKQIRMLAQYYVDLMMKLGLVRFSMLLALALVVLAIVVQMAVTMVLHGQVESIDVIRSIFFGLLITPWAV

YFLSVVVEQLEESRQRLSRLVDKLEEMRERDLKLNVQLKDNIAQLNQEIGEREKAEAERETTLEQLKIEM

KEREETQIQLEQQSSFLRSFLDASPDLVFYRNEDKEFSGCNRAMELLTGKSEKQLIHLKPQDVYSEEAAE

KVLETDEKVFRHNVSLTYEQWLDYPDGRKACFEIRKVPYYDRVGKRRGLMGFGRDITERKRYQDALERAS

RDKTTFISTISHELRTPLNGIVGLSRILLDTELTSEQEKYLKTIHVSAVTLGNIFNDIIDMDKMERRKVQ

LDNQPVDFTSFLADLENLSGLQAQQKGLRFVLEPSLPLPHKVITDGTRLRQILWNLISNAVKFTPQGGGV

NVRVRYDEGDILHFEVEDSGIGIPEAEQDKIFAMYYQVKDSHGGKPATGTGIGLAVSRRLARNMGGDISV

TSQPGKGATFTLTVHAPAIAEEVEDTLAEDDMPLPALNVLLVEDIELNVIVARSVLEKLGNSVDVAMTGK

AALEMFEPGEYDLVLLDIQLPDMTGLDISRELKQRFAADELPPLVALTANVLKNKKEYLDAGMDDVLSKP

LSVPALTAMIKKFWDAPDEEAQEAPAADLHKADAVLDTDMLEQYIELVGPKLINDGLAVFEKMMPGYMSV

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AWVAKASKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004181418.1\_504 [gene=elbB] [locus\_tag=BN49\_RS03725] [protein=isoprenoid biosynthesis glyoxalase ElbB] [protein\_id=WP\_004181418.1] [location=530087..530740] [gbkey=CDS]

MKKIGVVLGGCGVYDGSEIHEAVITLLAIARNGAQAVCFAPDKPQRDVINHLTGEAMPEQRNVLVEAARI

ARGDILPLAQARAETLDALIVPGGFGAAKNLSSFAAEGSECQVDPDLRALALAMHQTGKPLGFMCIAPAM

LPKIFAFPLRITIGTDLDTADVVEEMGAEHVPCPVDDIVVDEDNKVVTTPAYMLAEDIAQAATGIEKLVA

RVLALSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144927.1\_505 [gene=mtgA] [locus\_tag=BN49\_RS03730] [protein=monofunctional biosynthetic peptidoglycan transglycosylase] [protein\_id=WP\_004144927.1] [location=530737..531462] [gbkey=CDS]

MRLRIAPFALLKRLALRLLLIAAVFWGGGIALFSVLPVPFSAVMLERQVSAWLSGDFHYLAHSDWVAMDK

ISPWMGLAVIAAEDQKFPEHWGFDVSAIEKALAHNERHETRIRGASTLSQQTAKNLFLWDGRSWLRKGLE

AGLTVGIETVWSKKRILTVYLNIAEFGDGIFGVEAAAQRYFHKPASQLTPGEAALLAAVLPNPIRYRADA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918431.1\_506 [gene=npr] [locus\_tag=BN49\_RS03735] [protein=PTS phosphocarrier protein NPr] [protein\_id=WP\_002918431.1] [location=complement(531526..531798)] [gbkey=CDS]

MTVKQTVEITNKLGMHARPAMKLFELMQNFDAEVLLRNDEGTEAEANSVIALLMLDSAKGRQIEVEASGP

QEVEALAAVIALFNAGFDED

>lcl|NZ\_FO834906.1\_prot\_WP\_002918428.1\_507 [gene=rapZ] [locus\_tag=BN49\_RS03740] [protein=RNase adapter RapZ] [protein\_id=WP\_002918428.1] [location=complement(531795..532649)] [gbkey=CDS]

MVLMIVSGRSGSGKSVALRALEDMGFYCVDNLPVVLLPDLARSLADRNISAAVSIDVRNMPESPEIFEQA

MQNLPECFSPQLLFLDADRNTLIRRYSDTRRLHPLSSKNLSLESAIDEESDLLEPLRSRADLIVDTSEMS

VHELAEMLRTRLLGKRERELTMVFESFGFKHGIPIDADYVFDVRFLPNPHWDPKLRPMTGLDKPVAAFLD

RHTEVHNFIYQTRSYLELWLPMLETNNRSYLTVAIGCTGGKHRSVYIAEQLADYFRSRGKNVQSRHRTLE

KRKS

>lcl|NZ\_FO834906.1\_prot\_WP\_004144926.1\_508 [gene=ptsN] [locus\_tag=BN49\_RS03745] [protein=PTS IIA-like nitrogen regulatory protein PtsN] [protein\_id=WP\_004144926.1] [location=complement(532695..533183)] [gbkey=CDS]

MMNNDSALQLSNVLNQECTRSQVHCQSKKRALEIISELAAKQLSLPPQVVFEAILTREKMGSTGIGNGIA

IPHGKLEEDTLRAVGVFVQLETPIAFDAIDNQPVDLLFALLVPADQTKTHLHTLSLVAKRLADKAICRRL

RAAQSDEELYEIITEAGSSDDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918423.1\_509 [gene=hpf] [locus\_tag=BN49\_RS03750] [protein=ribosome hibernation promoting factor] [protein\_id=WP\_002918423.1] [location=complement(533254..533541)] [gbkey=CDS]

MQLNITGHNVEITPAMREFVTAKFSKLEQFFDRINQVYIVLKVEKVTQIADANLHVNGGEIHASAEGQDM

YAAVDGLIDKLARQLTKHKDKLKQH

>lcl|NZ\_FO834906.1\_prot\_WP\_002918420.1\_510 [gene=rpoN] [locus\_tag=BN49\_RS03755] [protein=RNA polymerase factor sigma-54] [protein\_id=WP\_002918420.1] [location=complement(533564..534997)] [gbkey=CDS]

MKQGLQLRLSQQLAMTPQLQQAIRLLQLSTLELQQELQQALESNPLLEQTDLHDEVEAKEVEDRESLDTV

DALEQKEMPDELPLDASWDEIYTAGTPSGNGVDYQDDELPVYQGETTQTLQDYLMWQVELTPFTDTDRAI

ATSIVDAVDDTGYLTIQIEDIVDSIGDDEIGLEEVEAVLKRIQRFDPVGVAAKDLRDCLLIQLSQFAKET

PWLEEARLIISDHLDLLANHDFRTLMRVTRLKEEVLKEAVNLIQSLDPRPGQSIQTSEPEYVIPDVLVRK

VSGRWTVELNADSIPRLKINQQYAAMGNSARNDADGQFIRSNLQEARWLIKSLESRNDTLLRVSRCIVEQ

QQAFFEQGEEYMKPMVLADIAQAVEMHESTISRVTTQKYLHSPRGIFELKYFFSSHVNTEGGGEASSTAI

RALVKKLIAAENPAKPLSDSKLTSMLSEQGIMVARRTVAKYRESLSIPPSNQRKQLV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529639.1\_511 [gene=lptB] [locus\_tag=BN49\_RS03760] [protein=LPS export ABC transporter ATP-binding protein] [protein\_id=WP\_016529639.1] [location=complement(535045..535770)] [gbkey=CDS]

MATLTAKNLAKAYKGRRVVEDVSLTVNSGEIVGLLGPNGAGKTTTFYMVVGIVPRDAGNIIIDDEDISLL

PLHARARRGIGYLPQEASIFRRLSVYDNLMAVLQIRDDLTSEQREDSAKELMEEFHIEHLRDSLGQALSG

GERRRVEIARALAANPKFILLDEPFAGVDPISVIDIKRIIEHLRDSGLGVLITDHNVRETLAVCERAYIV

SQGHLIAHGTPQQILEDEQVKRVYLGEDFRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002918415.1\_512 [gene=lptA] [locus\_tag=BN49\_RS03765] [protein=lipopolysaccharide ABC transporter substrate-binding protein LptA] [protein\_id=WP\_002918415.1] [location=complement(535777..536322)] [gbkey=CDS]

MKFRTNKLSLKIALAGALLAASLPALAKTGDTDQPIHIESDQQSLDMQGNVVTFTGNVVVTQGTIKINAD

KVVVTRPGNEKGKEVIEGFGNPATFYQMQDNGKPVKGRASKMRYELQNDYVVLTGNAYLEQLDSNIKGDK

ITYLVKEQKMQAFSDKGRRVTTVLVPSELQDKSGNQQKKSN

>lcl|NZ\_FO834906.1\_prot\_WP\_002918413.1\_513 [gene=lptC] [locus\_tag=BN49\_RS03770] [protein=LPS export ABC transporter periplasmic protein LptC] [protein\_id=WP\_002918413.1] [location=complement(536291..536866)] [gbkey=CDS]

MSKTRRWVIILLSLLALILIGLNLANTDDTAQPEVNPNDPTYKSEHTDTVVYSPEGALSYRLIAEHVEYF

SDQEVSWFTKPVMTTFDTNKVPTWSVRADKAKLTNDRMLYLYGHVEVNALAPDSQLRKITTDNAQINLVT

QDVTSDDMVTLYGTTFNSSGLKMRGNLRSKNAELIEKVRTSYEIQNKQTQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002918405.1\_514 [gene=kdsC] [locus\_tag=BN49\_RS03775] [protein=3-deoxy-manno-octulosonate-8-phosphatase KdsC] [protein\_id=WP\_002918405.1] [location=complement(536863..537429)] [gbkey=CDS]

MNNADAQLATCYGPVSQAFVDRAAKIRLLILDVDGVLSDGLIYMGNHGEELKAFNVRDGYGIRCALTSGI

EVAIITGRKAKLVEDRCQTLGITHLYQGQSDKLLAFRDLTDKLHVRPEEVAYIGDDLIDWPVMAEVGLSV

AVADAHPLLLPRANYVTRINGGRGAVREVCDLLLLAQGKLDEAKGQSI

>lcl|NZ\_FO834906.1\_prot\_WP\_002918399.1\_515 [gene=kdsD] [locus\_tag=BN49\_RS03780] [protein=arabinose-5-phosphate isomerase KdsD] [protein\_id=WP\_002918399.1] [location=complement(537444..538430)] [gbkey=CDS]

MSQIDLPTDFDFQQAGRQVLEIEREGLAQLDQYINEDFTHACETIFRCGGKVVVMGMGKSGHIGRKMAAT

FASTGTSAFFVHPGEAAHGDLGMVTPQDVVIALSNSGESNEILALIPVLKRQQVKLICITSRPESSMARA

ADIHLCVKVPKEACPLGLAPTSSTTAALVMGDALAVALLEARGFTAEDFALSHPGGALGRKLLLRVNDIM

HTGDEIPHVGLQATLRDALLEITRKNLGMTAICDDDMNIIGIFTDGDLRRVFDTGVDMRDASIADVMTRG

GIRIRPGTLAVDALNLMQSRHITCVLVADGDHLLGVVHMHDLLRAGVV

>lcl|NZ\_FO834906.1\_prot\_WP\_016531106.1\_516 [locus\_tag=BN49\_RS03785] [protein=calcium/sodium antiporter] [protein\_id=WP\_016531106.1] [location=complement(538445..539422)] [gbkey=CDS]

MLLATALLIIGLLLVVYSADRLVYAASILCRMLGIPPLIIGMTVVSIGTSLPEIMVATAASLHGQTDLAV

GTALGSNITNILLILGLAALLRPFTVHSDILRRELPLMLLVSVLAGLVLYDGQLTRLDGLFLLALALLWL

LFTIKIARLAERQGSDSLTREQLAELPREGSLPVALLWLGVAMIVMPIATRMVVDNSTVLANYFAISELT

VGLTVVAIGTSLPELATAIAGARKGEDDIAIGNIIGANILNIALVLGLPALIAPGSFATEAFTRDYGVML

LVSLIFAVLCWRRQQQPGRLVGALLVGGFVVWLAMLFWTAPLFVE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150950.1\_517 [gene=mlaF] [locus\_tag=BN49\_RS03790] [protein=phospholipid ABC transporter ATP-binding protein MlaF] [protein\_id=WP\_004150950.1] [location=539632..540444] [gbkey=CDS]

MSQTQANLVEVRGIRFSRGDRVIFDDISLSVPRGKITAIMGPSGIGKTTLLRLIGGQIPPDRGEILFDGE

NVPQMTRSRLYTVRKRMSMLFQSGALFTDLNVFDNVAYPLREHTHLPPALLHTTVMMKLEAVGLRGAAKL

MPSELSGGMARRAALARAIALEPDLIMFDEPFVGQDPITMGVLVKLISELNSTLGVTCIVVSHDVPEVLS

IADYAYIVADKKIVAHGSAQSLRENTDPRVRQFIDGIADGPVPFRYPAGDYHHDLLGIGS

>lcl|NZ\_FO834906.1\_prot\_WP\_004150949.1\_518 [gene=mlaE] [locus\_tag=BN49\_RS03795] [protein=lipid asymmetry maintenance ABC transporter permease subunit MlaE] [protein\_id=WP\_004150949.1] [location=540452..541234] [gbkey=CDS]

MLFNALAALGHRGIKTTATFGRAGLMLFNAVVGKPEFRKHAPLLVRQLYNVGVLSMLIIIVSGLFIGMVL

GLQGYLVLTTYSAETSLGMLVALSLLRELGPVVAALLFAGRAGSALTAEIGLMRATEQLSSMEMMAVDPL

RRVISPRFWAGVISLPLLTIIFVAVGIWGGALVGVSWKGIDGGFFWTAMQNAVDWRMDLVNCLIKSLVFA

ITVTWIALFNGYDAIPTSAGISRATTRTVVHASLAVLGLDFVLTALMFGN

>lcl|NZ\_FO834906.1\_prot\_WP\_002918387.1\_519 [gene=mlaD] [locus\_tag=BN49\_RS03800] [protein=outer membrane lipid asymmetry maintenance protein MlaD] [protein\_id=WP\_002918387.1] [location=541239..541790] [gbkey=CDS]

MQTKKTEIWVGVFLLVALLAALFVCLKAANVTSLRTEPTYRLYATFDNIGGLKARSPVRIGGVVVGRVAD

ITLDPKTYLPRVELDIDERYNHIPDTSSLAIRTSGLLGEQYLALNVGFEDPDLGTTILKDGGTIQDTKSA

MVLEDLIGQFLYNSKGGDNQNSGNDKAEAEGHTDATPAAGTTH

>lcl|NZ\_FO834906.1\_prot\_WP\_002918386.1\_520 [gene=mlaC] [locus\_tag=BN49\_RS03805] [protein=phospholipid-binding protein MlaC] [protein\_id=WP\_002918386.1] [location=541809..542444] [gbkey=CDS]

MFKRLLMVAMLVIAPLTAVQAADQSNPYKLMNEAAQKTFDRLKNEQPKIKANPNYLRDIVDQELLPYVQV

KYAGALVLGRYYKEATPAQREAYFAAFREYLKQAYGQALAMYHGQTYQIAPEQPLGSATIVPIRVTIIDP

NGRPPVRLDFQWRKNTQTGNWQAYDMIAEGVSMITTKQNEWSDLLRTKGVDGLTAQLKAISAQPITLEQK

K

>lcl|NZ\_FO834906.1\_prot\_WP\_004185850.1\_521 [gene=mlaB] [locus\_tag=BN49\_RS03810] [protein=lipid asymmetry maintenance protein MlaB] [protein\_id=WP\_004185850.1] [location=542444..542731] [gbkey=CDS]

MSGQLSWTREGETLALHGELDQDLLVPLWEARAQATAGTAIIDLSQTTRVDTAGLALLVHFMALIRRQGR

EAQLVGKSENLQTLIGLYNLPADLI

>lcl|NZ\_FO834906.1\_prot\_WP\_004144910.1\_522 [gene=ibaG] [locus\_tag=BN49\_RS03815] [protein=BolA family iron metabolism protein IbaG] [protein\_id=WP\_004144910.1] [location=542871..543125] [gbkey=CDS]

MENHEIQTVLMNALPLQEVHVSGDGSHFQVIAVGEMFDGMSRVKKQQSVYAPLMEYIADNRIHALSIKAF

TPQEWARDRKLNGF

>lcl|NZ\_FO834906.1\_prot\_WP\_002918382.1\_523 [gene=murA] [locus\_tag=BN49\_RS03820] [protein=UDP-N-acetylglucosamine 1-carboxyvinyltransferase] [protein\_id=WP\_002918382.1] [location=543179..544438] [gbkey=CDS]

MDKFRVQGPTRLQGEVTISGAKNAALPILFSALLAEEPVEIQNVPKLKDIDTTMKLLSQLGAKVERNGSV

WIDAGPVDVFCAPYDLVKTMRASIWALGPLVARFGQGQVSLPGGCAIGARPVDLHISGLEQLGAEIKLEE

GYVKASVSGRLKGAHIVMDKVSVGATVTIMSAATLAEGTTIIENAAREPEIVDTANFLNALGAKITGQGS

DRITIEGVQRLGGGVYRVLPDRIETGTFLVAAAISGGKILCRNAQPDTLDAVLAKLRDAGADIETGEDWI

SLDMHGNRPKAVNVRTAPHPGFPTDMQAQFTLLNLVAEGTGVITETIFENRFMHIPELIRMGAHAEIESN

TAICHGVKQLSGAQVMATDLRASASLVLAGCIAEGTTIVDRIYHIDRGYERIEDKLQALGANIQRVKGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002918381.1\_524 [gene=sfsB] [locus\_tag=BN49\_RS03825] [protein=DNA-binding transcriptional regulator SfsB] [protein\_id=WP\_002918381.1] [location=complement(544494..544766)] [gbkey=CDS]

MDKFIDWHPADIVAGLRKRGTSLAAESRRHGLSSSTLANALTRPWPKGELIIATALETQPWVIWPSRYHD

PVTHEFIDRTQMMRQKKIDK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530973.1\_525 [gene=ispB] [locus\_tag=BN49\_RS03830] [protein=octaprenyl diphosphate synthase] [protein\_id=WP\_016530973.1] [location=complement(544964..545935)] [gbkey=CDS]

MNLEKINELTAQDMAGVNATILEQLNSDVQLINQLGYYIVSGGGKRIRPMIAVLAARTVGYQGSAHVTIA

ALIEFIHTATLLHDDVVDESDMRRGKATANAAFGNAASVLVGDFIYTRAFQMMTQLGSLKILEVMSEAVN

VIAEGEVLQLMNVNDPDITEENYMRVIYSKTARLFEAASQCAGLLADCTAEEERALQDYGRYLGTAFQLI

DDLLDYSSDGERLGKNVGDDLNEGKPTLPLLHAMHHGTPDQSAMIRGAIEQGNGRHLLDAVLETMATCGS

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918379.1\_526 [gene=rplU] [locus\_tag=BN49\_RS03835] [protein=50S ribosomal protein L21] [protein\_id=WP\_002918379.1] [location=546195..546506] [gbkey=CDS]

MYAVFQSGGKQHRVSEGQTVRLEKLDIATGEAVEFAEVLMIANGEEIKIGVPFVEGGVIKAEVVAHGRGE

KVKIVKFRRRKHYRKQQGHRQWFTDVKITGISA

>lcl|NZ\_FO834906.1\_prot\_WP\_002434222.1\_527 [gene=rpmA] [locus\_tag=BN49\_RS03840] [protein=50S ribosomal protein L27] [protein\_id=WP\_002434222.1] [location=546527..546784] [gbkey=CDS]

MAHKKAGGSTRNGRDSEAKRLGVKRFGGEAVLAGSIIVRQRGTKFHAGTNVGCGRDHTLFALTDGKVKFE

VKGPKNRKFISIVAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004149938.1\_528 [locus\_tag=BN49\_RS03845] [protein=DMT family transporter] [protein\_id=WP\_004149938.1] [location=546878..547843] [gbkey=CDS]

MKQQAGIGIILALTTAMCWGALPIAMKQVLEVMAPPTVVFYRFLMASIGLGAILAIKGKLPPMRIFRKPR

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MFFNTSLIEIFTRLTDYTWGVIFGVAAATVWVSYGVAQKVLLRRLASQQILFLLYTLCTIALLPLAEPGV

ISRLSSWQLACLIFCGLNTLVGYGALAEAMARWQAAQVSALITLTPLFTLLFSDLLSMAWPDVFARPMLN

LIGYLGAFVVVAGAMYSAIGHRLWGRWRKREAVVPLPRSGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002918377.1\_529 [gene=cgtA] [locus\_tag=BN49\_RS03850] [protein=Obg family GTPase CgtA] [protein\_id=WP\_002918377.1] [location=547859..549037] [gbkey=CDS]

MKFVDEATILVVAGDGGNGCVSFRREKYIPKGGPDGGDGGDGGDVWLEADENLNTLIDYRFEKSFRAERG

QNGQSRDCTGKRGKDVTVKVPVGTRVIDQGTGETMGDMTKHGQRLMVAKGGWHGLGNTRFKSSVNRTPRQ

KTMGTPGDKRDLQLELMLLADVGMLGMPNAGKSTFIRAVSAAKPKVADYPFTTLVPSLGVVRMDNEKSFV

VADIPGLIEGAAEGAGLGIRFLKHLERCRVLLHLIDIDPIDGSDPVENARIIIGELEKYSEKLASKPRWL

VFNKIDLMDKAEAEAKAKAIAEALGWEEKFYLISAASQQGVKELCWDVMTFIIENPIVQAEEEQKPEKVE

FMWDDYHRQQLEEAEAEAEDDEDWDDDWDEDDEEGVEFIYKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002918376.1\_530 [gene=dacB] [locus\_tag=BN49\_RS03855] [protein=serine-type D-Ala-D-Ala carboxypeptidase] [protein\_id=WP\_002918376.1] [location=complement(549089..550522)] [gbkey=CDS]

MRFPRFIIGLTAGIALSAQAANIDEYINQLPAGANLAFMAQKVGASTPEIDYHSQQMALPASTQKVITAL

AALLQLGPDFRFTTTLETKGSLDGGVLKGDLIARFGGDPTLKRQDIRNMVATLKKAGVQRIEGNVLIDTS

VFASHDKAPGWPWNDLTQCFSAPPAAAIVDRNCFSVSLYSAQKPGDVAFIRVASYYPVTMFSQVRTLARG

SSEAQYCELDVVPGDLNRYTLTGCLPQRSEPLPLAFAIQDGASYAGAILKAELAQAGITYSGTLLRQTLA

NEPGTVLATSQSAPLHDLLRIMLKKSDNMIADTVFRTIGHARFGVPGTWRAGSDAVRQILRQQAGVDLGN

TIIADGSGLSRHNLIAPATMMQVLQYIAQHDTELNFISMLPLAGHDGSLQYRAGLHQAGVDGKVSAKTGS

LQGVYNLAGFITTASGQKMAFVQYLSGYAVEPADQRNRRIPLVRFESRLYKDLYQNN

>lcl|NZ\_FO834906.1\_prot\_WP\_002918375.1\_531 [gene=greA] [locus\_tag=BN49\_RS03860] [protein=transcription elongation factor GreA] [protein\_id=WP\_002918375.1] [location=550758..551234] [gbkey=CDS]

MQAIPMTLRGAEKLREELDYLKSVRRPEIIAAIAEAREHGDLKENAEYHAAREQQGFCEGRIKDIEAKLS

NAQVIDITKMPNNGRVIFGSTVSVLNLDTDEEQTYRIVGDDEADFKQNLISVNSPIARGLIGKEQDDVVT

IRTPGGEVEYEITKVEYL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530974.1\_532 [gene=yhbY] [locus\_tag=BN49\_RS03865] [protein=ribosome assembly RNA-binding protein YhbY] [protein\_id=WP\_016530974.1] [location=complement(551387..551680)] [gbkey=CDS]

MNLSTKQKQHLKGLAHPLKPVVMLGNNGLTEGVLAEIEQALGHHELIKVKIASEDRETKALIVEAIVRET

GACIVQVIGKTLVLYRPTPERKISLPR

>lcl|NZ\_FO834906.1\_prot\_WP\_002918373.1\_533 [gene=rlmE] [locus\_tag=BN49\_RS03870] [protein=23S rRNA (uridine(2552)-2'-O)-methyltransferase RlmE] [protein\_id=WP\_002918373.1] [location=551804..552433] [gbkey=CDS]

MTGKKRSASSSRWLQEHFSDKYVQQAQKKGLRSRAWFKLDEIQQSDKIFKPGMTVVDLGAAPGGWSQYAV

TQIGNSGRIIACDLLPMDPIVGVDFLQGDFRDELVLKALLERVGDSKVQVVMSDMAPNMCGTPAVDIPRA

MYLVELALEMSRDVLAPGGSFVVKVFQGEGFDEYLREIRSLFTKVKVRKPDSSRARSREVYIVATGRKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002918372.1\_534 [gene=ftsH] [locus\_tag=BN49\_RS03875] [protein=ATP-dependent zinc metalloprotease FtsH] [protein\_id=WP\_002918372.1] [location=552533..554467] [gbkey=CDS]

MAKNLILWLVIAVVLMSVFQSFGPSESNGRKVDYSTFLQEVNQDQVREARINGREINVTKKDSNRYTTYI

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VPFFTISGSDFVEMFVGVGASRVRDMFEQAKKAAPCIIFIDEIDAVGRQRGAGLGGGHDEREQTLNQMLV

EMDGFEGNEGIIVIAATNRPDVLDPALLRPGRFDRQVVVGLPDVRGREQILKVHMRRVPLAPDIDAAIIA

RGTPGFSGADLANLVNEAALFAARGNKRVVSMVEFEKAKDKIMMGAERRSMVMTEAQKESTAYHEAGHAI

IGRLVPEHDPVHKVTIIPRGRALGVTFFLPEGDAISASRQKLESQISTLYGGRLAEEIIYGPEHVSTGAS

NDIKVATNLARNMVTQWGFSDKLGPLLYAEEEGEVFLGRSVAKAKHMSDETARIIDQEVKSLIERNYGRA

RQLLNDNMDILHAMKDALMKYETIDAPQIDDLMARREVRPPAGWEEPGSSNNSDNNGTPRAPRPVDEPRT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918371.1\_535 [gene=folP] [locus\_tag=BN49\_RS03880] [protein=dihydropteroate synthase] [protein\_id=WP\_002918371.1] [location=554561..555409] [gbkey=CDS]

MKLVAQGSTLDLSHPHVMGILNVTPDSFSDGGAHNSLIEAVKHANLMINAGATIIDIGGESTRPGAAEVS

VEEELARVIPVVEAIAQRFEVWISVDTSKAEVIRQSARAGAHIINDIRSLTEPGALQAAAETGLPVCLMH

MQGQPKTMQEAPKYEDVFADVERFFNEHIVRCEQAGIAKEKLLLDPGFGFGKNLSHNYQLLARLGEFHHF

GLPLLVGMSRKSMVGQLLNVGPSERLNGSLACAVIAAMQGAQIIRVHDVKETVEALRVVEATLAAKGKKR

YE

>lcl|NZ\_FO834906.1\_prot\_WP\_002918370.1\_536 [gene=glmM] [locus\_tag=BN49\_RS03885] [protein=phosphoglucosamine mutase] [protein\_id=WP\_002918370.1] [location=555402..556739] [gbkey=CDS]

MSNRKYFGTDGIRGRVGDAPITPEFVLKLGWAAGKVLARHGSRKIIIGKDTRISGYMLESALEAGLAAAG

LSASFTGPMPTPAIAYLTRAFRAEAGIVISASHNPFYDNGIKFFSIEGTKLPDDVEEAIEAEMEKELTCV

DSAELGKASRIVDAAGRYIEFCKGTFPNELSLGTLKVVVDCAHGATYHIAPNVFRELGAQVIAMGCEPDG

LNINEEVGATDVRALQARVLAEKADLGIAYDGDGDRVIMVDHEGNKVDGDQILYIIAREGLRQGQLRGGA

VGTLMSNMGLELALKQLGIPFARAKVGDRYVLEMLQEKGWRIGAENSGHVILLDKTTTGDGIVASLQVVA

AMVRNHMSLHDLCSGMKMFPQLLVNVRFTEGSGNPLENEHVKAVTAEVEAALGKRGRVLLRKSGTEPLIR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918369.1\_537 [gene=secG] [locus\_tag=BN49\_RS03890] [protein=preprotein translocase subunit SecG] [protein\_id=WP\_002918369.1] [location=556969..557298] [gbkey=CDS]

MYEALLVVFLIVAIGLVGLVMLQQGKGADMGASFGAGASGTLFGSSGSGNFMTRMTGILAALFFIISLAL

GNINSNKTSKGSEWDNLSAPKTEQTQPTAPAQPTSDIPH

>lcl|NZ\_FO834906.1\_prot\_WP\_014906872.1\_538 [locus\_tag=BN49\_RS30835] [protein=hypothetical protein] [protein\_id=WP\_014906872.1] [location=557692..557940] [gbkey=CDS]

MRRYFQDNTALISRLNHSLKSHYLQDVERRDVFDRHSEAYKVYGALTRLEQMASMNEVYRKENNVAGLQE

INRVLKSVPLTS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530976.1\_539 [locus\_tag=BN49\_RS03905] [protein=YfaZ family outer membrane protein] [protein\_id=WP\_016530976.1] [location=complement(557982..558533)] [gbkey=CDS]

MKSIAATMVAVTIALGASSAACAAVNLHGEAGAEFTNLSASFGAGEPGMTFSSQWAHSDNDGDSVGLGMG

YNFNLGPFLMTLGGKAVYLNPKDGDEGYAIAAGGGAELPLGQYFTLFGEGYYSPDSMSSGVEDYVEANAG

VRLNVLPSLNIEAGYRYIDMAGKDGNRDNTLADGAYAGVNFRF

>lcl|NZ\_FO834906.1\_prot\_WP\_004174150.1\_540 [locus\_tag=BN49\_RS03910] [protein=winged helix-turn-helix transcriptional regulator] [protein\_id=WP\_004174150.1] [location=complement(558875..559504)] [gbkey=CDS]

MNIKPPIRPQKTIDRLIDVLEPHATPVNAIARKRLTWEYKGKTQLFIFKKGELSIIRNSDRLLMVTVYEP

HLFGVAEMLQPSRSHSLRAEVSCELLRIDHDLASALFRQHNLWEEVTSLLAYHTSYMVYRDDLVLQQRTY

SVIRNHLLEMMLLSEETRQRVSILEYIQDRTLLSRSSILNVLSALKKGGYIAFARGGYLQNIVSLPEKF

>lcl|NZ\_FO834906.1\_prot\_WP\_004144895.1\_541 [gene=argG] [locus\_tag=BN49\_RS03915] [protein=argininosuccinate synthase] [protein\_id=WP\_004144895.1] [location=complement(559674..561017)] [gbkey=CDS]

MTTILKHLPVGQRIGIAFSGGLDTSAALLWMRKKGAVPYAYTANLGQPDEDDYDAIPRRAKEYGAEGARL

IDCRKQLVAEGIAAIQCGAFHNTTGGLTYFNTTPLGRAVTGTMLVAAMKEDGVNIWGDGSTYKGNDIERF

YRYGLLTNAELQIYKPWLDSDFINELGGRHEMSEFMIACGFDYKMSVEKAYSTDSNMLGATHEAKDLEFL

NSSVKIVNPIMGVKFWDENVKIPAEEVTVRFEQGHPVALNGKTFADDVEMMLEANRIGGRHGLGMSDQIE

NRIIEAKSRGIYEAPGMALLHIAYERLLTGIHNEDTIEQYHAHGRQLGRLLYQGRWFDSQALMLRDSLQR

WVASQITGEVTLELRRGNDYSILNTVSDNLTYKAERLTMEKGDSMFTAEDRIGQLTMRNLDITDTREKLF

GYAQSGLLSASSATGLPQVENLENKGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002918364.1\_542 [gene=rimP] [locus\_tag=BN49\_RS03930] [protein=ribosome maturation factor RimP] [protein\_id=WP\_002918364.1] [location=561610..562062] [gbkey=CDS]

MSTLEQKLTEMLTAPVEALGFELVGIEFIRGRTSTLRIYIDSEDGINVDDCADVSHQVSAVMDVEDPITV

AYNLEVSSPGLDRPMFTAEHYQRFTGEEVALVLRMAVQNRRKWQGIIKAVDGEMITVTVEGKDEVFALSN

IQKANLVPHF

>lcl|NZ\_FO834906.1\_prot\_WP\_002918252.1\_543 [gene=nusA] [locus\_tag=BN49\_RS03935] [protein=transcription termination factor NusA] [protein\_id=WP\_002918252.1] [location=562090..563577] [gbkey=CDS]

MNKEILAVVEAVSNEKALPREKIFEALESALATATKKKYEQEIDVRVEIDRKSGDFDTFRRWLVVEEVTQ

PTREITLEAARFEDESMNVGDYVEDQIESVTFDRITTQTAKQVIVQKVREAERAMVVDQFREHEGEIITG

VVKKVNRDNITLDLGNNAEAVILREDMLPRENFRPGDRIRGVLYAVRPEARGAQLFVTRSKPEMLIELFR

IEVPEIGEEVLEIKAAARDPGSRAKIAVKTNDKRIDPVGACVGMRGARVQAVSTELGGERIDIVLWDDNP

AQFVINAMAPADVASIVVDEDKHTMDIAVEAGNLAQAIGRNGQNVRLASQLSGWELNVMTVDDLQAKHQA

EAHAAIDTFTKYLDIDEDFATVLVEEGFSSLEELAYVPMKELLEIDGLDEATVEALRERAKNALTTLALA

QEESLGDNKPADDLLNLEGLDRALAFKLAARGVCTLEDLAEQGVDDLADIEGMTDEKAGELIMAARNICW

FGDEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918250.1\_544 [gene=infB] [locus\_tag=BN49\_RS03940] [protein=translation initiation factor IF-2] [protein\_id=WP\_002918250.1] [location=563602..566292] [gbkey=CDS]

MTDVTIKALASEIQTSVDRLIQQFADAGIRKSADDSVTSQEKQTLLTHLNREHGSAPDKLTLQRKTRSTL

NIPGTGGKSKSVQIEVRKKRTFVKRDPQEAERLAAEEQAQREAEEQARREAEEAAKREAQLKAEREAAEQ

AKREVADKAKREAAEKDKVSNQHTDEMTKTAQAEKIRRENEAAELKRKSEEEARRKLEEEARRVAEEARR

MAEENEKNWSETSDSPEDSSDYHVTTSQHARQAEDDNDREVEGGRGRSRSSKAARPAKKGNKHAESKADR

EEARAAVRGGKGGKHRKGSALQQGFQKPAQAVNRDVVIGETITVGELANKMAVKGSQVIKAMMKLGAMAT

INQVIDQETAQLVAEEMGHKVILRRENELEEAVMSDRDTGAAAEPRAPVVTIMGHVDHGKTSLLDYIRST

KVASGEAGGITQHIGAYHVETDNGMITFLDTPGHAAFTSMRARGAQATDIVVLVVAADDGVMPQTIEAIQ

HAKAAQVPVVVAVNKIDKPEADPDRVKNELSQYGILPEEWGGESQFVHVSAKAGTGIDDLLDAILLQAEV

LELKAVRNGMASGAVIESFLDKGRGPVATVLVREGTLHKGDIVLCGFEYGRVRAMRDELGREVLEAGPSI

PVEILGLSGVPAAGDEVTVVRDEKKAREVALYRQGKFREVKLARQQKSKLENMFANMTEGEVHEVNIVLK

ADVQGSVEAISDSLLKLSTDEVKVKIIGSGVGGITETDATLAAASNAILVGFNVRADASARKVIEAESLD

LRYYSVIYNLIDEVKAAMSGMLSPELKQQIIGLAEVRDVFKSPKFGAIAGCMVTEGTIKRHNPIRVLRDN

VVIYEGELESLRRFKDDVNEVRNGMECGIGVKNYNDVRVGDMIEVFEIIEIQRSID

>lcl|NZ\_FO834906.1\_prot\_WP\_002918248.1\_545 [gene=rbfA] [locus\_tag=BN49\_RS03945] [protein=30S ribosome-binding factor RbfA] [protein\_id=WP\_002918248.1] [location=566395..566796] [gbkey=CDS]

MAKEFGRPQRVAQEMQKEIAIILQREIKDPRLGMMTTVSGVEMSRDLAYAKVYVTFLNDKDEAAVKAGIK

ALQEASGFIRSLLGKAMRLRIVPELTFFYDNSLVEGMRMSNLVTSVVKHDDERRVNPDDSKED

>lcl|NZ\_FO834906.1\_prot\_WP\_004144892.1\_546 [gene=truB] [locus\_tag=BN49\_RS03950] [protein=tRNA pseudouridine(55) synthase TruB] [protein\_id=WP\_004144892.1] [location=566796..567740] [gbkey=CDS]

MSRPRRRGRDVHGVLLLDKPQGASSNDVLQKVKRIYNANRAGHTGALDPLATGMLPICLGEATKFSQYLL

DSDKRYRVIAKLGQRTDTSDADGQVVEERPLTFSDEQLAAALDSFRGETQQVPSMYSALKYQGKKLYEYA

RQGIEVPREARPITVYELLFIRREGDELELEIHCSKGTYIRTIIDDLGEKLGCGAHVIFLRRLAVSKYPV

ERMVTLEQLQALVDEAAAQDIPAAQLLDPLLMPMDSPASDYPLVNIPETSAVYFKNGNPVRQSGAPLNGL

VRVMESESGKFLGMGEIDDEGRVAPRRLVVEYPA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918244.1\_547 [gene=rpsO] [locus\_tag=BN49\_RS03955] [protein=30S ribosomal protein S15] [protein\_id=WP\_002918244.1] [location=567889..568158] [gbkey=CDS]

MSLSVEAKAKIVSEFGRGENDSGSTEVQVALLTAQINHLQGHFAEHKKDHHSRRGLLRMVSQRRKLLDYL

KRKDVARYSALIERLGLRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004150944.1\_548 [gene=pnp] [locus\_tag=BN49\_RS03965] [protein=polyribonucleotide nucleotidyltransferase] [protein\_id=WP\_004150944.1] [location=568401..570536] [gbkey=CDS]

MLNPIVRKFQYGQHTVTLETGMMARQATAAVMVSMDDTAVFVTVVGQKKAKPGQDFFPLTVNYQERTYAA

GKIPGGFFRREGRPSEGETLIARLIDRPVRPLFPEGFVNEVQVIATVVSVNPQVNPDIVAMIGASAALSL

SGIPFNGPIGAARVGYINDQYVLNPTQEELKSSKLDLVVAGTEAAVLMVESEAELLSEDQMLGAVVFGHE

QQQIVIQNINDLVKEAGKPRWDWQPEAVNEALNARVAALAESRLSDAYRITDKQERYAQVDVIKSETIAT

LVAEDETLDANELGEILHAIEKNVVRSRVLAGEPRIDGREKDMIRGLDVRTGVLPRTHGSALFTRGETQA

LVTATLGTARDAQNIDELMGERTDSFLFHYNFPPYSVGETGMVGSPKRREIGHGRLAKRGVLAVMPTIEE

FPYTVRVVSEITESNGSSSMASVCGASLALMDAGVPVKAAVAGIAMGLVKEGDNFVVLSDILGDEDHLGD

MDFKVAGSRDGISALQMDIKIEGITKEIMQVALNQAKGARLHILGVMEQAINAPRGDISEFAPRIHTIKI

NPDKIKDVIGKGGSVIRALTEETGTTIEIEDDGTVKIAATDGDKAQHAIRRIEEITAEIEVGRIYNGKVT

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APEAPAAEQGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002918241.1\_549 [gene=nlpI] [locus\_tag=BN49\_RS03970] [protein=lipoprotein NlpI] [protein\_id=WP\_002918241.1] [location=570645..571529] [gbkey=CDS]

MKPFLRWCFVATALTLAGCSSTAWRKDAVLAVPLQPTLQQEVILARMEQILASRALSDDERAQLLYERGV

LYDSLGLRALARNDFSQALAIRPDMPEVFNYLGIYLTQAGNFDAAYEAFDSVLELDPTYNYAHLNRGIAL

YYGGRAKLAQDDLLAFYQDDPNDPFRSLWLYIAERKLDEKRALEALRERLNKSDKEQWGWNIVEFYLGDI

SEKELMTRLKADATDNTSLAEHLSETNFYLGKYYLSLGDKDSATALFKLAVANNVHNYVEHRYALLELSL

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>lcl|NZ\_FO834906.1\_prot\_WP\_085903200.1\_550 [gene=yrbN] [locus\_tag=BN49\_RS30205] [protein=protein YrbN] [protein\_id=WP\_085903200.1] [location=571634..571714] [gbkey=CDS]

MKITVNFHDELCRLAAINFEAHVLHG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529474.1\_551 [locus\_tag=BN49\_RS03975] [protein=DEAD/DEAH family ATP-dependent RNA helicase] [protein\_id=WP\_016529474.1] [location=571707..573623] [gbkey=CDS]

MAEFETTFADLGLKAPILEALTDLGYEKPSPIQAECIPHLLDGRDVLGMAQTGSGKTAAFSLPLLNNIDP

ELRAPQILVLAPTRELAVQVAEAMTEFSKHMRGVNVVALYGGQRYDVQLRALRQGPQIVVGTPGRLLDHL

KRGTLDLSKLSGLVLDEADEMLRMGFIEDVETIMAQIPEGHQTALFSATMPEAIRRITRRFMKEPQEVRI

QSSVTTRPDISQSYWTAYGMRKNEALVRFLEAEDFDAAIIFVRTKNATLEVAEALERNGYNSAALNGDMN

QALREQTLERLKDGRLDILIATDVAARGLDVERISLVVNYDIPMDSESYVHRIGRTGRAGRAGRALLFVE

NRERRLLRNIERTMKLTIPEVELPNAELLSKRRLEKFAAKVQQQLESSDLDQYRALLAKIQPTAEGEELD

VETLAAALLKMAQGERSLIVPPDAPMRPRREFRDRDDRFDRRGDRNDRGPRGDREDRPKRERRDVGDMEL

YRIEVGRDDGVEVRHIVGAIANEGDISSRYIGNIKLFASHSTIELPKGMPGEVLQHFTRTRILNKPMNMQ

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RRRFGGDA

>lcl|NZ\_FO834906.1\_prot\_WP\_004185824.1\_552 [gene=mtr] [locus\_tag=BN49\_RS03980] [protein=tryptophan permease] [protein\_id=WP\_004185824.1] [location=573768..575012] [gbkey=CDS]

MATLTTTATRPSLFGGVVIIGGTIIGAGMFSLPVVMSGAWFFWSLAALVFTWFCMLHSGLMILEANLNYR

IGSSFDTITKDLLGKGWNLVNGVSIAFVLYILTYAYISASGSILHHTFSELSLKVPARAAGFGFALLVAF

IVWMSTKAVSRMTAIVLGAKVITFFLTFGSLLGHVEPTTLFNVAEKNASYAPYLLMTLPFCLASFGYHGN

VPSLMKYYGKDPRTIIRCLTYGTLLALGLYVVWLLVTMGNIPRPQFIDIAQKGGNIDVLVQALSGVLNSR

SLDLLLVVFSNFAVASSFLGVTLGLFDYLADLFGFDDSAMGRFKTALLTFIPPMIGGLVKPDGFLYAIGY

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918234.1\_553 [locus\_tag=BN49\_RS03985] [protein=LLM class flavin-dependent oxidoreductase] [protein\_id=WP\_002918234.1] [location=complement(575057..576064)] [gbkey=CDS]

MTDKSVPFSVLDLAPIPQGSSAKEAFTHSLDLARLAESRGYHRYWLAEHHNMVGIASAATSVLIGYLAAN

TTTLHLGSGGVMLPNHSPLVIAEQFGTLNTLYPGRIDLGLGRAPGSDQPTMRALRRHMSGDVDNFPRDVA

ELVDWFDARDPNPHVRPVPGYGERIPVWLLGSSLYSAQLAAQLGLPFAFASHFAPDMLFQALHLYRSNFK

PSARLEKPYAMVCINIIAADSNRDAEFLFTSMQQAFVKLRRGETGQLPPPVENMHQLWSASEQYGVQQAL

SMSLVGDKTKVRHGLESILRETEADEIMVNGQIFDHQARLHSFDLAMQVKEELLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002918233.1\_554 [locus\_tag=BN49\_RS03990] [protein=U32 family peptidase] [protein\_id=WP\_002918233.1] [location=complement(576208..577086)] [gbkey=CDS]

MKYSLGPVLYYWPKETLEDFYQQAANCSADTIYLGEAVCSKRRATKVGDWIEMAKTLAASGKQVVLSTLA

LVQASSELGELKRYVDNGEFLIEASDLGVVNLCAERKLPFVAGHALNCYNAVTLRLLRKQGMVRWCMPVE

LSRDWLANLLTQCEELGIRNQFEVEVLSYGHLPLAYSARCFTARSEDRPKDECETCCIKYPTGRSMLSQE

NQQVFVLNGIQTMSGYVYNLGNELTSMHGLVDMVRLSPMGNETFAMLEAFRANENGAAPLDLTSNSDCNG

YWKRLPGLVLQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918232.1\_555 [locus\_tag=BN49\_RS03995] [protein=U32 family peptidase] [protein\_id=WP\_002918232.1] [location=complement(577092..578087)] [gbkey=CDS]

MELLCPAGNLPALKAAIENGADAVYIGLKDDTNARHFAGLNFTEKKLQEAVSFVHQHRRKLHIAINTFAH

PDGYARWQRAVDMAAQLGADALILADIAMLEYAAERYPHIERHVSVQASATNEEAIRFYHRNFDVARVVL

PRVLSIHQVKQLARATPVPLEVFAFGSLCIMAEGRCYLSSYLTGESPNTVGACSPARFVRWQQTPQGLES

RLNEVLIDRYQDGENAGYPTLCKGRYLVDGERYHALEEPTSLNTLELLPELMAANIASVKIEGRQRSPAY

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>lcl|NZ\_FO834906.1\_prot\_WP\_002918231.1\_556 [locus\_tag=BN49\_RS04000] [protein=SCP2 domain-containing protein] [protein\_id=WP\_002918231.1] [location=578309..578833] [gbkey=CDS]

MLDKLRSRLVHFGPSLMSVPVKLAPFALKRQVLEQVLSWQFRQALAEGELEFLEGRWLSIHVRDIGLLWY

TSVVDGRLVVSQQADADVSFSADASDLLMIAARKQDPDTLFFQRRLVIEGDTELGLYVKNLMDAIELEQM

PKALRVMLLQLADFVEAGLKSPQKPEQTSVGEAC

>lcl|NZ\_FO834906.1\_prot\_WP\_002918229.1\_557 [locus\_tag=BN49\_RS04005] [protein=N-acetyltransferase] [protein\_id=WP\_002918229.1] [location=578827..579330] [gbkey=CDS]

MLIRVEIGIDAPGIDALLRRTFGRDAEAQLVHDLREDGLITLGVVATDDEGQVIGYVAFSPVAVEGEELQ

WVGLAPLAVDERYRGQGIGRQLVYEGLDSLNEFGYAAVVTLGDPDLYRRFGFEPAARFDLRCRWPDSAEA

FQVHRLADDALDGVHGQVEYSEHFNRL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529428.1\_558 [locus\_tag=BN49\_RS04010] [protein=GIY-YIG nuclease family protein] [protein\_id=WP\_016529428.1] [location=complement(579317..579607)] [gbkey=CDS]

MTVCWFLYLIRTADNRLYTGITTDVPRRFRQHQAGKGAKALRGKGDLQLAFSHEVGEHSLALRLEYRIKQ

LTKREKERLVAGEDAFETLLARLKDD

>lcl|NZ\_FO834906.1\_prot\_WP\_002918223.1\_559 [locus\_tag=BN49\_RS04015] [protein=YhbP family protein] [protein\_id=WP\_002918223.1] [location=579657..580100] [gbkey=CDS]

MDTLAAIGRWLSKQHVVTWCVSREDELWCANAFYVYDPDTVAFYLLSEEHTRHGQMTGQRAKVAGTVNGQ

PKTVALIRGVQFKGEIRRLSGDEEARMRQRYVKRFPVARMLSAPVWEIRPDEIKFTDNTLGFGKKLHWRR

DAGAEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002918221.1\_560 [locus\_tag=BN49\_RS04020] [protein=type 1 glutamine amidotransferase] [protein\_id=WP\_002918221.1] [location=complement(580062..580598)] [gbkey=CDS]

MSKKIAVLITDDFEDSEFTSPAEAFKLAGHQVITIEKQAGKTVKGKQGEAEVAIDRAIDDVTPGEFDALL

LPGGYSPDQLRGDERFVTFTRDFVNGGKPVFAICHGPQLLISADVIRGRKLTAVKPIVVDVKNAGGEFYD

QEVVVDNEQLVTSRTPDDLPAFNREALRLLGAGITPPV

>lcl|NZ\_FO834906.1\_prot\_WP\_016531003.1\_561 [locus\_tag=BN49\_RS04025] [protein=NAD(P)H-binding protein] [protein\_id=WP\_016531003.1] [location=580727..581374] [gbkey=CDS]

MSQVLLTGATGLVGGHLLRLLQNEPRISTIAAPTRRPLAPAEGVFNPHDPQLTDALAQVVDPVDIVFCCL

GTTRREAGSKEAFVHADYTLVVDTALTGKRLGAQHMLVVSAMGANAHSPFFYNRVKGEMEAALIEQDWPR

LTIARPSMLSGEREKKRANETFLAPLFRLLPGNWKSIAARDVATALLAEALSPTHEGVRILTSSELRERA

ARQAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004188467.1\_562 [locus\_tag=BN49\_RS04030] [protein=permease] [protein\_id=WP\_004188467.1] [location=581450..582490] [gbkey=CDS]

MAGQSSSQAASPFQWWKPALFFLVVIVGLWYVKWQPYYGKAFTAAETHSIGKSILAQADANPLMAAWDYA

MVYFLAVWKAAVLGVLLGSLIQVLIPRDWLLRTLGQSRFQGTLLGAIFSLPGMMCTCCAAPVAAGMRKQQ

VSMGGALAFWMGNPLLNPATLVFMGFVLGWQFALVRLVAGLATVLTVATLVQKWVKEAATQPVAVPAAPS

EATQGGFFSRWLRALWTLFWNTIPVYILAVLVLGAARVWLFPHADGVVDNTLFWVIAMAIAGCLFVIPTA

AEIPIVQTMMLAGMGTAPALALLITLPAVSVPSLIMLRKAFPAKALWLTGGLVALCGAIVGALALV

>lcl|NZ\_FO834906.1\_prot\_WP\_002918214.1\_563 [gene=yraP] [locus\_tag=BN49\_RS04035] [protein=division/outer membrane stress-associated lipid-binding lipoprotein] [protein\_id=WP\_002918214.1] [location=complement(582612..583187)] [gbkey=CDS]

MKALSPLAILLSALLLQGCVAAAVVGTAAVGTKAATDPRTVGTQVDDSTLELRVNSALSKDEQIKKQARI

NVTAYQGKVLLTGQSPTPDLSARAKQIAMGVEGTTEVFNEVRQGQPIGLGTASSDTWITTKVRSQLLSTD

QVKSSNVKVTTENSEVFLMGLVTDREGRAAADIASRVSGVSRVTTAFTYIK

>lcl|NZ\_FO834906.1\_prot\_WP\_002918211.1\_564 [gene=diaA] [locus\_tag=BN49\_RS04040] [protein=DnaA initiator-associating protein DiaA] [protein\_id=WP\_002918211.1] [location=complement(583197..583787)] [gbkey=CDS]

MLDRIKACFTESIQTQIAAAEALPDAISRAAMTLVQSLLNGNKILCCGNGTSAANAQHFAASMINRFETE

RPGLPAIALNTDNVVLTAIANDRLHDEIYAKQVRALGHAGDVLLAISTRGNSRDIVKAVEAAVTRDMTIV

ALTGYDGGELAGLLGQQDVEIRIPSHRSARIQEMHMLTVNCLCDLIDNTLFPHQDD

>lcl|NZ\_FO834906.1\_prot\_WP\_002918206.1\_565 [locus\_tag=BN49\_RS04045] [protein=YraN family protein] [protein\_id=WP\_002918206.1] [location=complement(583813..584199)] [gbkey=CDS]

MAQVPAGKNRSGQLSKQTGDAWENQARRWLEGQGLRFIAANARERGGEIDLIMRDGTVTVFIEVRYRRSA

RYGDAAASVTPQKQQRLLKAARLWLCRQNGSFETVDCRFDVVAFTGNDIQWLKNAFGE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042292.1\_566 [locus\_tag=BN49\_RS04050] [protein=penicillin-binding protein activator] [protein\_id=WP\_046042292.1] [location=complement(584157..586265)] [gbkey=CDS]

MVPSTFLRSKPARCLPVLLATLIFAGCGTHTQDQSAAFMQGTSQANSSFYLQQMQQSTNDSKTNWQLLAI

RALLQEGKKQQAIDLFNQLPANLNSTQAREQSLLAVEVKLAQNDYQAARNLLAKIDPTSLEQPQQARYWQ

AQIDASQGKPSLTLLRALIAQQPLLSDAKQRQKNIDATWQALTSMPQDQANALVINADENILQGWLDLQR

MWFDNRNDPTLLKAGVKDWQTRYPQNPGAKMLPTALVNMQNYKPASINKIALFLPLNGQASIFGRTIQQG

FEAAKNGAPSVTGSAVPAQVAQAANVSGNDDVVSPSQAEISDLTAAGSRADPVQAPTQDQAAPAAEPAAQ

APATSATPQTTASPATQPVTAPAAQPQPVVATAANPSAELKIYDTTSQPISQLLAQAQQDGATLVVGPLL

KENVEEVIKSNTPLNVLALNQPEKVESRANLCYFALSPEDEARDAARHIHQQGKQTPLLLVPRGALGDRV

VSAFADEWLKLGGASVLQQRFGSTAELRAGVNGGGGIALSGTPVSTLPSAQNSILGSADEMPVSSGGSVD

AAYILATPEQIAYIKPMIAMRNGSQSNVTLYASSRSAQGTAGPDFRLEMEGLQYSEIPMLAGSNPSLMQQ

ALSAVRNDYSLARLYAMGADAWSLANHFTQMRQTPGFELNGNTGDLTANQDCVINRKLSWLKYQQGKIVP

AS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042294.1\_567 [gene=rsmI] [locus\_tag=BN49\_RS04055] [protein=16S rRNA (cytidine(1402)-2'-O)-methyltransferase] [protein\_id=WP\_046042294.1] [location=586329..587192] [gbkey=CDS]

MKQHESADNSQGQLYIVPTPIGNLSDITQRALEVLQAVDLIAAEDTRHTGLLLQHFAINARLFALHDHNE

QQKAETLLAKLKEGQNIALVSDAGTPLINDPGYHLVRTCREANIRVVPLPGPCAAIAALSAAGLPSDRFC

YEGFLPAKSKGRRDTLKALEEEPRTLIFYESTHRLVESLEDICAVLGEFRYVVLARELTKTWESIHGAPI

GELVAWVKEDENRRKGEMVLIVEGFKAQEEALPAAALRTLALLQAELPLKKAAALAAEIHGVKKNALYKY

ALEQQGE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042296.1\_568 [gene=garD] [locus\_tag=BN49\_RS04060] [protein=galactarate dehydratase] [protein\_id=WP\_046042296.1] [location=complement(587393..588964)] [gbkey=CDS]

MADIAIRQQSPTAFYIKVDPTDNVAIIVNDRGLTAGTRFPDGLTLVEHIPQGHKVALVDIPAHGEIIRYG

EVIGYAVRDIPQGSWIDESLVELPTAPPLNTLPLATKVPEQLPPLEGYTFEGYRNADGSVGTKNLLGITT

SVHCVAGVVDYVVKIIERDLLPNYPNVDGVVGLNHLYGCGVAINAPAAVVPIRTIHNIALNPNFGGEVMV

IGLGCEKLQPERLLQGTEDVKSIPVDSASIVSLQDEKHVGFKSMVDDILQVAERHLAKLNQRQRETCPAS

ELVVGMQCGGSDAFSGVTANPAVGYASDLLVRCGATVMFSEVTEVRDAIHLLTPRAINEEVGKRLLEEMA

WYDNYLDMGKTDRSANPSPGNKKGGLANVVEKALGSIAKSGKSAIVEVLSPGQRPTKRGLIYAATPASDF

VCGTQQVASGITVQVFTTGRGTPYGLMAVPVIKMATRTELANRWYDLMDINAGTIATGEETIEDVGRKLF

EFILDVASGRKKTFSDQWGLHNQLAVFNPAPVT

>lcl|NZ\_FO834906.1\_prot\_WP\_016531008.1\_569 [locus\_tag=BN49\_RS04070] [protein=MFS transporter] [protein\_id=WP\_016531008.1] [location=589357..590688] [gbkey=CDS]

MILDSTLDEKKGIPTRYLILLMIFVVTAVNYGDRATLSIAGTEVAKELGLSAVSMGYIFSAFGWAYLLMQ

IPGGWLLDKFGSKKVYSYSLFFWSRFTFLQGFIDVFPLAWAGVSMFFMRFMLGFSEAPSFPANARIVAAW

FPAKERGTASAIFNAAQYFSLALFSPLLGWLTFALGWEHVFTVMGIIGFVLTIIWVKFVHNPTDHPRMSA

AELKYISEGGAVVDMDHKKEATPAAGPKMDYIRQLLTNRMMLGVFFGQYFLNTITWFFLTWFPIYLVQDK

GMSILKVGFVASIPALFGFAGGVLGGLFSDYLIGRGCTLTFARKLPIVLGMLLASSIILCNYTASTPLVI

TLMALAFFGKGFGALGWPVISDVAPKEIVGLCGGVFNVFGNVASIATPLVIGYIVSELHSFNGALIFVGG

SALMMMVCYLFVVGDIKRMELQK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531009.1\_570 [gene=garL] [locus\_tag=BN49\_RS04075] [protein=2-dehydro-3-deoxyglucarate aldolase] [protein\_id=WP\_016531009.1] [location=590715..591485] [gbkey=CDS]

MDNAIFPNKFKAALAAHQVQIGCWCALANPISTEVLGLAGFDWLVLDAEHAPNDVTTLIPQLMALKGSSS

AQVVRVPTNEPIIIKRMLDIGFYNFLVPFVETAEQAAQAVASTRYPPEGIRGVSVSHRGNMFGTVPDYFA

QSNKNISILVQIESQTGVDNVEAIAATEGVDGVFVGPSDLAAALGHLGNAAHPEVQRAIQYIFASAKKHG

KPSGILAPVEADARRYLEWGATFVAVGSDLGVFRSATQKLADAFKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002917952.1\_571 [gene=garR] [locus\_tag=BN49\_RS04080] [protein=2-hydroxy-3-oxopropionate reductase] [protein\_id=WP\_002917952.1] [location=591512..592402] [gbkey=CDS]

MTIKVGFIGLGIMGKPMSKNLLKAGYSLVVSDRNPEAIADVIAAGAETATTPKAIAEQCEVIITMLPNSP

HVKEVALGENGIIEGAKPGTVVIDMSSIAPLASREISEALKAKGIDMLDAPVSGGEPKAIDGTLSVMVGG

DKAIFDKYYDLMKAMAGSVVHTGDIGAGNVTKLANQVIVALNIAAMSEALTLATKAGVNPDLVYQAIRGG

LAGSTVLDAKAPMVMDRNFKPGFRIDLHIKDLANALDTSHGVGAQLPLTAAVMEMMQALRADGLGTADHS

ALACYYEKLAKVEVTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004900844.1\_572 [gene=garK] [locus\_tag=BN49\_RS04085] [protein=glycerate 2-kinase] [protein\_id=WP\_004900844.1] [location=592467..593612] [gbkey=CDS]

MKIVIAPDSYKESLSASEVAQAIEKGFREIFPDAQYVSLPVADGGEGTVEAMIAATQGKEHFAWVTGPLG

ERVKACWGMSGDGVTAFIEMAAASGLGLVPPDKRNPLITTSRGTGELILQALEHGAERIIIGIGGSATND

GGAGMMQALGARLCDAEGQEIGHGGGSLSRLSRIDLSAIDPRLRDRMIHVACDVTNPLVGERGASRIFGP

QKGATEAMIVELDRNLAHYADVIKASLQVDVKSIPGAGAAGGMGAALMAFLNAELRSGIEIVTEALKLEE

QIHDCSLVVTGEGRLDSQSVHGKVPVGVARVAKKYRKPVIGIAGSLTHDVGVVHQHGIDAVFSVLTSVST

LEEAFRGAFDNIYRASRNIAATLQVGMTTEG

>lcl|NZ\_FO834906.1\_prot\_WP\_004150939.1\_573 [locus\_tag=BN49\_RS04090] [protein=OB-fold putative lipoprotein] [protein\_id=WP\_004150939.1] [location=complement(594141..594605)] [gbkey=CDS]

MLLRFRVLPLVFVISLLSGCGLASKAFYSAGDKLFQPGDDAVASMQTYSVAQFLQPFTLNPAKASSDYLG

KWVKVRGVIVDIRRKSGIAGSYYFIVTMRDEQNKTDKRLTFNFGSHNSADVEALSNGSVATIVGQVHQVQ

DSTIPTLQNPKVVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004149907.1\_574 [locus\_tag=BN49\_RS04100] [protein=Spy/CpxP family protein refolding chaperone] [protein\_id=WP\_004149907.1] [location=594913..595323] [gbkey=CDS]

MKLITRIAFATLLTTGFSITAQAADVKAAPAPAQDPIVQHLKLTNDQVAKIKSLHQQLESNVQQISQQEI

KDGALINVIDSGKWDEKAVNDQLAAFSKIDQQVRYYRVKYYFEVNKVLTPEQRTQVKKDLADALSE

>lcl|NZ\_FO834906.1\_prot\_WP\_002917926.1\_575 [locus\_tag=BN49\_RS30840] [protein=hypothetical protein] [protein\_id=WP\_002917926.1] [location=complement(595397..595564)] [gbkey=CDS]

MSKKKNRKKASPTPLAPVQPQVAGAASFGYDEMLSELEAIVAEAEIRLRDEESLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002917925.1\_576 [locus\_tag=BN49\_RS04110] [protein=pirin family protein] [protein\_id=WP\_002917925.1] [location=complement(595589..596290)] [gbkey=CDS]

MITTRTAKQCGQADFGWLQARYTFSFGHYFDPKLLGFASLRVLNQEVLAPGASFQARTYPKVDILNLILE

GEAEYRDSDGNHVQAKAGEALLIATQPGVSYSEHNLSKEQSLTRMQLWLDACPQRENPLQQKINVADATL

QLLASPEGGDNSLQLRQQAWVYHIALEKGEQINVQLHGPRAYLQSIHGSVHAVAQEQQKQALTCGDGAFI

RDEANITLVADTPLRALLIDLPV

>lcl|NZ\_FO834906.1\_prot\_WP\_004144865.1\_577 [locus\_tag=BN49\_RS04115] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004144865.1] [location=596395..597291] [gbkey=CDS]

MAKERALTLEALRVMDAIDRRGSFAAAADELGRVPSALSYTMQKLEEELDVVLFDRSGHRTKFTNVGRML

LERGRVLLEAADKLTTDAEALSRGWETHLTIVTEALVPTPDLFPLIEKLATKSNTQLSIITEVLAGAWER

LEQGRADIVVAPDMHFRSSSEINSRKLYSVLSVYVAAPDHPIHQEPEPLSEVTRVKYRGVAVADTARERP

VLTVQLLDKQPRLTVSTIEDKRQALLAGLGVATMPYPLVEKDIAEGRLRVVSPEYTNEIDIIMAWRRDSM

GEAKSWCLREIPKLFAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002917923.1\_578 [locus\_tag=BN49\_RS04120] [protein=DUF805 domain-containing protein] [protein\_id=WP\_002917923.1] [location=complement(597333..597701)] [gbkey=CDS]

MDWYLKVLKNYIGFGGRARRKEYWMFILVNLILTGVLSIIDKMLGWQRAGGEGILTTIYGVLVFLPWWAV

QFRRLHDTDRSAWWLLLLLIPVIGWLVILIFNCQRGTEGNNRFGPDPKPFSY

>lcl|NZ\_FO834906.1\_prot\_WP\_002917922.1\_579 [locus\_tag=BN49\_RS04125] [protein=glutathione S-transferase family protein] [protein\_id=WP\_002917922.1] [location=complement(597828..598814)] [gbkey=CDS]

MGQLVDGVWQDTWYDTKSTGGRFKRSVSAFRNWLTADGAAGPSGEGGFAAEKDRYHLYVSLACPWAHRTL

IMRKLKGLEPFLPVSVVNPLMLENGWTFDDSFPEATGDTLYQHDFLYQLYLHADPHYTGRVTVPVLWDKK

QQTIVSNESAEIIRMFNTAFDGLGARAGDYYPPALREQIDELNGWIYDNVNNGVYKAGFATSQQAYDEAV

DAVFTSLERLEQILGQHRYLTGNQLTEADIRLWTTLVRFDPVYVTHFKCDKRRISDYLNLYGFLRDIYQM

PGIAETVSFPHIRHHYYRSHKTINPTGIISIGPQQDLNEPHGRDQRFR

>lcl|NZ\_FO834906.1\_prot\_WP\_002917920.1\_580 [locus\_tag=BN49\_RS04130] [protein=DoxX family protein] [protein\_id=WP\_002917920.1] [location=complement(598895..599287)] [gbkey=CDS]

MKKLEDVGVLVARILMPILFITAGWGKITGYAGTQQYMEAMGVPGALLPLTILLEFGGGLAILFGFLTRT

TALFTAGFTLLTAFLFHSNFAEGVNSLMFMKNLTIAGGYLLLAITGPGAFSIDRVLNKKW

>lcl|NZ\_FO834906.1\_prot\_WP\_002917918.1\_581 [locus\_tag=BN49\_RS04135] [protein=YqjK-like family protein] [protein\_id=WP\_002917918.1] [location=complement(599632..599928)] [gbkey=CDS]

MNGRQERERQKTQLLRQIQQQRLELSACRRHWHEATAPLDRGWHTLLSLRSWLMVGSGLMAVWSVRHPHF

LMRWTKRGLGLWSTWRLVRGILRQSAVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002917917.1\_582 [locus\_tag=BN49\_RS04140] [protein=phage holin family protein] [protein\_id=WP\_002917917.1] [location=complement(599925..600323)] [gbkey=CDS]

MANTQHTQGPGQRVFSIGQRIVTLLVEMVETRLRLVVVELEEEKANLFQLLIMTGLTLLFAAFGLMSLLV

LVIWAVDAQYRLHVMIATTVVLLLAAAIVGILTLRKARRSTLLRLTRKELENDRALLEEDKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002917916.1\_583 [locus\_tag=BN49\_RS04145] [protein=YqjD family protein] [protein\_id=WP\_002917916.1] [location=complement(600326..600631)] [gbkey=CDS]

MAKENVTDDLRAELKTLADTLEEVLNSSADKSKEEMGKLRSKAESALKESRARLGETSEAILRQTRETAA

RADDYVRENPWTGVGIGAAVGLVLGVLLSRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004144860.1\_584 [locus\_tag=BN49\_RS04150] [protein=DUF1090 domain-containing protein] [protein\_id=WP\_004144860.1] [location=complement(600677..601045)] [gbkey=CDS]

MKHRIALLLVLTSLSASALAASPCQEKEQDIQREISYAEKHHNQSRIDGLNTALRQVRENCSDSKLKADH

QQKIAKQREEIAERQRDLQEARKKGDADKINKRQHKLNEAQQELKTLESRDY

>lcl|NZ\_FO834906.1\_prot\_WP\_004218213.1\_585 [gene=mzrA] [locus\_tag=BN49\_RS04155] [protein=EnvZ/OmpR regulon moderator MzrA] [protein\_id=WP\_004218213.1] [location=complement(601195..601572)] [gbkey=CDS]

MKRPSLRQFSWLLGGSLLLGALFWLWLAVQQQEATLAIRPVGQGIGMPDGFSVWHHLDANGIRFKSITPQ

KDGLLIKFDSTAQGAAAKEVLGRALPHGYIIALLEDDNSPTAWLSRLRDAPHRLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002917909.1\_586 [locus\_tag=BN49\_RS04160] [protein=DedA family protein] [protein\_id=WP\_002917909.1] [location=complement(601581..602243)] [gbkey=CDS]

MELFTQLLNALWAQDYETLANPSMIGMLYFVLFMILFLENGLLPAAFLPGDSLLVLVGVLIAKGAMGFPE

TLLLLTAAASLGCWLSYIQGRWLGNTRIVQNWLSHLPSHYHQRAHHLFHKHGLSALLIGRFIAFVRTLLP

TIAGLSGLNNARFQFFNWMSGLLWVLILTSLGYLLGKTPVFLKYEDQLMSCLMLLPVALLVFGLIGSLVV

LWKKKYRSRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002917907.1\_587 [gene=exuR] [locus\_tag=BN49\_RS04165] [protein=transcriptional regulator ExuR] [protein\_id=WP\_002917907.1] [location=complement(602585..603361)] [gbkey=CDS]

MEIIEPRRLYQQLAAELKTRIEQGVYLVGDKLPAERFIADEKNVSRTVVREAIIMLEVEGYVEVRKGSGI

HVISNHPKYQQVADESLEFANYGPFELLQARQLIESNIAEFAATQVTKQDIMKLMEIQEKARNEKCFRDS

EWDLQFHVQVALATQNSALAAIVEKMWTQRVHNPYWKKLHEHIDLRTVDNWCDDHDQILKALLRKDPNAA

KLAMWQHLENTKQMLFNETSDDFEFNADRYLFAENPVVHLDTAVNGAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004174208.1\_588 [locus\_tag=BN49\_RS04170] [protein=MFS transporter] [protein\_id=WP\_004174208.1] [location=complement(603489..604790)] [gbkey=CDS]

MRKIKGLRWYMIALVTLGTVLGYLTRNTVAAAAPTLMEELHISTQQYSYIIAAYSAAYTVMQPVAGYVLD

ILGTKIGYAFFAIAWAVFCGSTALAGSWGGLALARGAVGAAEAAMIPAGLKASSEWFPAKERSIAVGYFN

VGSSIGAMIAPPLVVWAIVMHSWQMAFIISGVLSFAWAIAWLIFYKHPRDQKKLSDEERDYIIGGQESQH

QTNNAKKMSPWQILRNRQFWGIALPRFLAEPAWGTFNAWIPLFMFKVYGFNLKEIAMFAWMPMLFADLGC

IVGGYLPPLFQRWFGVNLIVSRKMVVTMGALLMIGPGMIGLFTSPYVAIALLCIGGFAHQALSGALITLS

SDVFGRNEVATANGLTGMAAWLASTMFALVVGALADTIGFSPLFAVLAVFDLLGALVIWTVLKNKPADDD

STPLSSRKPATQS

>lcl|NZ\_FO834906.1\_prot\_WP\_002917899.1\_589 [gene=uxaC] [locus\_tag=BN49\_RS04175] [protein=glucuronate isomerase] [protein\_id=WP\_002917899.1] [location=605271..606683] [gbkey=CDS]

MTSFMTEDFLLDTEFARRLYHDYAKDQPIFDYHCHLPPQQVAENYRFKNLYDIWLKGDHYKWRAMRTNGV

PERLCTGDASDREKFDAWAATVPHTIGNPLYHWTHLELRRPFGITGKLLSPSTADEIWDQCNDLLAQDAF

SARGIMKQMNVKMVGTTDDPIDSLEHHAAVAKDNSFDIKVLPSWRPDKAFNIELATFNDYMAKLGEVSDT

DIRRFADLQSALTKRLDHFAAHGCKVSDHALDVVLFAEATDAELDDILARRLAGETLSEHEVAQFKTAVL

VFLGAEYARRGWVQQYHIGALRNNNLRQFKLLGPDVGFDSINDRPMAEELSKLLSKQNEENLLPKTILYC

LNPRDNEVLGTMIGNFQGEGMPGKMQFGSGWWFNDQKDGMERQMTQLAQLGLLSRFVGMLTDSRSFLSYT

RHEYFRRILCQMIGRWVAAGEAPADIALLGEMVKNICFNNARDYFAIELN

>lcl|NZ\_FO834906.1\_prot\_WP\_032103056.1\_590 [locus\_tag=BN49\_RS04180] [protein=altronate dehydratase family protein] [protein\_id=WP\_032103056.1] [location=606702..608189] [gbkey=CDS]

MQYIKIHSQDNVAVALTDIAAGSVVTIDNDSVTLGQDIVRGHKFALRAIAKGENVVKYGLPIGHALADIA

PGEHVHAHNTRTNLSDLDAYRYQPDLVAQPPQPADREVQIYRRANGDVGVRNELWILPTVGCVNAMARQM

QNRFLKETYGAEDIDGVHLFSHTYGCSQLGDDHINTRTMLQNMVRHPNAGAVLVVGLGCENNQVEAFRET

LGEFDPQRVHFMVCQHQDDEVEAGIEHLHQLYEVMRQDKRQPGKLSELKFGLECGGSDGLSGITANPMLG

RFSDYVIANGGTTVLTEVPEMFGAEQLLMSHCRDEATFDKLVTMVNDFKQYFIAHDQPIYENPSPGNKAG

GITTLEDKSLGCTQKAGSSQVVDVLRYGERLKVHGLNLLSAPGNDAVATSALAGAGCHMVLFSTGRGTPY

GGFVPTVKIATNSELAAKKKHWIDFDAGQLLHGKTMPQLLEEFVDAIVAFANGKPTCNEQNDFRELAIFK

SGVTL

>lcl|NZ\_FO834906.1\_prot\_591 [locus\_tag=BN49\_RS04185] [protein=YgjV family protein] [pseudo=true] [location=608319..608873] [gbkey=CDS]

MTAYWLAQGVGVIAFLIGITTFINRDERRFRLQLAVYSAIIGVHFFLMGAGPAGMSAGLNALRTVISLRT

RSLWVMTVFILLTLILGLGKLQHAMELLPIIGTVAST\*ALFRCKGLTVRCVMWCSTACWVTHNLWLGSIG

GTLIEGSFLIVNGLNIIRFRRMQKRGIDPFKVENAVQEESPSAR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530910.1\_592 [gene=sstT] [locus\_tag=BN49\_RS04190] [protein=serine/threonine transporter SstT] [protein\_id=WP\_016530910.1] [location=complement(608889..610136)] [gbkey=CDS]

MTTRTPSSGWLSRLAQGSLVKQILIGLVLGVLLALVSKPAAIAVGLLGTLFVGALKAVAPVLVLMLVMAS

IANHQHGQKTSIRPILFLYLPGTFSAALTAVLFSFLFPSTLHLTTAADSITPPSGIVEVLRGLLMSMVSN

PIDALLNANYIGILVWAVGLGFALRHGNDTTKNLINDVSHAVTFIVKVVIRFAPLGIFGLVSSTLATTGF

ETLWGYAQLLLVLVGCMLLVALVINPLLVFWKIRRNPYPLVLTCLRESGVYAFFTRSSAANIPVNMALCE

KLNLDRDTYSVSIPLGATINMAGAAITITVLTLAAVHTLNIPVVLPTALLLSVVASLCACGASGVAGGSL

LLIPLACNMFGIPNDVAMQVVAVGFIIGVLQDSCETALNSSTDALFTAAACMAEDDQLAKNALRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004185787.1\_593 [locus\_tag=BN49\_RS04195] [protein=TerC family protein] [protein\_id=WP\_004185787.1] [location=complement(610403..611374)] [gbkey=CDS]

MNTVGTPLLWGGFAVVVAIMLAIDLLLQGRRGSHSMTMKQAAGWSILWVTLSLLFNAAFWWYLVQTQGRA

VADPQALAFLTGYLIEKALAVDNVFVWLMLFSYFAVPPALQRRVLVFGVLGAIVLRTIMIFAGSWLISQF

DWLLYVFGAFLLFTGVKMALAKEDDSGIGDKPLVRWIRSHLRMTDKIESERFFTRKNGVLFATPLLLVLI

LVELSDVIFAVDSIPAIFAVTTDPFIVLTSNLFAILGLRAMYFLLAGVAERFSMLKYGLSVILVFIGVKM

LIVDFYHIPVAISLGVVGGILAVTLLINAWVNRQHDKQRKLPE

>lcl|NZ\_FO834906.1\_prot\_594 [locus\_tag=BN49\_RS04200] [protein=Gfo/Idh/MocA family oxidoreductase] [pseudo=true] [location=complement(611646..612635)] [gbkey=CDS]

MIRFAVVGTNWITKQFVDAAHETGKYKLTAIYSRSLEQAQAFAKDYPVEHLFTSLDELAQSPDVDAVYIA

SPNSLHFPQTRLFLSHKKHVICEKPLASNLQEVEAAIALAKENNVVLFEAFKTASLPNFLLLKETLAKVG

KLRKAFINYCQYSSRYQRYLDGENPNTFNPAFSNGSIMDIGFYCLASAVALWGEPQAVLATASLLDSGVD

AQGTVVLSYGDFDVTLHHSKVSDSAIPSEIQGEDGALVIEKISECQKLAFVPRGGKA\*DLTQPQHINTML

YEAETFARLVETQDVDHPGLAVSRITAKLSSEIRRQTGVIFPADTQPLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144843.1\_595 [locus\_tag=BN49\_RS04205] [protein=M48 family metallopeptidase] [protein\_id=WP\_004144843.1] [location=complement(612709..613209)] [gbkey=CDS]

MTKLIYLQGYPESLLAQVTTLIEQGRLGEVLQKRYPQGHDVNSDKALYQYTQDLKNRFLRGAAPINKVMY

DSKIHVLNNALGLHTAISRVQGGKLKAKAEIRVATVFRDAPEAFLRMIVVHELAHLKEKDHNKAFYQLCC

HMEPQYHQLEFDTRLWLTHLSLNRSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144842.1\_596 [locus\_tag=BN49\_RS04210] [protein=XRE family transcriptional regulator] [protein\_id=WP\_004144842.1] [location=complement(613229..613831)] [gbkey=CDS]

MNVKVNITTDSGSDVDQVSRAVATRLKAYRKAKKMSLDELSRRASISKGMLVEMEKEAANPSIAILCKLA

AALGVSVADIVNVASEPALHIIPAEQIPTLWQGPLGGSARLLAGTAGPNMIELWRWEMQPGEAFASPGHP

ATTFELLHVEAGALTLTLGETCRTVAAGESAVARTEIEHGYRNEGTAPLVFTMTVAELPS

>lcl|NZ\_FO834906.1\_prot\_WP\_002917889.1\_597 [locus\_tag=BN49\_RS04215] [protein=B3/4 domain-containing protein] [protein\_id=WP\_002917889.1] [location=613875..614582] [gbkey=CDS]

MRSVTPSIESAVSRLAPGFRALSIVVESAPVADPAVAEQALAEACLAVQQDDVPWAQAHLAAWDEAFSAF

GAKAKRTPCSAQALRKRVLKEGSLPAIDPVVDIYNAISIRYAVPVGGENLAAYRGEPRLAIARGDEPFDT

LKSAEPVVEYPEPGEVIWRDDIGVTCRRWNWRQGVRTRLDSGAQTMWFILESLPAMPLSALHEAGERLVG

YLQQLMPGARASITLLRADDEGDLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531665.1\_598 [gene=rlmG] [locus\_tag=BN49\_RS04220] [protein=23S rRNA (guanine(1835)-N(2))-methyltransferase RlmG] [protein\_id=WP\_016531665.1] [location=614668..615798] [gbkey=CDS]

MSQAELNGELFTLERFPPNAEEEALQAWEAADEYLLQQVNDVDGLTLIFNDGFGALACALADRNPVSIND

SFISELATRHNLRMNGIDEESVRFQDSLSPLPAAPALVLIKVPKQLALLEQQLRALREVVTPETRIIAAA

KARDVHNSTLALFEKILGTSTTSLAWKKARLIHCVFTAPELADAPQTYSWKLDGTPWTIHNHANVFARSG

LDIGARFFLQHLPSDLEGEIADLGCGNGVIGLQALAQNPNASVMFTDESHMAVASSRLNVERNLPDDIAR

CEFMVNNSLSGIEPDRFTAILCNPPFHQQHAITDHIAWQMFNDARRSLKYGGELYVVGNRHLDYFRKLKR

AFGNCTTIATNNKFVILKATKVRKQR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531664.1\_599 [locus\_tag=BN49\_RS04225] [protein=NADPH-dependent 2,4-dienoyl-CoA reductase] [protein\_id=WP\_016531664.1] [location=complement(615907..617928)] [gbkey=CDS]

MSRYPSLFAPLELGFTTLKNRVLMGSMHTGLEELPDGAQRLAAFYAERARHGVALIVTGGIAPAPSGVTM

AGGAVLNDASHLAHHRHITDAVHQEGGKIALQILHTGRYSYQPALVAPSALQAPINRFTPHELSHDEILT

LIDDFAHCAQLAREAGYDGVEVMGSEGYLINEFLAARTNQRDDQWGGDYARRMRFAVEVVKAVRQRAGHD

FIIIYRLSMLDLVNDGSTLAEVTELAKAIEAAGATIINTGIGWHEARIPTIATPVPRGAFSWVTRKLKGA

VSIPLITTNRINDPQVAEDILARGDADMVSMARPFLADAEFISKAQDDRADQINTCIGCNQACLDRIFVG

KVTSCLVNPRACHETLMPVLPANAPKRLAVVGAGPAGLAFAVNAAARGHHVTLFDALPEIGGQFNIAKQI

PGKEEFHETLRYYRTMLDLHGVDLRLNTHVTTDDLLAFDETILATGIAPRLPAIDGIDHPKVLSYLDVLR

DKAPVGAKVAIIGCGGIGFDTAMFLSQSGVATSQDIGEFCREWGIDTSLQTAGGLSAEGPQLSKSPRQIV

MLQRKASKPGEGLGKTTGWIHRATLLARGVKMIPAVSYEKIDDEGLHVTIGGERQLLAVDQVVICAGQEP

RRELADPLRAAGKTVHLIGGCDVAAELDARRAIAQGTKLALAI

>lcl|NZ\_FO834906.1\_prot\_WP\_046042307.1\_600 [gene=lsrK] [locus\_tag=BN49\_RS04230] [protein=autoinducer-2 kinase] [protein\_id=WP\_046042307.1] [location=complement(618121..619719)] [gbkey=CDS]

MSYLLALDAGTGSIRAVIFDLNGRQLAVGQAEWKHLSVDNVPGSMEFDLTTNWQLACQCIRQALDAARLS

AADIQSVACCSMREGIVLYDRNGEAIWACANVDARASREVAELKEIHDYRFESEVYEVSGQTLALSAMPR

LLWLAHHRPDIYRKAATITMISDWLAAKLSGELAVDPSNAGTTGMLDLFSRDWRPALLDMAGLRADMLSP

VKETGTLLGAVTEAAAQQSGLRAGTPVVMGGGDVQLGCLGLGVVHAGQTAVLGGTFWQQVVNLPQVRTDP

QMNIRVNPHVIPGMAQAESISFFTGLTMRWFRDAFCAEEKLIAERLGVDAYSLLEEMASRVPAGSHGVMP

IFSDAMHFKQWYHAAPSFINLSIDPEKCNKATLFRALEENAAIVSACNLAQISQFSGVTFESLVFAGGGS

KGALWSQILSDVTGLPVRVPVVREATALGCAIAAGTGAGLYDDMASTGERLVSWHREFTPNPQHRELYQE

MMSKWQTVYADQLGLVDSGLTTSMWQAPGLERRQRVASSPSP

>lcl|NZ\_FO834906.1\_prot\_WP\_004144837.1\_601 [gene=lsrR] [locus\_tag=BN49\_RS04235] [protein=transcriptional regulator LsrR] [protein\_id=WP\_004144837.1] [location=complement(619757..620728)] [gbkey=CDS]

MSEKRITEENRYAGLALAEEELVARVAWCYYHDGLTQNDIGERLGLPRLKISRLLEKGRQSGVIRVQINS

RYEGCLALESELQQRFGLKIARVLPALNTPPMNTRLGIGAAQSLMGILQPGQLLAVGFGEATMSCLQHLS

GFIGSQQVRLVTLSGGVGPYMTGIGQLDAACSVSIIPAPLRVSSAEVAEILRRESSVRDVILAATAADAA

VVGIGAIDQRRDATILRSGYISEGEQLMYARKGAVGDILGYFLQADGRPVEGLEIHRELLGVTLDELAQL

PTIVGVAGGEEKAQAIYAALIGKRINGLVTEETTARAVLTLAS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042309.1\_602 [gene=lsrA] [locus\_tag=BN49\_RS04240] [protein=autoinducer 2 ABC transporter ATP-binding protein LsrA] [protein\_id=WP\_046042309.1] [location=620947..622434] [gbkey=CDS]

MKPLLEARQIRKQFSGVAVLKGIDFTLCAGQVHALMGGNGAGKSTLMKIIAGVETPDSGELTIGDRAFAR

LSPALAHQLGIYLVPQEPMLFPNLSVRENILFRLPKRADTTARLQEKLQQLNCQINLDASASTLEVADQQ

MVEILRGLMREARILILDEPTASLTPGETERLFSQIRALQALDVGIVFISHKLPEIRQLASHISVMRDGA

VVLSGEAATYRDEQLISAMTPASRDHTLSDTQKLWLALPGNRRTQAQDFPVLRVEDLTGEGFIDLNLEIR

AGEIVGLAGLVGSGRTEFAETLYGLRPPRAGRIWLENREISNDSTRARLASGLVYLPEDRQVSGLFLDAP

VRWNTVMFNQPSWWQQGKREAAVVERYHRALGIKLADGDQPVRTLSGGNQQKVLLARCLEANPLLLIVDE

PTRGVDVSARADIYQLLKSVAVQNVAVLMISSDLDEFIGLADRVLVMHQGRYSGELARQAVTVDRMMTLA

FGGQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181392.1\_603 [gene=lsrC] [locus\_tag=BN49\_RS04245] [protein=autoinducer 2 ABC transporter permease LsrC] [protein\_id=WP\_004181392.1] [location=622431..623465] [gbkey=CDS]

MKTLLKNRELSAFFAIVALFVVLVALNPAYFSLQTLAMIFSSSQILCLLALGATLVMLTRNIDVSVGSTV

GLCAIAVGVALNNGYGLATAIAFALAIGALAGAFNGLLVVGLRIPAIVATLGTLGLYRGVMLLWTGGKWI

EGLPDSLKSLSEPAFIGVSPLGWLVLALLLAGGWLLSRTAFGRDFYAVGDNLAAARQLGVAVNRTRMLAF

TLNGMLAACAGIVFAAQIGFVPNQTGSGLEMKAIAACVLGGISLLGGTGTLLGAFLGAFFLTQIDTVLVL

FRLPAWWNDFIAGLVLLGVLVLDGRLRQALARHQRALKYSRFQPGNKGGKQVARFPERKSKEVA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531103.1\_604 [locus\_tag=BN49\_RS04250] [protein=ABC transporter permease] [protein\_id=WP\_016531103.1] [location=623466..624464] [gbkey=CDS]

MKLKLNWESALLALLIVEILLFGALNPRMLDLNMLLFSTSDFICIGIVALPLTLVIISGGIDISLGSTIG

LCAIALGVMTQAGWPLWLAVSLTLLLGLLCGVFNAALIHYTGISPLVITLGTLYLYGGGALLLSGMAGAT

GYEGIGGFPDSFTAFANLTLAGLPLPLVLFAIITFFFWLLTHRGRFGRHLFLLGQNPRAARYAALSVNGI

PYVLYGLVGVASAVAALVMVSYFGSARSDLGRDLLMPALTAAVLGGANIYGGSGSILGTALAALLVGYLQ

QGLQMVGIPNQVSSALSGALLVVVVMGRSLSLHREWVRATWRRLFSHKTIGA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531102.1\_605 [gene=lsrB] [locus\_tag=BN49\_RS04255] [protein=autoinducer 2 ABC transporter substrate-binding protein LsrB] [protein\_id=WP\_016531102.1] [location=624466..625467] [gbkey=CDS]

MKLKLIVLALAMSVVTAQAADRIAFIPKLVGVGFFTSGGNGAKEAGKALGVDVTYDGPTEPSVSGQVQLI

NNFVNQGYNAIIVSAVSPDGLCPALKRAMQRGVKVLTWDSDTRPECRSIYINQGTPQQLGGLLVEMAEKQ

VTKPTAKVAFFYSSPTVTDQNQWVKEAKAKIEKEHPQWQIVTTQFGYNDATKSLQTAEGILKAYPDLDAI

IAPDANALPAAAQAAENLKRQGVAIVGFSTPNVMRPYVERGTVKAFGLWDVVQQGRIAVNVADRLLKKGD

LNVGDSVEVKDIGSLKVEPNSVQGYQYEAKGNGIVLLPERVVFSKENINNYDF

>lcl|NZ\_FO834906.1\_prot\_WP\_002917724.1\_606 [gene=lsrF] [locus\_tag=BN49\_RS04260] [protein=3-hydroxy-5-phosphonooxypentane-2,4-dione thiolase] [protein\_id=WP\_002917724.1] [location=625479..626366] [gbkey=CDS]

MADLDDIKEGKDFGIDRPQQNTLYTLKGCGSLDWGMQSRLARIFNPHSNRTVMLAFDHGYFQGPTTGLER

IDLSIAPLFADTDVLMCTRGVLRSQVPAATNKPVVLRASGGNSILSELSNECVAVAMEDALRLNVCAVAA

QVYIGSEYEHQSINNIIKLVDAGNRYGMPVLAVTGVGKEMTRDARYFSLASRIAAEMGAQFVKTYFVEEG

FEKVTASCPVPIVIAGGKKLPEHEALEMCWRAIDQGASGVDMGRNIFQSSAPRAMLKAVKKVVHENLNAR

EAYQFWQEEKQGELK

>lcl|NZ\_FO834906.1\_prot\_WP\_002917723.1\_607 [gene=lsrG] [locus\_tag=BN49\_RS04265] [protein=(4S)-4-hydroxy-5-phosphonooxypentane-2,3-dione isomerase] [protein\_id=WP\_002917723.1] [location=626363..626659] [gbkey=CDS]

MNVTLVEINIKPERVDEFLEVFRANHEGALQEPGNLRFDVLQDPEVKTRFFIYEAYKDDEAVLAHKKTPH

YLACVEKLEEMMSQPRQKRSFIGLLPQV

>lcl|NZ\_FO834906.1\_prot\_WP\_042941333.1\_608 [gene=ygjG] [locus\_tag=BN49\_RS04270] [protein=putrescine aminotransferase] [protein\_id=WP\_042941333.1] [location=complement(626706..628085)] [gbkey=CDS]

MNRLPSSASALACSAHALNLIEKRTLDHEEMKALNQEVREYFKEHVNPGFLEYRKSVTASGDYGAVEWQA

GGLNTLVDTQGQEFIDCLGGFGIFNVGHRNPVVVSAVENQLAKQPLHSQELLDPLRAMLAKTLAALTPGK

LKYSFFCNSGTESVEAAIKLAKAYQSPRGKFTFIATSGAFHGKSLGALSATAKSTFRKPFMPLLPGFRHV

PFGDINAMRTMLSECKKTGDDVAAVILEPIQGEGGVILPPTGYLPAVRKLCDEFGALLILDEVQTGMGRT

GKMFACEHENVQPDILCLAKALGGGVMPIGATVATEEVFSVLFDNPFLHTTTFGGNPLACAAALATINVL

LTQNLPAQAAQKGDMLLDGFRLLAQEYPDLVNEVRGKGMLMAIEFVDNEIGYDFASEMFRQRVLVAGTLN

NAKTIRIEPPLTLTLEQCEQVLKAARKALAALRVSVEEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002917718.1\_609 [locus\_tag=BN49\_RS04275] [protein=PadR family transcriptional regulator] [protein\_id=WP\_002917718.1] [location=complement(628343..628897)] [gbkey=CDS]

MRHHHEEGRGPRGRHGDPSEHGDHGRRGGGRRQRFFGHGELRLIILDILSRSASHGYELIKEIETLTQGN

YSPSPGVIYPTLDLLQDQGLISVEDDNGRKKILISEEGKQLHAENQEHLAHIQERLQARMVGCELRRDPQ

MKRALENFKAVLDLKVNQQASSAAQLKQIIGIIDRAAMEISQLD

>lcl|NZ\_FO834906.1\_prot\_WP\_023283008.1\_610 [locus\_tag=BN49\_RS04285] [protein=siderophore-interacting protein] [protein\_id=WP\_023283008.1] [location=629135..629911] [gbkey=CDS]

MMTKTKADKYPQRVRNELRFRELTVLRVERAGAAFQRIVLGGEALEGFASHGFDDHTKLFFPEPGAAFTP

PQVSEEGIDWGEGVRPATRDYTPLYDAERHELAYDFYIHDGGIASRWALEAKVGDKLVIGGPRGSLVVPE

DYAWQLYVCDESGMPALRRRLLGLRQLPARPQVTAIVTIADASYKDYLADLDGFNIEWVVGHNPAFVAER

LAQVKVPAEDYFIWLTGEGAVVKSLLARFEDESIDQQLVRSQAYWHSK

>lcl|NZ\_FO834906.1\_prot\_WP\_023283007.1\_611 [locus\_tag=BN49\_RS04290] [protein=glycerone kinase] [protein\_id=WP\_023283007.1] [location=complement(630067..631716)] [gbkey=CDS]

MSQFFFNQRASLVNDVIEGTIIASPWNNLACLESDPAIRVVVRRDLNKNNVAVISGGGAGHEPAHVGFIG

KGMLTAAVCGDLFASPSVDAVLTAIQAVTGEAGCLLIVKNYTGDRLNFGLAAEKARRLGYNVEMLIVGDD

ISLPDNKQPRGIAGTILVHKVAGYFAERGFNLATVLREAQYAASHTASIGVALASCHLPQEADSAPRHQA

GHAELGMGIHGEPGASTIATQNSAEIVNLMVEKLTAALPETGRLAVMLNNLGGVSVAEMAILTRELANTP

LQARIDWLIGPASLVTALDMKGFSLTAIVLEESIEKALLSDVETASWQKPVQPRTINVVPSTLDSARVDF

TPSANPQVGDYVAQVTGALIDLEEHLNALDAKVGDGDTGSTFAAGAREIAERLERQQLPLNDLPTLFALI

GERLTVVMGGSSGVLMSIFFTAAGQKLGQGASVAEALNAGLEQMKFYGGADEGDRTMIDALQPALAALLA

EPENLQAAFAAAQAGADRTCQSSKAGAGRASYLNSDSLLGNMDPGAHAVAMVFKALAER

>lcl|NZ\_FO834906.1\_prot\_WP\_032103066.1\_612 [gene=dhaM] [locus\_tag=BN49\_RS04295] [protein=dihydroxyacetone kinase phosphoryl donor subunit DhaM] [protein\_id=WP\_032103066.1] [location=complement(631792..633213)] [gbkey=CDS]

MVNLVIVSHSARLGEGVGELARQMLINDGCKLAIAAGIDDPDSPIGTDPLKVMEAIESVADTDHVLVMMD

IGSALLSAETALDLLDPAIAAKVRLCAAPLVEGTLAATVSAASGAGIDKVIADAMSALEAKRVQLGLPSP

TSDAAPAPMLADDGDTKSVSVIINNHNGLHVRPASKLVAALAGFNADLLLEKNGKCVKPDSLNQIALLQV

RRNDKLRLLARGPDADAALAAFQALAADNFGESPAAQPAAAPATPERVEGAALRYPLALIQPLRPAAADA

AREQQRLRQAIDQTLADLIALTELAENKFNADIAAIFAGHHTLLDDDDLFDAANDRLLTEQCSAEWAWHQ

VLMELSQQYRQLDDPYLQARYIDIEDILQRTLRHLQGVQERVPTPGEPTIIIADNIYPSTVLQLDASFVK

GLCLRDGSEQAHGAIIARAAGIAWLSQQGEALNSVQPGETIVLDMRHQRLIRD

>lcl|NZ\_FO834906.1\_prot\_WP\_004181378.1\_613 [gene=dhaL] [locus\_tag=BN49\_RS04300] [protein=dihydroxyacetone kinase subunit DhaL] [protein\_id=WP\_004181378.1] [location=complement(633224..633856)] [gbkey=CDS]

MSLNRTQIVDWLYRCGDIFTKESDFLTGLDKEIGDADHGLNMHRGFSKVVEKLPSIADKDIGFILKNTGM

TLLSNVGGASGPLFGTFFIRAAQVTQAHQSLTLDELYLMIREGADGVVNRGKAEPGDKTMCDVWLPVVDS

LRQSSEQHLSIAAALDAACEVAERAAHATITMQARKGRASYLGERSIGHQDPGATSVLFMVQMLAAAAKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002917682.1\_614 [gene=dhaK] [locus\_tag=BN49\_RS04305] [protein=dihydroxyacetone kinase subunit DhaK] [protein\_id=WP\_002917682.1] [location=complement(633867..634937)] [gbkey=CDS]

MKKLINRVEDVLNEQLQGLAKAHPQLTLHQDPLYVTRTDAPVAGKVALLSGGGSGHEPMHCGYIGQGMLS

GACPGEIFTSPTPDKMFECAMQIDGGEGVLLIIKNYTGDILNFETATELLHESGIKVTTVVVDDDVAVKD

SLYTAGRRGVANTVLIEKLVGAAAERGDSLEACAELGRRLNNLGHSIGIALGACTVPAAGQPSFTLKDDE

MEFGVGIHGEPGIDRRRFSSLDQTVDEMFDTLLENGAYSRTLRQWDTVKGAWQEVQQSKTALQNGDRVIA

LVNNLGATPLSELYGVYNRLAQRCEASGIIIERNLIGSYCTSLDMAGFSITLLKVDDETLTLWDAPVHTP

ALNWGN

>lcl|NZ\_FO834906.1\_prot\_WP\_032415719.1\_615 [locus\_tag=BN49\_RS04310] [protein=hypothetical protein] [protein\_id=WP\_032415719.1] [location=complement(635093..635278)] [gbkey=CDS]

MFDPLFSRSRQKISKKFFSTRFASYPDRRLWQKKKSAPARIFTISSAKTFHKETKSGSNVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002917681.1\_616 [locus\_tag=BN49\_RS04315] [protein=glycerol dehydrogenase] [protein\_id=WP\_002917681.1] [location=635548..636645] [gbkey=CDS]

MLKVIQSPAKYLQGPDAAVLFGQYAKNLAESFFVIADDFVMKLAGEKVVNGLQSHDIRCHAERFNGECSH

AEINRLMAILQKQGCRGVVGIGGGKTLDTAKAIGYYQKLPVVVIPTIASTDAPTSALSVIYTEAGEFEEY

LIYPKNPDMVVMDTAIIAKAPVRLLVSGMGDALSTWFEAKACYDARATSMAGGQSTEAALSLARLCYDTL

LAEGEKARLAAQAGVVTEALERIIEANTYLSGIGFESSGLAAAHAIHNGFTILEECHHLYHGEKVAFGTL

AQLVLQNSPMDEIETVLGFCQRVGLPVTLAQMGVKEGIDEKIAAVAKATCAEGETIHNMPFAVTPESVHA

AILTADLLGQQWLAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002917680.1\_617 [gene=dhaR] [locus\_tag=BN49\_RS04320] [protein=dihydroxyacetone kinase operon transcriptional regulator DhaR] [protein\_id=WP\_002917680.1] [location=636747..638672] [gbkey=CDS]

MTVQTQDTGKAVSSVIAQSWHRCSKFMQRETWQTPHQAQGLTFDSICRRKTALLTIGQAALEDAWEFMDG

RPCALFILDESACILSRCGEPQTLAQLAALGFRDGSYCAESIIGTCALSLAAMQGQPINTAGDRHFKQAL

QPWSFCSTPVFDNHGRLFGSISLCCLVEHQSSADLSLTLAIAREVGNSLLTDSLLAESNRHLNQMYGLLE

SMDDGVMAWNEQGVLQFLNVQAARLLHLDAQASQGKNIADLVTLPALLRRAIKHARGLNHVEVTFESQHQ

FVDAVITLKPIVEAQGNSFILLLHPVEQMRQLMTSQLGKVSHTFEQMSADDPETRRLIHFGRQAARGGFP

VLLCGEEGVGKELLSQAIHNESERAGGPYIAVNCQLYADSVLGQDFMGSAPTDDENGRLSRLELANGGTL

FLEKIEYLAPELQSALLQVIKQGVLTRLDARRLIPVDVKVIATTTVDLANLVEQNRFSRQLYYALHSFEI

VIPPLRARRNSIPSLVHNRLKSLEKRFSSRLKVDDDALAQLVAYSWPGNDFELNSVIENIAISSDNGHIR

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DASQFKRKHQA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529557.1\_618 [locus\_tag=BN49\_RS04325] [protein=cob(I)yrinic acid a,c-diamide adenosyltransferase] [protein\_id=WP\_016529557.1] [location=complement(638650..639180)] [gbkey=CDS]

MYRIYTRTGDKGTTALYGGSRIEKDHIRVEAYGTVDELISQLGVCYATTRDAGLRESLHQIQQTLFVLGA

ELASDARGLTRLSQTIGEEEISALERLIDRNMAESGPLKQFVIPGKNLSSAQLHVARTQARRLERLLTAM

DRAHPLREALKRYSNRLSDALFSMARIEETRPDACA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529556.1\_619 [locus\_tag=BN49\_RS04330] [protein=glycerol dehydratase reactivase beta/small subunit family protein] [protein\_id=WP\_016529556.1] [location=complement(639181..639534)] [gbkey=CDS]

MSLSPPGVRLFYDPRGHHAGAINELCWGLEEQGVPCQTITYDGGGDAAALGALAARSSPLRVGIGLSAAG

EIALTHAQLPADAPLATGHVTDSGDHLRTLGANAGQLVKVLPLSERN

>lcl|NZ\_FO834906.1\_prot\_WP\_004150927.1\_620 [gene=dhaT] [locus\_tag=BN49\_RS04335] [protein=1,3-propanediol dehydrogenase] [protein\_id=WP\_004150927.1] [location=complement(639555..640718)] [gbkey=CDS]

MSYRMFDYLVPNVNFFGPNAISVVGERCQLLGGKKALLVTDKGLRAIKDGAVDKTLHYLREAGIEVAIFD

GVEPNPKDTNVRDGLAVFRREQCDIIVTVGGGSPHDCGKGIGIAATHEGDLYQYAGIETLTNPLPPIVAV

NTTAGTASEVTRHCVLTNTETKVKFVIVSWRNLPSVSINDPLLMIGKPAALTAATGMDALTHAVEAYISK

DANPVTDAAAMQAIRLIARNLRQAVALGSNLQARENMAYASLLAGMAFNNANLGYVHAMAHQLGGLYDMP

HGVANAVLLPHVARYNLIANPEKFADIAELMGENITGLSTLDAAEKAIAAITRLSMDIGIPQHLRDLGVK

EADFPYMAEMALKDGNAFSNPRKGNEQEIAAIFRQAF

>lcl|NZ\_FO834906.1\_prot\_WP\_015875176.1\_621 [locus\_tag=BN49\_RS04340] [protein=heme-binding protein] [protein\_id=WP\_015875176.1] [location=complement(640740..641168)] [gbkey=CDS]

MNKSQQVQTITLAAAQQMAAAVEKKATEINVAVVFSVVDRGGNTLLIQRMDEAFVSSCDISLNKAWSACS

LKQGTHEITSAVQPGQSLYGLQLTNQQRIIIFGGGLPVIFNEQVIGAVGVSGGTVEQDQLLAQCALDCFS

AL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529555.1\_622 [locus\_tag=BN49\_RS04345] [protein=propanediol/glycerol family dehydratase large subunit] [protein\_id=WP\_016529555.1] [location=641582..643240] [gbkey=CDS]

MKRSKRFAVLAQRPVNQDGLIGEWPEEGLIAMDSPFDPVSSVKVDNGLIVELDGKRRDQFDMIDRFIADY

AINVERTEQAMRLEAVEIARMLVDIHVSREEIIAITTAITPAKAVEVMAQMNVVEMMMALQKMRARRTPS

NQCHVTNLKDNPVQIAADAAEAGIRGFSEQETTVGIARYAPFNALALLVGSQCGRPGVLTQCSVEEATEL

ELGMRGLTSYAETVSVYGTEAVFTDGDDTPWSKAFLASAYASRGLKMRYTSGTALMGYSESKSMLYLESR

CIFITKGAGVQGLQNGAVSCIGMTGAVPSGIRAVLAENLIASMLDLEVASANDQTFSHSDIRRTARTLMQ

MLPGTDFIFSGYSAVPNYDNMFAGSNFDAEDFDDYNILQRDLMVDGGLRPVTEAETIAIRQKAARAIQAV

FRELGLPPIADEEVEAATYAHGSNEMPPRNVVEDLSAVEEMMKRNITGLDIVGALSRSGFEDIASNILNM

LRQRVTGDYLQTSAILDRQFEVVSAVNDINDYQGPGTGYRISAERWAEIKNIPGVVQPDTIE

>lcl|NZ\_FO834906.1\_prot\_WP\_002917672.1\_623 [locus\_tag=BN49\_RS04350] [protein=propanediol/glycerol family dehydratase medium subunit] [protein\_id=WP\_002917672.1] [location=643253..643837] [gbkey=CDS]

MQQTTQIQPSFTLKTREGGVASADERADEVVIGVGPAFDKHQHHTLIDMPHGAILKELIAGVEEEGLHAR

VVRILRTSDVSFMAWDAANLSGSGIGIGIQSKGTTVIHQRDLLPLSNLELFSQAPLLTLETYRQIGKNAA

RYARKESPSPVPVVNDQMVRPKFMAKAALFHIKETKHVVQDAEPVTLHVDLVRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002917670.1\_624 [locus\_tag=BN49\_RS04355] [protein=glycerol dehydratase small subunit DhaB3] [protein\_id=WP\_002917670.1] [location=643840..644265] [gbkey=CDS]

MSEKTMRVQDYPLATRCPEHILTPTGKPLTDITLEKVLSGEVGPQDVRISRQTLEYQAQIAEQMQRHAVA

RNFRRAAELIAIPDERILAIYNALRPFRSSQAELLAIADELEHTWHATVNAAFVRESAEVYQQRHKLRKG

S

>lcl|NZ\_FO834906.1\_prot\_WP\_016529554.1\_625 [locus\_tag=BN49\_RS04360] [protein=diol dehydratase reactivase subunit alpha] [protein\_id=WP\_016529554.1] [location=644278..646101] [gbkey=CDS]

MPLIAGIDIGNATTEVALASDDPQARAFVASGIVATTGMKGTRDNIAGTLAALEQALAKTPWSMSDVSRI

YLNEAVPVIGDVAMETITETIITESTMIGHNPQTPGGVGVGVGTTIALGRLATLPAAQYAEGWIVLIDDA

VDFLDAVWWLNEALDRGINVVAAILKKDDGVLVNNRLRKTLPVVDEVTLLEQVPEGVMAAVEVAAPGQVV

RILSNPYGIATFFGLSPEETQAIVPIARALIGNRSAVVLKTPQGDVQSRVIPAGNLYISGEKRRGEADVA

EGAEAIMQAMSACAPVRDIRGEPGTHAGGMLERVRKVMASLTGHEMSAIYIQDLLAVDTFIPRKVQGGMA

GECAMENAVGMAAMVKADRLQMQVIARELSARLQTEVVVGGVEANMAIAGALTTPGCAAPLAILDLGAGS

TDAAIVNAEGQITAVHLAGAGNMVSLLIKTELGLEDLSLAEAIKKYPLAKVESLFSIRHENGAVEFFREA

LSPAVFAKVVYIKEGELVPIDNASPLEKIRLVRRQAKEKVFVTNCLRALRQVSPGGSIRDIAFVVLVGGS

SLDFEIPQLITEALSHYGVVAGQGNIRGTEGPRNAVATGLLLAGQAN

>lcl|NZ\_FO834906.1\_prot\_WP\_046042320.1\_626 [locus\_tag=BN49\_RS04365] [protein=aquaporin] [protein\_id=WP\_046042320.1] [location=646155..646958] [gbkey=CDS]

MNQTSTLTGQCVAEFLGTGLLIFFGAGCVAALRVAGASFGQWEISIIWGLGVAMAIYLTAGVSGAHLNPA

VTIALWLFACFERRKVLPFIVAQTAGAFCAAALVYGLYRQLFLDLEQSQHIVRGTAASLNLAGVFSTYPH

PQITFIQAFAVETTITAILMAMIMALTDDGNGIPRGPLAPLLIGLLIAVIGASMGPLTGFALNPARDFGP

KLFTSLAGWGSIAFTGGLAIPYFLVPLLAPVVGAIIGAFLYRKLIGRHLPCECGIDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002917655.1\_627 [gene=hdeB] [locus\_tag=BN49\_RS04370] [protein=acid-activated periplasmic chaperone HdeB] [protein\_id=WP\_002917655.1] [location=complement(647014..647319)] [gbkey=CDS]

MNLPKALVLTVAATTFCLMTSPAFAVEETTPQNMTCQEFMDMNPKSMTPVAFWVVNRNTDFSGGDYVDWH

EVETVSVPKMLQECHKNPAAKLGDLSAVIKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002917651.1\_628 [locus\_tag=BN49\_RS04375] [protein=HdeD family acid-resistance protein] [protein\_id=WP\_002917651.1] [location=complement(647346..647921)] [gbkey=CDS]

MFMFSHYTLNAFSPRVFIRYKRHACLMAVLLFICGACCLAWPLVAGWYLATVTGMLLMICGFYSLYSLIV

FRQQHWKSRLVALIFAIAWIVLGLSFVVNPLNGMSSLAILFGFLFVLGGISRIVNGCQTRKQSGAGWNIF

IGLLDLLIACLWLAMNPQQSWLFITAFIGVEMIFSAIGLLVLRNKMKHAQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144810.1\_629 [locus\_tag=BN49\_RS04380] [protein=YfdX family protein] [protein\_id=WP\_004144810.1] [location=648162..648824] [gbkey=CDS]

MLTDFNQESTMKKVILASLLATMMSTSPVWATDSATAAPAAAATTQVQKEAADVLQVAVQGANAMRDIQF

ARLALFHGQPDSAKKLTDDAAALLAADDASWAKFVKTDAKAKMIADRYVIINASIALSEDYVATPEKESA

IQSANEKLAKGDQKGAIDTLRLAGIGVIENQYLMPLNQTRKAVAQAQELLKAGKYYEANLVLKGAEEGIV

VDSEMLVAGN

>lcl|NZ\_FO834906.1\_prot\_WP\_020864858.1\_630 [locus\_tag=BN49\_RS04385] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_020864858.1] [location=complement(648915..652157)] [gbkey=CDS]

MAVRLILSVVVGLALSLSPAAYAMKQLELKSHSHIAAIDIPLSGKEKAWLAAQPTLTVGTWLPERTPIVY

DGDEKSYQGINADYLALMAHSLGLKVIIRQYDTEQQALTALADRQVDTLLTQVAHRDALAPSLDQSAPLL

KTWPTLVTSLKSPLPPLTTDRRVTLACTRDCAFFDIIQQAFPNAKITLYDSDYQALASVVSGENQYFIGN

NITTGHCISKYFSQSLVIAHYFRQQEQHNRFVTRDDRPELHQLLDRFIHAVDSDTAMRIMQNWLNRGDLS

FLNTPLTFSPEEQRWLQKHRRVRLLVNPYFPPFTLVDNEDELRGIMADMLNIVSLQTGLQFDPILVRNRQ

ALAKRMEKEDWAIMPAATLTPQPQAYVTLSDPLINVAFVLVARGSAPDQHLLTRSARIALPVGPIAAHDL

KARFPLINWVETDNVGVAMKMVEEGEVDAAVASELSARYMIDHYYPQGLHYTRIDGLPVAAIRLAIPRDE

PVLAAILNKALQVIPPRDILQMTEKWSKISSQQIENWSQYSRQFYQLIAFALVLIAISLGWGLSLCREVR

KRKDSQQRLEEELAQKEALSCALEREKDKAIQATKAKSRFLASMSHELRTPVSAIVGFLELLAKPELNVG

QRKEALELAGSTAQTLLGLIGNILDIDKIESGKYQVTPQWSDVAQLVSQQCHTFDALAQQKGIDLHYHNA

LQEGTMLWVDPQALRQILNNLIGNALKFTVEGAIQVSCRLTPANETQGELALMVSDSGCGISEAEQATLF

HRYAQARQGRQQTGSGLGLVICKELVALMQGRLEMVSRPGVGTTFTITLPVKASRCAIHAPQASPARPQA

LPGLAILIADDHPTNRLLLKRQLSTIGYSVDEACDGEEAENKLASKHYDLLITDLNMPKKDGLELAASLR

RRYPGLVIWGVTASALPQSREACLASGMNMCLFKPVSVQTLSHELSRLAVGRSSPHATRHLKLSVLSENT

GGDQALMNEMLETFRDASAADLQAAGQAIARHEPQIFLRALHRLHGSAQILGITRQLAGVSESGRFASKG

AHSCCSAVMVQRITGVMREIDGEIDALIGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004174237.1\_631 [gene=evgA] [locus\_tag=BN49\_RS04390] [protein=acid-sensing system DNA-binding response regulator EvgA] [protein\_id=WP\_004174237.1] [location=complement(652162..652776)] [gbkey=CDS]

MNAIIIDDHPLARIAIRNLLDSNGITVAAELDSGAHAVQTAESMQPDLLIVDVDIPELSGIEVLEQLRKR

RYQGTIIIISAKNELFYGKRSADCGANGFVSKKEGMNNILAAIDAANNGYSYFPFSLERFCTHGITDQDR

LDTLSTQEMKVFRYILSGVDYTTIGSKMNISNKTVSTYKVRLMDKLGCSTLLELYDFAQRNKIG

>lcl|NZ\_FO834906.1\_prot\_WP\_026005884.1\_632 [locus\_tag=BN49\_RS04395] [protein=HdeA/HdeB family chaperone] [protein\_id=WP\_026005884.1] [location=653078..653443] [gbkey=CDS]

MAKEKRAFWRKWVWKHLMAGITVLAMSCAAVGKDVVPDEARTRDMMRCQDYLQLDPRAWTPMVIWLMNDP

FSLEPPEWTDFHEAELVLTPILTEICRQEPDVWLTSLRERLNSYQQVRSLN

>lcl|NZ\_FO834906.1\_prot\_WP\_004185740.1\_633 [locus\_tag=BN49\_RS04400] [protein=hypothetical protein] [protein\_id=WP\_004185740.1] [location=complement(653512..653784)] [gbkey=CDS]

MKEAAAFAFNVDASQVTISDTRQQDVKTNFVVTIGKTSHRCYVTKAAEPKLYGLIPLGGGSTVSDAICAG

ANPTLASKTCDALSQKAGRC

>lcl|NZ\_FO834906.1\_prot\_WP\_002917636.1\_634 [gene=mug] [locus\_tag=BN49\_RS04410] [protein=G/U mismatch-specific DNA glycosylase] [protein\_id=WP\_002917636.1] [location=654520..655026] [gbkey=CDS]

MISDILAPGLRVVFCGINPGKSSAHTGFHFAHPGNRFWKVIHQAGFTDRQLRPEEELQLLDTRCGITMLV

ERPTVQASEVALQELRSGGRELVRKIEEYQPQALAVLGKQAFELAFNQRGAKWGKQAMTIGTTQVWVLPN

PSGLNRATLDKLVAAYRELDDALATRGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004174339.1\_635 [gene=rpoD] [locus\_tag=BN49\_RS04415] [protein=RNA polymerase sigma factor RpoD] [protein\_id=WP\_004174339.1] [location=complement(655126..656967)] [gbkey=CDS]

MEQNPQSQLKLLVQRGKEQGYLTYAEVNDHLPEDIVDSDQIEDIIQMINDMGIQVMEEAPDADDLMLAEN

TADEDAAEAAAQVLSSVESEIGRTTDPVRMYMREMGTVELLTREGEIDIAKRIEDGINQVQCSVAEYPEA

ITYLLEQYDRVEAEEARLSDLITGFVDPNAEEDMAPTATHVGSELSQEEMDDDEDEDEDEDADDNSDDDN

SIDPELAREKFAELRTQYELTRDTIKAKGRSHAAAQEEILKLSEVFKQFRLVPKQFDYLVNSMRSMMDRV

RTQERIIMKLCVEQCKMPKKNFITLFTGNETSETWFNAAVAMNKPWSEKLLEVKEDVQRGLQKLQQIEEE

TGLTIEQVKDINRRMSIGEAKARRAKKEMVEANLRLVISIAKKYTNRGLQFLDLIQEGNIGLMKAVDKFE

YRRGYKFSTYATWWIRQAITRSIADQARTIRIPVHMIETINKLNRISRQMLQEMGREPTPEELAERMLMP

EDKIRKVLKIAKEPISMETPIGDDEDSHLGDFIEDTTLELPLDSATTESLRAATHDVLAGLTAREAKVLR

MRFGIDMNTDHTLEEVGKQFDVTRERIRQIEAKALRKLRHPSRSEVLRSFLDD

>lcl|NZ\_FO834906.1\_prot\_WP\_004149864.1\_636 [gene=dnaG] [locus\_tag=BN49\_RS04420] [protein=DNA primase] [protein\_id=WP\_004149864.1] [location=complement(657186..658931)] [gbkey=CDS]

MAGRIPRVFISDLLARTDIVDLIDARVKLKKQGKNFHACCPFHNEKTPSFTVNGEKQFYHCFGCGAHGNA

IDFLMNYDKLEFVETVEELAAMHNLEVPYEAGNGPSQIERHQRQNLYQLLDGLNAFYQQSLMQPAADPAR

QYLAKRGLSSEVITRFAIGYAPPGWDNVLKRFGGNQENRQSLIDAGMLVTNDQGRSYDRFRERVMFPIRD

KRGRVIGFGGRVLGDALPKYLNSPETDIFHKGRQLYGLYEAQQDNPEPPRLLVVEGYMDVVALAQYDINY

AVASLGTSTTADHIQLLFRVTNNVICCYDGDRAGRDAAWRALETALPYMTDGRQLRFMFLPDGEDPDTLV

RKEGKAAFEARMEQAQPLSTFLFNSLLPQVDLSTPDGRAQLSTLALPLITQVPGETLRIYLRQELGNKLG

ILDDAQLERLMPKQAENGAPRPAPQLKRTTMRILIGLLVQNPDLAPLVPPLEGLDSRKMPGLSLFSELVK

SCLAQPGLTTGQLLEQYRGTKEAATLEKLSMWDDIADKDIAEQTFTDSLNHMFDSLLELRQEELIARDRT

HGLSSEERRELWTISQELAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_001144069.1\_637 [gene=rpsU] [locus\_tag=BN49\_RS04425] [protein=30S ribosomal protein S21] [protein\_id=WP\_001144069.1] [location=complement(659043..659258)] [gbkey=CDS]

MPVIKVRENEPFDVALRRFKRSCEKAGVLAEVRRREFYEKPTTERKRAKASAVKRHAKKLARENARRTRL

Y

>lcl|NZ\_FO834906.1\_prot\_WP\_002916879.1\_638 [gene=tsaD] [locus\_tag=BN49\_RS04430] [protein=tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD] [protein\_id=WP\_002916879.1] [location=659496..660509] [gbkey=CDS]

MRVLGIETSCDETGIAIYDDQQGLLANQLYSQVKLHADYGGVVPELASRDHVRKTVPLIQAALKEAGLTA

KDIDAVAYTAGPGLVGALLVGATVGRSLAFAWNVPAIPVHHMEGHLLAPMLEDNPPAFPFVALLVSGGHT

QLISVTGIGQYELLGESIDDAAGEAFDKTAKLLGLDYPGGPMLSKMASQGTEGRFVFPRPMTDRPGLDFS

FSGLKTFAANTIRSNGDDEQTRADIARAFEDAVVDTLMIKCRRALEQTGFKRLVMAGGVSANRTLRAKLA

EMMQKRGGEVFYARPEFCTDNGAMIAYAGMVRLQTGAKAELGVTVRPRWPLAELPAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181356.1\_639 [locus\_tag=BN49\_RS04435] [protein=cytosine permease] [protein\_id=WP\_004181356.1] [location=complement(660554..662161)] [gbkey=CDS]

MSSLDLNPELPATTRTSGSRETLEDYTLRYAPLSFRRWGPGVVAVTALGGIAYLADFSIGASIGMAWGTS

NAIYSILVAALVIFLTGIPLAITAARYNIDLDLITRSAGFGYFGSVITSIIFAGFTFIFFALEGSIMAQG

LLVGLGIPLWMGYLIATLMVLPLVVYGMKALTRLQVWTTPLWLVLMVVPVVWLIVKDPQLVDGFLHFAGK

NSASTVDITAIMLGAGVCLSLIMQIGEQIDYLRFMPPKTAENRKSWWLAVFSAGPGWVVLGAIKQIIGAF

LGFYLLTRFPAVHNTEPVQQFVSVFDNLVPGWLALTLAVVLVVISQIKINVTNAYSGSLAWTSAWTRTTK

RYPGRIIFVVVNLAIALALMEGDMFSALSWILGFYSNFAIAWVVVVATDITFNKGLLKLAPAQPEYRRGM

IYNVNPVGVVSFGLAAGLSICAFFGLLGATLAPFSPLIALVVAFVMTPLMGLLTRGRYYIKQVDDGIAEP

RYDAAGNASTTVYQCVSCEEEYERPDVMHSHKHQGAICSLCKSME

>lcl|NZ\_FO834906.1\_prot\_WP\_002916877.1\_640 [gene=ureG] [locus\_tag=BN49\_RS04440] [protein=urease accessory protein UreG] [protein\_id=WP\_002916877.1] [location=complement(662315..662932)] [gbkey=CDS]

MNSYKHPLRVGVGGPVGSGKTALLEALCKAMRDTWQLAVVTNDIYTKEDQRILTEAGALAPERIVGVETG

GCPHTAIREDASMNLAAVEALSEKFGNLDLIFVESGGDNLSATFSPELADLTIYVIDVAEGEKIPRKGGP

GITKSDFLVINKTDLAPYVGASLEVMASDTQRMRGDRPWTFTNLKQGDGLSTIIAFLEDKGMLGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532672.1\_641 [locus\_tag=BN49\_RS04445] [protein=urease accessory protein UreF] [protein\_id=WP\_016532672.1] [location=complement(662941..663615)] [gbkey=CDS]

MSTAEQRLRLMQLASSNLPVGGYSWSQGLEWAVEAGWVPDVAAFERWQRRQMTEGFFTVDLPLFARLYRA

CEQGDIAAAQRWTAYLLACRETRELREEERNRGAAFARLLSDWQPDCPPPWRSLCQQSQLAGMAWLGVRW

RIALPEMALSLGYSWIESAVMAGVKLVPFGQQAAQQLILRLCDHYAAEMPRALAAPDGDIGSATPLAAIA

SARHETQYSRLFRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002916875.1\_642 [gene=ureE] [locus\_tag=BN49\_RS04450] [protein=urease accessory protein UreE] [protein\_id=WP\_002916875.1] [location=complement(663617..664093)] [gbkey=CDS]

MLYLTQRLEIPAAATASVTLPIDVRVKSRVKVTLNDGREAGLLLPRGLLLRGGDVLSNEEGTEFVQVIAA

DEGVSVVRCDDPFMLAKACYHLGNRHVPLQIMPGELRYHHDHVLDDMLRQFGLTVTFGQLPFEPEAGAYA

SESHGHHHAHHDHHAHSH

>lcl|NZ\_FO834906.1\_prot\_WP\_046042331.1\_643 [gene=ureC] [locus\_tag=BN49\_RS04455] [protein=urease subunit alpha] [protein\_id=WP\_046042331.1] [location=complement(664103..665806)] [gbkey=CDS]

MSNISRQAYADMFGPTVGDKVRLADTELWIEVEDDLTTYGEEVKFGGGKVIRDGMGQGQMLAADCVDLVL

TNALIVDHWGIVKADIGVKDGRIFAIGKAGNPDIQPNVTIPIGAATEVIAAEGKIVTAGGIDTHIHWICP

QQAEEALVSGVTTMVGGGTGPAAGTHATTCTPGPWYISRMLQAADSLPVNIGLLGKGNVSQPDALREQVA

AGVIGLKIHEDWGATPAAIDCALTVADEMDIQVALHSDTLNESGFVEDTFAAIGGRTIHTFHTEGAGGGH

APDIITACAHPNILPSSTNPTLPYTLNTIDEHLDMLMVCHHLDPDIAEDVAFAESRIRRETIAAEDVLHD

LGAFSLTSSDSQAMGRVGEVILRTWQVAHRMKVQRGALAEETGDNDNFRVKRYIAKYTINPALTHGIAHE

VGSIEVGKLADLVVWSPAFFGVKPATVIKGGMIAIAPMGDINASIPTPQPVHYRPMFGALGSARHHCRLT

FLSQAAAANGVAGRLNLRSAIAVVKGCRTVQKADMVHNSLQPNITVDAQTYEVRVDGELITSEPADVLPM

AQRYFLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002916872.1\_644 [locus\_tag=BN49\_RS04460] [protein=urease subunit beta] [protein\_id=WP\_002916872.1] [location=complement(665799..666119)] [gbkey=CDS]

MIPGEYHVKPGQIALNTGRATCRVVVENHGDRPIQVGSHYHFAEVNPALKFDRQQAAGYRLNIPAGTAVR

FEPGQKREVELVAFAGHRAVFGFRGEVMGPLEVNDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916871.1\_645 [locus\_tag=BN49\_RS04465] [protein=urease subunit gamma] [protein\_id=WP\_002916871.1] [location=complement(666129..666431)] [gbkey=CDS]

MELTPREKDKLLLFTAALVAERRLARGLKLNYPESVALISAFIMEGARDGKSVASLMEEGRHVLTREQVM

EGVPEMIPDIQVEATFPDGSKLVTVHNPII

>lcl|NZ\_FO834906.1\_prot\_WP\_016532675.1\_646 [locus\_tag=BN49\_RS04470] [protein=urease accessory protein UreD] [protein\_id=WP\_016532675.1] [location=complement(666441..667265)] [gbkey=CDS]

MHGTVLPPLKKGWQATLDLRFHQAGGKTVLASAQHVGPLTVQRPFYPEEETCHLYLLHPPGGIVGGDELT

ISAHLAPGCHTLITMPGASKFYRSSGAQALVRQHLTLAPQATLEWLPQDAIFFPGANARLFTTFHLCASS

RLLAWDLLCLGRPVIGETFSHGTLSNRLEVWVDDEPLLVERLQLQEGELSSVAERPWVGTLLCYPATDAL

LDGVRDALAPLGLYAGASLTDRLLTVRFLSDDNLICQRVMRDVWQFLRPHLTGKSPVLPRIWLT

>lcl|NZ\_FO834906.1\_prot\_WP\_004144529.1\_647 [locus\_tag=BN49\_RS04475] [protein=short-chain dehydrogenase] [protein\_id=WP\_004144529.1] [location=667255..667401] [gbkey=CDS]

MPCNVAPLQNQDKTAAMSIDRREFIPVIRNAYVIRNPERRDGREGKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_020324810.1\_648 [locus\_tag=BN49\_RS30845] [protein=hypothetical protein] [protein\_id=WP\_020324810.1] [location=complement(667412..667531)] [gbkey=CDS]

MERQKLRWRLAARRNPIRRLFRRAQAADQDIDGKDYPGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004144530.1\_649 [gene=plsY] [locus\_tag=BN49\_RS04485] [protein=glycerol-3-phosphate 1-O-acyltransferase PlsY] [protein\_id=WP\_004144530.1] [location=complement(667663..668280)] [gbkey=CDS]

MSAIAPGLVLLAYLCGSISSAILVCRLAGLPDPRDSGSGNPGATNVLRIGGKGAAVAVLIFDVLKGMLPV

WGAWALGLTPFWLGLVAIAACVGHIWPVFFHFRGGKGVATAFGAIAPIGLDLTGVMAGTWLLTILLSGYS

SLGAIVSALIAPFYVWWFKPQYTFPVSMLSCLILLRHHDNIQRLWRRQESKIWTRVKKKKTPEQK

>lcl|NZ\_FO834906.1\_prot\_WP\_004150923.1\_650 [gene=folB] [locus\_tag=BN49\_RS04490] [protein=bifunctional dihydroneopterin aldolase/7,8-dihydroneopterin epimerase] [protein\_id=WP\_004150923.1] [location=668388..668771] [gbkey=CDS]

MDIVFIEQLSVITTIGVYDWEQTIEQKLVFDIEIAWDNRKAAASDDVSDCLSYADISERVIAHVEGGKFA

LVERVAEEVADLLLETFQSPWVRIKVSKPGAVARAANVGVIIERGLNLKQNFSGHTC

>lcl|NZ\_FO834906.1\_prot\_WP\_004144532.1\_651 [gene=bacA] [locus\_tag=BN49\_RS04495] [protein=undecaprenyl-diphosphate phosphatase] [protein\_id=WP\_004144532.1] [location=668970..669791] [gbkey=CDS]

MSDIHSLLVAAILGVVEGLTEFLPVSSTGHMIIVGHLLGFEGDTANTFEVVIQLGSILAVVVMFWRRLFG

LIGIHFGKPPAHEGQGSGRLSLIHILLGMIPAVVMGLIFHDTIKSLFNPVNVMYALIVGGVLLIAAEVLK

PKQPRAVGIDDMTYRQAFVIGCFQCLALWPGFSRSGATISGGMLMGVSRYAASEFSFLLAVPMMMGATVL

DVYKSIGFLNMGDVPMFAVGFVMAFIVALIAIKTFLQLIKRISFIPFAIYRFIVAAAVYVVFF

>lcl|NZ\_FO834906.1\_prot\_WP\_016532678.1\_652 [locus\_tag=BN49\_RS04500] [protein=multifunctional CCA addition/repair protein] [protein\_id=WP\_016532678.1] [location=complement(669803..671044)] [gbkey=CDS]

MKSYLVGGAVRDALLGLPVKDRDWVVVGATPQQMLDAGYQQVGRDFPVFLHPQSREEYALARTERKSGAG

YTGFTCYAAPDVTLEADLLRRDLTVNALAQDADGAIIDPYGGQNDLRQRLLRHVSPAFSEDPLRVLRVAR

FAARYAHLGFRIAEETQALMAAMVEAGELAHLTPERVWKETESALTTRNPQVFFQTLRDCQALKVLFPEI

DALYGVPAPAKWHPEIDTGLHTLMTVTMAAMLSPDVDVRFATLCHDLGKGLTPKALWPRHHGHGPAGVKL

VEQLCARLRVPNDIRDLAKLVAEYHDLIHTLPILQPKTLVKLFDSIDAWRKPQRVQQIALTSEADVRGRT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002916862.1\_653 [locus\_tag=BN49\_RS04505] [protein=TIGR04211 family SH3 domain-containing protein] [protein\_id=WP\_002916862.1] [location=complement(671106..671726)] [gbkey=CDS]

MPKLRLITFTLLALSAATAVHAEEKRYVSDELNTWVRSGPGDNYRLVGTINAGEEVSVLQTNDSTSYAQI

RDSNGRTAWIPLKELSNEPSLRTRVPDLENQVKTLTDKLNNIDATWNQRTADMQKKVAGSDSVINALKDE

NQKLKNELVVAQKKVNAANLQLDDKQRTIIMQWFMYGGGVLGVGLLLGLVLPHLVPSRKRKDRWMN

>lcl|NZ\_FO834906.1\_prot\_WP\_004174351.1\_654 [locus\_tag=BN49\_RS04510] [protein=inorganic triphosphatase] [protein\_id=WP\_004174351.1] [location=671941..673239] [gbkey=CDS]

MAQEIELKFIVAQDGVETLREQLNALEAKHTPAGQLLNIYYETADNWLRRHDMGLRIRGDQGRYEMTLKI

AGRVVGGLHQRPEYNIPLDKPELALERLPAEVWPQGELPAALAEHVQPLFSTDFARERWVIQEGKSEIEI

ALDRGEVKAGEHQEPICELELELLAGETADLLRLAHRLLESGVLRQGSLSKAARGYHLAQGNNERPVTRL

AVLPVAAKASVEQGLEAALESALAHWLYHDEIWLRGNAKAKAEILLAIARVRHALVLFGGIVPRKATTHL

RALLNDADAVLLAADTADEALFRTEVVGAKLALTEWLIQRGWRPFLNEAGEKKIAGSFKRFADIHLSRVA

AELRSAVQHLAVEDAADQLPKLSRDIDSVQLLAGAYGDAVAPWLENWQELQRAIEHDDRSVFEYFRRQAL

AAEPFWLHSGKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004174352.1\_655 [gene=glnE] [locus\_tag=BN49\_RS04515] [protein=bifunctional [glutamate--ammonia ligase]-adenylyl-L-tyrosine phosphorylase/[glutamate--ammonia-ligase] adenylyltransferase] [protein\_id=WP\_004174352.1] [location=673260..676097] [gbkey=CDS]

MMPLSPQLQQHWQTVADRLPADFPVAELSPQARSVMAFSDFVEQSVIAQPGWLNELADSAPAAEEWRHYE

AWLQERLQAVTDEAGLMRELRLFRRQMMVRIAWAQALSLVREEETLQQLSVLAETLIVAARDWLYAACCK

EWGTPCNAEGQPQPLLILGMGKLGGGELNFSSDIDLIFAWPEHGATRGGRRELDNAQFFTRLGQRLIKAL

DQPTQDGFVYRVDMRLRPFGDSGPLVLSFAALEDYYQEQGRDWERYAMVKARIMGDNDGAYASELRAMLR

PFVFRRYIDFSVIQSLRNMKGMIAREVRRRGLKDNIKLGAGGIREIEFIVQVFQLIRGGREPALQQRALL

PTLAAIDELHLLPEGDAMLLRAAYLFLRRLENLLQSINDEQTQTLPQDELNRARLAWGMHTDDWETLSAQ

LANHMANVRRVFNELIGDDEAQSPDEQLAEYWRELWQDALEEDDASPALAHLNDADRRSVLALIADFRKE

LDRRTIGPRGRQVLDQLMPHLLSEICSRADAPLPLARITPLLTGIVTRTTYLELLSEFPGALKHLITLCA

ASPMVASQLARHPLLLDELLDPNTLYQPTATDAYRDELRQYLLRVPEEDEEQQLEALRQFKQAQQLHIAA

ADIAGTLPVMKVSDHLTWLAEAILDAVVQQAWGQMVARYGLPTHLHDRQGRGFAVVGYGKLGGWELGYSS

DLDLVFLHDCPAEVMTDGEREIDGRQFYLRLAQRIMHLFSTRTSSGILYEVDARLRPSGAAGMLVTTADA

FADYQQNEAWTWEHQALVRARVVYGDPALQARFDAIRRDILTTPREGATLQTEVREMREKMRAHLGNKHP

NRFDIKADAGGITDIEFITQYLVLRYASDKPKLTRWSDNVRILELLAQNDIMDEEEARALTHAYTTLRDA

LHHLALQELPGHVAPEAFSREREQVSASWQKWLMA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042336.1\_656 [gene=hldE] [locus\_tag=BN49\_RS04520] [protein=bifunctional D-glycero-beta-D-manno-heptose-7-phosphate kinase/D-glycero-beta-D-manno-heptose 1-phosphate adenylyltransferase HldE] [protein\_id=WP\_046042336.1] [location=676156..677589] [gbkey=CDS]

MKVTLPEFERAGVLVVGDVMLDRYWYGPTSRISPEAPVPVVKVENIEERPGGAANVAMNIASLGATSRLV

GLTGIDDAARALSQALANVNVKCDFVSVPTHPTITKLRVLSRNQQLIRLDFEEGFSGVDPQPMHERIQQA

LGSIGALVLSDYAKGALTSVQTMIRLAREAGVPVLIDPKGTDFERYRGATLLTPNLSEFEAVVGKCQDEA

QIVERGMKLIAEFELSALLVTRSEQGMTLLQPGRPPLHMPTQAQEVYDVTGAGDTVIGVLAATLASGNTL

EEACYFANAAAGVVVGKLGTSTVSPVELENAVRGRAESGFGVMSEEELKQAVAAARKRGEKVVMTNGVFD

ILHAGHVSYLANARKLGDRLIVAVNSDASTKRLKGETRPVNPLEQRMIVLGALEAVDWVVSFEEDTPQRL

IAGILPDLLVKGGDYKPEQIAGSEEVWANGGEVLVLNFEDGCSTTNIIKKIQKDSDK

>lcl|NZ\_FO834906.1\_prot\_WP\_004144536.1\_657 [locus\_tag=BN49\_RS30850] [protein=hypothetical protein] [protein\_id=WP\_004144536.1] [location=complement(677667..677816)] [gbkey=CDS]

MVHAHTPSAVDVLISHMPFTHFSIYAYLNAICTKNALNMIIYCAKSFST

>lcl|NZ\_FO834906.1\_prot\_WP\_004174354.1\_658 [gene=glgS] [locus\_tag=BN49\_RS04530] [protein=cell surface composition regulator GlgS] [protein\_id=WP\_004174354.1] [location=677808..678005] [gbkey=CDS]

MNHNDMYSMKNFDFLARSFARMHAQGQPIDLQAIVGNMDEEHREWFCQRYELYCRQVSSQAEAAH

>lcl|NZ\_FO834906.1\_prot\_WP\_004174355.1\_659 [locus\_tag=BN49\_RS04535] [protein=accessory factor UbiK family protein] [protein\_id=WP\_004174355.1] [location=complement(678041..678313)] [gbkey=CDS]

MIDPKKIEQIARQVHESMPKGLRDLGEDVEKKIRQALQSQLTRLDLVSREEFDVQTQVLLRTREKLALLE

QRLNDLENRPATTPGSEEQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004185664.1\_660 [gene=ribB] [locus\_tag=BN49\_RS04540] [protein=3,4-dihydroxy-2-butanone-4-phosphate synthase] [protein\_id=WP\_004185664.1] [location=678691..679344] [gbkey=CDS]

MNQTLLSSFGTAFERVEHALDALREGRGVMVLDDEDRENEGDMIFAAETMTVEQMALTIRHGSGIVCLCL

TEERRKQLDLPMMVENNTSAYGTGFTVTIEAAEGVTTGVSAADRVTTVRAAIADGAKPSDLNRPGHVFPL

RAQPGGVLTRGGHTEATIDLVTLAGFKPAGVLCELTNDDGTMARAPECIKFAQQHNMAVVTIEDLVAYRR

EHERKAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002916852.1\_661 [gene=zupT] [locus\_tag=BN49\_RS04545] [protein=zinc transporter ZupT] [protein\_id=WP\_002916852.1] [location=complement(679406..680176)] [gbkey=CDS]

MSSPLILTLLAGSATFIGAIFGVIGQKPSNRLLGFSLGFAAGIMLLISLMEMLPAALAAEGMSPLLGYGM

FVVGLLGYFGLDRLLPHAHPQDLMTPAMPRPRNLRRTAILLTLGISLHNFPEGIATYVTASNNLELGMGV

ALAVALHNIPEGLAVAGPVYAATGSRSKAVLWAGLSGMAEILGGVLAWLILGSLVSPLVMGAIMAAVAGI

MVALSVDELMPLAKEIDPQSNPSYGVLCGMSVMGLSLVVLQTMGIG

>lcl|NZ\_FO834906.1\_prot\_WP\_004174357.1\_662 [gene=ygiD] [locus\_tag=BN49\_RS04550] [protein=4,5-DOPA dioxygenase extradiol] [protein\_id=WP\_004174357.1] [location=680363..681154] [gbkey=CDS]

MSRTRMPALFLGHGSPMNVLEDNRYTRAWAQLGETLPRPKAIVVVSAHWFTRGTGVTAMEAPKTIHDFGG

FPQALYDTHYPAPGSPALAQRLVELLSPVPVTLDTEAWGFDHGSWGVLIKMYPQADIPMVQLSIDSTKPP

AWHLEMGRKLASLRDEGIMLVASGNVVHNLRTARWHGENTPYPWAESFNNYVKANLQWQGLDEQHPLVNY

LAHEGGSLSNPTAEHFLPLLYVLGTWDGVEAMTIPVDGIEMGSLSMLSVLVGA

>lcl|NZ\_FO834906.1\_prot\_WP\_004900674.1\_663 [locus\_tag=BN49\_RS04555] [protein=glutathionylspermidine synthase family protein] [protein\_id=WP\_004900674.1] [location=complement(681199..682359)] [gbkey=CDS]

MERVSITERPDWREKATEYGFNFHTMYGEPYWSEEAYYKLTLAQVEKLEAVTAELHQMCLQVVEKVIASD

ELMTKFRIPKHTWGFVRQSWKTNQPSLYSRLDLAWDGVGEPKLLENNADTPTSLYEAAFFQWIWLEDQLN

AGKLPAGSDQFNSLQEKLIDRFGELREQFGFQLLHMACCRDTVEDRGTVQYLQDCAAEAGLATEFLYVED

IGLGEKGQFTDLQDQVIGNLFKLYPWEFMLREMFSTKLEDAGVRWLEPAWKSIISNKALLPMLWEMFPNH

PNLLAAYFSEDAHPEMEKYVIKPIFSREGANVSIVENGKVVEAVEGPYGEEGTIVQAFYPLPKFGDSYTL

IGSWLINDQPAGIGIREDRALITQDLSRFYPHIFVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916849.1\_664 [locus\_tag=BN49\_RS04560] [protein=DUF1190 family protein] [protein\_id=WP\_002916849.1] [location=complement(682365..683036)] [gbkey=CDS]

MKRTKNINHSSFRKSWSARHLTPVALAVTAVFMLAGCEKSDETVSLYQNADDCSAANPGKAAECTTAYTN

AVKEAERTAPKYATREDCVAEFGEGQCQQTPAQAGVAPENQAQAQSSGSFWMPLMAGYMMGRLMGGGMAQ

QQPLFSSKNPASPAYGQYTDASGKSYGAAQPGRTMNVPKTAMAPKPATTTTVTRGGFGESVAKQSTMQRS

AAGSTSSSRSMGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004150921.1\_665 [gene=tolC] [locus\_tag=BN49\_RS04565] [protein=outer membrane channel protein TolC] [protein\_id=WP\_004150921.1] [location=complement(683204..684673)] [gbkey=CDS]

MKKLLPILIGLSLTGFSAMSQAENLLQVYQQARISNPDLRKSAADRDAAFEKINEARSPLLPQLGLGADY

TYTNGYRDSNGVNSNVTSGSLQLTQVLFDMSKWRALTLQEKTAGIQDVTYQTDQQTLILNTATAYFKVLA

AIDTLSYTEAQKQAIYRQLDQTTQRFNVGLVAITDVQNARSQYDAVLANEVTARNDLDNAVEGLRQVTGN

YYPELASLNVNGFKTNKPQAVNALLKEAENRNLSLLQARLSQDLAREQIRQAQDGHLPTLNLSASTGVSN

TRYNGSKTNTPLAYNDSDNGQNQIGLNFSLPLYQGGAVTSQVKQAQYNFVGASEQLESAHRSVVQTVRSS

FNNVNASISSINAYKQAVVSAQSSLDAMEAGYSVGTRTIVDVLDATTTLYNAKQQLSNARYNYLINELNI

KSALGTLNEQDLVALNNTLGKPISTSADSVAPENPQQDATADGYGNTTAAVKPASARTTQSSGSNPFRQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016532683.1\_666 [gene=nudF] [locus\_tag=BN49\_RS04570] [protein=ADP-ribose diphosphatase] [protein\_id=WP\_016532683.1] [location=684870..685502] [gbkey=CDS]

MSKPTQQGITFSKNDVEIIARETLYRGFFSLDLYRFRHRLFNGGMSREITREIFERGHAAVLLPFDPVRD

EVVLVEQIRIAAYDTSESPWLLEMVAGMIEAGETVEDVARREALEEAGLEVGRTKPILSYLASPGGTSER

LSILVGEVDASTAKGIHGLAEENEDIRVHVVSREQAYQWVEEGKIDNAASVIALQWLQLHYHNLRNEWTK

>lcl|NZ\_FO834906.1\_prot\_WP\_002916847.1\_667 [locus\_tag=BN49\_RS04575] [protein=DUF1249 family protein] [protein\_id=WP\_002916847.1] [location=685499..685921] [gbkey=CDS]

MKRYTPDFPEMMRLCETNFAQLRRLLPRTDAAGEKVSYQVGSAQYRLTIVESTRYTTLVAIEQTLPAVSY

WSLPSMTVRLYHDAMVAEVCSSQQIFRFKARYDYPNKKLHQRDEKHQINQFLADWLRYCLAHGAMAIPVC

>lcl|NZ\_FO834906.1\_prot\_WP\_002916846.1\_668 [gene=cpdA] [locus\_tag=BN49\_RS04580] [protein=3',5'-cyclic-AMP phosphodiesterase] [protein\_id=WP\_002916846.1] [location=685946..686773] [gbkey=CDS]

MESLLNLPLAGEARVRILQITDTHLFAEKHETLLGINTWDSYQAVLSAIHASQRPCDLIVATGDLAQDHS

SAAYQHFAEGIASFAAPCVWLPGNHDFQPAMYSTLQEAGISPAKRVFLGDRWQILLLDSQVFGVPHGELS

DFQLEWLEHKLAEAPERYTLLLLHHHPLPAGCSWLDQHSLRNAGALDSALSAWPRVKHLLCGHIHQELDL

DWNGRRMMATPSTCVQFKPHCANFTLDTVSPGWRWLELHPDGTLTTEVCRLEGAAFHPDIASEGY

>lcl|NZ\_FO834906.1\_prot\_WP\_002916845.1\_669 [gene=yqiA] [locus\_tag=BN49\_RS04585] [protein=esterase YqiA] [protein\_id=WP\_002916845.1] [location=686773..687348] [gbkey=CDS]

MATLLYLHGFNSSPRSAKATALKTWLAQHYPEITMVVPELPPYPAETAELLESIVLEHGGEPLGVVGSSL

GGYYATWLSQCFMLPAVVVNPAVRPFELLNNFLGHNENPYTGQQYVLESRHIYDLKVMQIDPLEAPDLLW

LLQQTGDEVLDYRQAVHYYASCRQTVEEGGNHAFVGFDDHFTQIIEFLGLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002916844.1\_670 [gene=parE] [locus\_tag=BN49\_RS04590] [protein=DNA topoisomerase IV subunit B] [protein\_id=WP\_002916844.1] [location=687379..689274] [gbkey=CDS]

MTQSSYNADAIEVLTGLEPVRRRPGMYTDTTRPNHLGQEVIDNSVDEALAGHAKRVEVILHADQSLEVID

DGRGMPVDIHPEEGVPAVELILCRLHAGGKFSNKNYQFSGGLHGVGISVVNALSKRVEVNVRRDGQVYSI

AFENGEKVEDLHVTGTCGKRNTGTSVHFWPDESFFDSPRFSVSRLTHLLKAKAVLCPGVEIVFRDQVNNS

EQSWCYADGLNDYLSEAVNGLPLLPEKPFVGAFSGETEAVDWALLWLPEGGELLTESYVNLIPTMQGGTH

VNGLRQGLLDAMREFCEYRNILPRGVKLSAEDIWDRCAYVLSVKMQDPQFAGQTKERLSSRQCAAFVSGV

VKDAFSLWLNQNVQAAELLAEMAISSAQRRLRAAKKVVRKKLTSGPALPGKLADCTAQDLNRTELFLVEG

DSAGGSAKQARDREYQAIMPLKGKILNTWEVSSDEVLASQEVHDISVAIGIDPDSDDLSQLRYGKICILA

DADSDGLHIATLLCALFVRHFRTLVKEGHVYVALPPLYRIDLGKEVYYALTEEEKTGVLEQLKRKKGKPN

VQRFKGLGEMNPMQLRETTLDPNTRRLVQLVISDEDEQQTTAIMDMLLAKKRSEDRRNWLQEKGDMADLE

V

>lcl|NZ\_FO834906.1\_prot\_WP\_002916842.1\_671 [locus\_tag=BN49\_RS04595] [protein=antibiotic biosynthesis monooxygenase] [protein\_id=WP\_002916842.1] [location=complement(689347..689661)] [gbkey=CDS]

MLTVIAEIRTRPGQHHRQAVLDQFAKIIPTVLQEAGCHGYAPLVDHAAGVSFQTTAPDSIVMVEQWESVA

HLEAHLQTPHMKAWSEAVKGDVLETSIRILQAGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002916840.1\_672 [locus\_tag=BN49\_RS04600] [protein=NAD(P)H-dependent oxidoreductase] [protein\_id=WP\_002916840.1] [location=complement(689743..690324)] [gbkey=CDS]

MSNILIINGAKKFAHSNGQLNDTLTEVAESYLRDAGHDVKSVRAESEYDVKEEVQNFLWADVVIWQMPGW

WMGAPWTVKKYMDDVFTEGHGSLYASDGRTRSDASKKYGSGGLVQGKKYMLSLTWNAPMEAFTDKDQFFH

GVGVDGVYLPFHKANQFLGMEALPTFIANDVIKMPDVPRYIAEYRKHLAEIFG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042343.1\_673 [gene=qseC] [locus\_tag=BN49\_RS04605] [protein=two-component system sensor histidine kinase QseC] [protein\_id=WP\_046042343.1] [location=complement(690431..691774)] [gbkey=CDS]

MKRLARLRLRLTLLFAVLTTAAWGMASVIAWQQTSKKLDKLFDTQQLLFARRLSVMHFDELRAPPALLGE

KKKVRHGHIDDDALAFAIFTRDGKMVLNDGENGEDIQWNSQREGFSDGYLRDDDDEWRFLWLTTADGRYR

IAVGQEWDYRREMAMDIVTSQLTPWMVALPLMFVLLIVLLSRELAPLKNLARTLRLRAPDSADSLSVEKI

PAEVRPLVEALNQLFRRTHDVMLRERRFTSDAAHELRSPLAALKVQTEVAQLSLDDPEGREKALDQLHQG

IDRATRLVDQLLTLSRLDSLAQLDDVQKVAIADLLQSAVMEMYHPAQQSGIELRLHLNASHIVRTGQPLL

LSLLVRNLLDNAVRYSPRGSQVDITLNAREFRVRDNGPGISPQALSRIGERFYRPPGQEAPGSGLGLSIV

RRIASLHGMQVDFANARDGGFEARVYW

>lcl|NZ\_FO834906.1\_prot\_WP\_004174368.1\_674 [gene=qseB] [locus\_tag=BN49\_RS04610] [protein=two-component system response regulator QseB] [protein\_id=WP\_004174368.1] [location=complement(691771..692430)] [gbkey=CDS]

MRILLVEDDKLIGDGIKAGLSKMGFSIDWFTAGLEGKNALYSAPYDAAILDLTLPGIDGLDILREWRDRG

RHEPVLILTARDALSQRVEGLRLGADDYLCKPFALIEVAARLEALIRRAHGQSSSELRHGKVILDPNRLT

ASLDGESLALKPKEFALLELLMRNAGRVLPRKLIEEKLYTWDDEVSSNAVEVHVHHLRRKLGSDFIRTVH

GIGYTLGDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002916833.1\_675 [locus\_tag=BN49\_RS04615] [protein=YgiW/YdeI family stress tolerance OB fold protein] [protein\_id=WP\_002916833.1] [location=692581..692976] [gbkey=CDS]

MKKIAAMTAIIALVSMPVLAAGQGGFTGPSTTTTTQAGGFTGPSGAVTTVANAKSLRDDTWVTLRGKIVE

RISDDLYKFQDASGVINVDIDHKRWNGVTVGPQDTVEIQGEVDKDWNSVEIDVKQIRKIAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002916831.1\_676 [locus\_tag=BN49\_RS04620] [protein=AraC family transcriptional regulator] [protein\_id=WP\_002916831.1] [location=693054..693923] [gbkey=CDS]

MNDIKASPAYVGRFQRVCRYIARHLDEPLSLETLSAIAHSSPYHFHRQFSAYTGIPLYRYIQWLRLRRAC

WRLAFNPRDKVIDIALDAGFQNAESFSRAFRTAFDQSPTQFRQQPDWAEWHRRVPKHTLQEQTSMDVNII

SCPSTRIAVLQHRGSPDLVNATAARFIAWRKTSGLSPVATSDTWGIAWDDPQTTPQEAFRFDICGTVDRP

VGENAFGVINGEIPGGRCAVVRHHGSLDTLANSVWFLYRDWLPASGETLRDFPVYFRYLNFVHEVAEHEL

QTDIYLPLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181324.1\_677 [gene=parC] [locus\_tag=BN49\_RS04625] [protein=DNA topoisomerase IV subunit A] [protein\_id=WP\_004181324.1] [location=694045..696303] [gbkey=CDS]

MSDMAERLALHEFTENAYLNYSMYVIMDRALPFIGDGLKPVQRRIVYAMSELGLNASAKFKKSARTVGDV

LGKYHPHGDSACYEAMVLMAQPFSYRYPLVDGQGNWGAPDDPKSFAAMRYTESRLSKYAELLLSELGQGT

VDWVPNFDGTLQEPKMLPARLPNILLNGTTGIAVGMATDIPPHNLREVAKAAITLIEQPKTTLDELLDIV

QGPDFPTEAEIITSRAEIRKIYQNGRGSVRMRAVWSKEDGAVVISALPHQVSGAKVLEQIAAQMRNKKLP

MVDDLRDESDHENPTRLVIVPRSNRVDMEQVMNHLFATTDLEKSYRINLNMIGLDGRPAVKNLLEILSEW

LVFRRDTVRRRLNHRLEKVLKRLHILEGLLVAFLNIDEVIEIIRTEDEPKPALMSRFGISETQAEAILEL

KLRHLAKLEEMKIRGEQSELEKERDQLQAILASERKMNNLLKKELQADADAFGDDRRSPLHEREEAKAMS

EHDMLPSEPVTIVLSQMGWVRSAKGHDIDAQGLSYKAGDSWKASAKGKSNQPVVFIDTTGRSYAIDPITL

PSARGQGEPLTGKLTLPPGATVEHMLMESDDQKLLMASDAGYGFVCTFNDLVARNRAGKALITLPDNAHV

MPPLVIEDESDMLLAITAAGRMLMFPVSDLPQLSKGKGNKIISIPAAEAAAGQDGLAHLFVLPPQSTLTI

HVGKRKIKLRPEELQKVTGERGRRGSLMRGLQKIDRVEIDSPRRAAAGDSEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916826.1\_678 [gene=plsC] [locus\_tag=BN49\_RS04630] [protein=1-acylglycerol-3-phosphate O-acyltransferase] [protein\_id=WP\_002916826.1] [location=696495..697232] [gbkey=CDS]

MLFIFRVIFVVIYCIVVCVLGCLYCLFSPRNPKHVATFGHLFGRLSPVFGLKVELRKPADAESYGNAIYI

ANHQNNYDMVTASNIVQAPTVTVGKKSLLWIPFFGQLYWLTGNLLIDRNNRTKAHGTIAEVVNAFKKRKI

SFWMFPEGTRSRGRGLLPFKTGAFHAAIAAGVPIIPVCVSNTSNKIKLNRWNNGLVIVEMLPPVDTTQFG

KDNVRALATHCRELMAAKIADLDNEVAEREAAGKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042347.1\_679 [gene=ftsP] [locus\_tag=BN49\_RS04635] [protein=cell division protein FtsP] [protein\_id=WP\_046042347.1] [location=697316..698728] [gbkey=CDS]

MSLSRRQFIKASGVALCAGAAPLKAHAAGQQPALPVPPLLESRRGQPLFLTLQRSHWSFTPGTRAPVWGI

NGRYMGPTIRVWNGDDVKLIYSNRLTENVAMTIRGLQVPGPLIGGAARMMSPNADWAPVLPIRQSAATLW

YQANTPNRMAKQVYNGLAGMWLVEDEVSKNLPIPNHYGVDDFPVIIQDKRLDNFGTPEYSEPGSGGFVGD

TLLVNGVQSPYVEVSRGWVRLRLLNASNSRRYQLQMSDGRLLHVISGDQGFLPAPVSLKQLSLAPGERRE

ILVDMTNGDEVSITCGEAASIVDRIRGFFEPSSILVSTLVLTLRPTGLLPLVTDSLPVRLLPTELLSGTP

IRSRDITLGDDPGINGQLWDPQRIDITAQQGTWERWTVRADRPQSFHIEGVMFQIRNVNGSSPFPEDRGW

KDTMWVDGQVELLVYYAQPSWPHFPFQYLSQTLELADRGSIGQMLVNTAP

>lcl|NZ\_FO834906.1\_prot\_680 [locus\_tag=BN49\_RS04640] [protein=YgiQ family radical SAM protein] [pseudo=true] [location=698762..701093] [gbkey=CDS]

MRKSSFISTIIPAYNPRPFGYFFIIFPGSNMSAISLIQPDRDLFSWPQYWAACFGPAPFLPMSREEMDQL

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MINRYTADRKLRHDDAYTAGNVAGKRPDRATLVYTQRCKEAWKDVPVILGGIEASLRRTAHYDYWSDTVR

RSVLVDSKADMLMFGNGERPLVEVAHRLAMGETIDQIRDVRNTAIMVKEALPGWSGVDSTRLDTPGKIDP

IPHPYGEDLPCADNKPVAPKKQEAKSITVQPPRPKPWEKTYVLLPSFEKVKGDKVLYAHASRILHHETNP

GCARALMQKHGERYIWINPPAIPLSTEEMDSVFALPYKRVPHPSYGDARIPAYEMIRFSINIMRGCFGGC

SFCSITEHEGRIIQSRSEDSIINEIEAIRDTVPGFTGVISDLGGPTANMYMLRCKSPRAEQTCRRLSCVY

PDICPHMDTNHEPTINLYRRARELKGIKKILIASGVRYDIAVEDPRYIKELATHHVGGYLKIAPEHTEEG

PLSKMMKPGMGSYDRFKELFDTYSKQAGKEQYLIPYFISAHPGTRDEDMVNLALWLKKHRFRLDQVQNFY

PSPLANSTTMYYTGKNPLGKIGYKSEEVVVPKGDKQRRLHKALLRYHDPANWPLIRQALEAMGKKHLIGS

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CEKRREV

>lcl|NZ\_FO834906.1\_prot\_WP\_004144550.1\_681 [locus\_tag=BN49\_RS04645] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004144550.1] [location=701093..701620] [gbkey=CDS]

MTPVILSRQQLDQLWEIDRSEIIDTLYRLDNGQLRAYREYYDVRGWDPHDRQVYTPIHEACYDRGGIFFA

FFDDEQMIAAAALDTLPRGMNGELRQLLFFYVGAGKRGQGWGRRLFQYALHQLPEMGASGLYISSIPNKN

TVDFYLAQGCRLADKPDPALFALEPEDIHLVCDRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916796.1\_682 [gene=dkgA] [locus\_tag=BN49\_RS04650] [protein=2,5-didehydrogluconate reductase DkgA] [protein\_id=WP\_002916796.1] [location=complement(701656..702483)] [gbkey=CDS]

MTHPTVIKLHDGNLMPQLGLGVWKAGNEEVVSAIHKALEVGYRSFDTAAAYQNETGVGNALHSAGVNRDE

LFITTKLWNDDQKRPHEALKESLSKLKLDYVDLYLIHWPVPAIGHYVEAWQALIELQQQGLTKSIGVCNF

QVPHLQKLIDETGVAPVINQIELHPLMQQRQLHAWNATHKIQTESWSPLAQGGEGVFDQKVIHQLADKYG

KTPAQIVIRWHLDSGLVVIPKSVTPSRIAENFDVWDFRLDKDELGAIAKLDQGKRLGPDPDQFGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004144551.1\_683 [gene=yqhD] [locus\_tag=BN49\_RS04655] [protein=alcohol dehydrogenase] [protein\_id=WP\_004144551.1] [location=complement(702629..703792)] [gbkey=CDS]

MNNFDLHTPTRILFGKGAIEKLREQIPAEARVLITYGGGSVKKTGVLDQVLTALNGLDVLEFGGIEPNPS

YETLMNAVKLAREEKVTFLLAVGGGSVLDGTKFIAAAAHYDADIDPWEILETYGSKIASAIPMGSVLTLP

ATGSESNKGAVISRKTTGDKRAFMSSHVQPQFAILDPVYTYTLPPRQVANGVVDAFVHTVEQYVTYPVDG

KIQDRFAEGILLTLIEDGPKALQEPENYNVRANIMWAATQALNGLIGAGVPQDWATHMLGHELTAMHGLD

HAQTLAIVLPALWNEKRDAKREKLLQYAERVWNITEGSDDQRIDAAIAATRQFFEQMGVPTRLSDYGLDG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004144552.1\_684 [locus\_tag=BN49\_RS04660] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004144552.1] [location=703989..704888] [gbkey=CDS]

MQHAEICRTLTEKINLLKDKHEMLSSLLPDVRLLYGTQPGPRTPVMYQPGIVFLFSGHKIGYINERTFRY

DTNEYLLLTVPLPFECETFATPEVPLAGMRLNVDILQLQELLMDIGEDPLFQPAVASSGINSAVLSEDIL

CAAERLLDVMERPLDARILGKQIVREILYYVLTGPCGGALLALVSRQTHFSLISRVLKHIESQYTENLSV

DRLAAEANMSVSAFHHNFKAVTSTSPLQYLKNYRLHKARMLMIHDGMKASAAAMRVGYESPSQFSREFKR

YFGLTPGEDAARIRTMQGM

>lcl|NZ\_FO834906.1\_prot\_WP\_002916791.1\_685 [locus\_tag=BN49\_RS04665] [protein=DedA family protein] [protein\_id=WP\_002916791.1] [location=complement(704938..705597)] [gbkey=CDS]

MVVIQEIVAALWQHDFAALANPHVVGVVYLVMFATLFLENGLLPASFLPGDSLLLLAGALIAKGVMDFVP

TIAILTAAASLGCWLSYVQGRWLGNTQTVKGWLAHLPHKYHQRATCMFDRHGLLALLAGRFLAFVRTLLP

TMAGISGLPNRRFQFFNWLSALLWVCVVTGLGYALSMIPFVKRHEDQVMTCLMILPIALLLAGLLGTLFV

VIKKKYCSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149836.1\_686 [gene=metC] [locus\_tag=BN49\_RS04670] [protein=cystathionine beta-lyase] [protein\_id=WP\_004149836.1] [location=complement(705729..706916)] [gbkey=CDS]

MADKHLDTALVNAGRSKKYTQGSVNSVIQRASSLVFDTVEAKKHATRNRANGELFYGRRGTLTHFSLQEA

MCELEGGAGCALFPCGAAAVANTILAFVEQGDHVLMTNTAYEPSQDFCTKILAKLGVTTSWFDPLIGADI

ARLVRPETRVVFLESPGSITMEVHDVPAIVAAVRQVAPEAIIMIDNTWAAGILFKALDFGIDISIQAGTK

YLIGHSDAMVGTAVANARCWPQLRENAYLMGQMLDADTAYMTSRGLRTLGVRLRQHHESSLRIAEWLAQH

PQVARVNHPALPGSKGHEFWKRDFTGSSGLFSFVLSKRLNDAELAEYLDNFSLFSMAYSWGGFESLILAN

QPEQIAHIRPDAEVDFSGTLIRLHIGLENVDDLQADLAAGFARIV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174395.1\_687 [gene=exbB] [locus\_tag=BN49\_RS04680] [protein=tol-pal system-associated acyl-CoA thioesterase] [protein\_id=WP\_004174395.1] [location=707167..707898] [gbkey=CDS]

MGNNLMQADLSVWGMYHHADIVVKVVMIGLILASVVTWAIFFGKGAEILASKRRLKREQQQLAEARSLDQ

ASDIASAFEAKSLTTQLINEAQNELELSAGAEDNEGIKERTGFRLERRVAAVGRHMGRGNGYLATIGAIS

PFVGLFGTVWGIMNSFIGIAQTQTTNLAVVAPGIAEALLATAIGLFAAIPAVVIYNIFARMIGSYKASLG

DVAAQVLLLQSRDLDLSASGVKPVRSAQKLRVG

>lcl|NZ\_FO834906.1\_prot\_WP\_002916785.1\_688 [gene=exbD] [locus\_tag=BN49\_RS04685] [protein=TonB system transport protein ExbD] [protein\_id=WP\_002916785.1] [location=707905..708330] [gbkey=CDS]

MAMRLNENLDDNGEMHEINVTPFIDVMLVLLIIFMVAAPLATVDVKVNLPASSSQPQPRPEKPIYLSVKA

DKSMFLGNDPVTEANMINALDSLTAGKKDTTVFFRADKTVDYETMMKVMDTLHQAGYLKIGLVGEETVKA

K

>lcl|NZ\_FO834906.1\_prot\_WP\_004105804.1\_689 [locus\_tag=BN49\_RS04690] [protein=TIGR00645 family protein] [protein\_id=WP\_004105804.1] [location=708469..708963] [gbkey=CDS]

MERFLENAMYASRWLLAPVYFGLSLGLIALTIKFFQEIFHILPHIFSVSESDMILTLLSLVDMTLVGGLL

VMVMFSGYENFVSQLDINEGKEKLSWLGKMDATSLKNKVAASIVAISSIHLLRVFMDAKNVPDNKLMWYV

IIHLTFVLSAFVMGYLDRLTKVKH

>lcl|NZ\_FO834906.1\_prot\_WP\_004144560.1\_690 [locus\_tag=BN49\_RS04695] [protein=dienelactone hydrolase family protein] [protein\_id=WP\_004144560.1] [location=709085..709972] [gbkey=CDS]

MTRLTAKDFPQQLLEYYDYYAHGKISKREFLQLAGKYTVGGMTALALFNLLKPDYALAEQVPFTDPDIRP

EYIHYPSPDGHGEVRAYLVTPTKIADKAPAVVVVHENRGLNPYIEDVARRVAKAGYIALAPDGLSAVGGY

PGNDDEGRALQQKVDPVKLMNDFFAAVAFMANYPQATGKVGITGFCYGGGVSNAAAVAIPELACAVPFYG

RQPPLKEVDKIKAPLLLHYAGLDSGINEGWPAYEQALKEHHKVYEAYFYQGVNHGFHNDSTPRYDRAAAD

LAWQRTLAWFEKYLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002916743.1\_691 [locus\_tag=BN49\_RS04700] [protein=DUF2623 domain-containing protein] [protein\_id=WP\_002916743.1] [location=710051..710338] [gbkey=CDS]

MENHFGKGLMAGLQASYADTAAHAANFCADYKRGFVLGYSHRMFEKTGDRQLSAWEAGILTRRYGLDRDM

VMDFFKEGGSGMAMRYFLAGYRLES

>lcl|NZ\_FO834906.1\_prot\_WP\_016531363.1\_692 [gene=yghU] [locus\_tag=BN49\_RS04705] [protein=glutathione-dependent disulfide-bond oxidoreductase] [protein\_id=WP\_016531363.1] [location=complement(710411..711277)] [gbkey=CDS]

MSEQNYQPPKVWEWKQNSGGAFANINRPVSGATHERVLPVGTHPLQLYSLGTHNGQKVTIMLEELLALGV

SGAEYDAWLIRIGEGDQFSSGFVEINPNSKIPALSDHSTTPPTRVFESGNILLYLAEKFGFFLPKDPAGR

TETLNWLFWLQGAAPFLGGGFGHFYNYAPVKIEYAIDRFTMEAKRQLDVLDKQLARGRYVAGEEYTIADM

AVWPWYGNVVLGNVYNAAEFLDAGSYKNVLRWAQDVGNRPAVKRGRIVNRTNGPLNEQLHERHDARDFDT

QTEDKRQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150918.1\_693 [locus\_tag=BN49\_RS04710] [protein=thioredoxin domain-containing protein] [protein\_id=WP\_004150918.1] [location=complement(711325..711885)] [gbkey=CDS]

MSTPSHLNAQPLVWGHGPRTFEVFLEPTCPYSVRAFNKLDDLLDEVGADNVTIKIRLQSQPWHLFSGVIV

RCILAASTLPHGREQAHKVMQAVADHREEFEFTDHCSGPNMNATPQQIIERIERYSHVLLGAAFARPELQ

DVIKWHSKYARQNGIHVSPTFMVNGLVQPDLGSGDDVSVWAARIMA

>lcl|NZ\_FO834906.1\_prot\_WP\_004217169.1\_694 [locus\_tag=BN49\_RS30855] [protein=hypothetical protein] [protein\_id=WP\_004217169.1] [location=711906..712028] [gbkey=CDS]

MFFCYITDNDITFVSGCRVIFLNGTISETNEWYHRYTSVW

>lcl|NZ\_FO834906.1\_prot\_WP\_002916740.1\_695 [gene=gss] [locus\_tag=BN49\_RS04720] [protein=bifunctional glutathionylspermidine amidase/synthase] [protein\_id=WP\_002916740.1] [location=712105..713970] [gbkey=CDS]

MSKGSTSSDAPFGTLLGYAPGGVAIYSSNYSSLNPQDYPDDATFRSYIGNEYMGHKWQCVEFARRFLFLT

YGFVFTDVGMAYEIFSLRFLREVVNDNILPLQAFANGSRRPPIAGSLLIWQKGGEFKHTGHVAVITQLVG

NKVRIAEQNVIHSPLPQGQQWTRELTLEVNDGRYTIKDTFADTEILGWMIQTADTEHSLPQPVLPGEAMA

IKGARLPNNGQFRGKWLNEKDPLQKAYVAANGHFINQDPYQYFTISESAEQELIKATNELHLMYLHATDK

VMKDDNLLALFDIPKILWPRLRLSWQRRRHHMITGRMDFCMDERGLKVYEYNADSASCHTEGGLILEQWL

KQGYYGTGHNPAEGLLDELAGAWKHSRARPFVHIMQDKDLEENYHAQFIQRSLTQAGFESKILFGLDELR

WDAAGQLIDADGRLVNCVWKTWAWETAIEQVREVSAEEYAAVPIRTGHPQNEVRLIDVLLRPEVLVFEPL

WTVIPGNKAILPVLWSLFPHHRYLLDTDFEVNDELAKTGYAVKPISGRCGNNIDLIGPQDELLDKTSGQF

VDRKNIYQQLWCLPKVDGKYIQVCTFTVGGNYGGTCLRGDSSLVVKKESDIEPLIVLKDKA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149825.1\_696 [locus\_tag=BN49\_RS04725] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_004149825.1] [location=714116..715297] [gbkey=CDS]

MHDRRLAARAGELKPSAVRELLKHSKLPGVISLGGGIPAPELFDTEGLELAVQKVMSERFNDAFQYGLTE

GYPPLRQAVSEICHSRGVACSAAQVYITSGSQQSLDIVARTLLDPGDTIVVERPTYLAALQVFQLAQANI

LSVDTDDDGMLVEQLADLLETTRVKAVYLVPTFGNPGGKTLSEARRRRLVELAKKYDFVILEDDPYGEIS

FTDAVRRPLYQHAVELGCEDQVVYTSTFSKILAPGMRIGWIVMPDWLAQQTVIVKQAADLHTNMLSQVIT

AEYLSLNRLDNQIALIREDYRKKCVALADALESRLGEHLEFSRPQGGMFLWARFRYPFDTMEWMKKTLEN

GVVYVPGEAFYHDKPDTRTLRLSYSTVSEAGLLTAVERLAASL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916738.1\_697 [locus\_tag=BN49\_RS04730] [protein=hypothetical protein] [protein\_id=WP\_002916738.1] [location=complement(715474..715662)] [gbkey=CDS]

MPVIIASSVKEAKALINGGKYREIILNFDIDADDFFSLASHSAGTKISIADRNDRSPVESAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004185642.1\_698 [locus\_tag=BN49\_RS04735] [protein=hypothetical protein] [protein\_id=WP\_004185642.1] [location=complement(715862..716206)] [gbkey=CDS]

MLKKLSLIIPLLALIALLVWWFTPHYTEEDEAYYRAVFCIIDHDDSRQFLHDMQNIVEGGNSDYALHKTH

YLPALGQRMLDTWRQLSPQEQQALRQDKQRCGEILREKQQGKSS

>lcl|NZ\_FO834906.1\_prot\_WP\_004174410.1\_699 [locus\_tag=BN49\_RS04740] [protein=short chain dehydrogenase] [protein\_id=WP\_004174410.1] [location=complement(716293..716895)] [gbkey=CDS]

MKIIVIGASGTIGRAVSEELSQRHEVIRVGRTRGDYQVDITSQESVEALFAQTGEVDAIVSTTGNLHFGP

LSTMTDSQFNLGLQDKLLGQIRLALVGQHFLRDGGSITLVSGIVAQEPIAQGVNATTVNAGLEGFVRAAA

CELPRGIRINLISPTVLSESLAAYGDFFPGFPSVPAAAVAQAYRRSIEGVQTGRIYPVGY

>lcl|NZ\_FO834906.1\_prot\_WP\_021314148.1\_700 [locus\_tag=BN49\_RS04745] [protein=LysR family transcriptional regulator] [protein\_id=WP\_021314148.1] [location=716993..717904] [gbkey=CDS]

MDKLRGMETFIAVVECGSFTGAASRLGLSAVMVGKYIAQLESQLATRLLERNTRRQSLTDAGRVYFDEAK

RVMEQVSIAESAVERLRLAPAGTLRVSAPTSFGASVIAPLTATFLQVWPAVRVELDLTNRMVDLVDEGFD

LAIRIGEIHQEDLVARYLAPYRMVICAAPAYLARYGTPGRPEDLADHLCLSHTVWTARNEWRLPGVEGEV

RWKRDAVLRCNDGYALRQAAIAGAGLLMQPEVLLADALASGSLVRVLEAWTPQPRPVHLLWRQDRRPLPK

LTQFIAHLQQGMADALTTTRASE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531357.1\_701 [locus\_tag=BN49\_RS04750] [protein=PLP-dependent aspartate aminotransferase family protein] [protein\_id=WP\_016531357.1] [location=complement(717905..719053)] [gbkey=CDS]

MSSIHTLSVHSGTFTDSHGAVMPPIYATSTFAQPAPGQHTGYEYSRSGNPTRHALETAIADLENGTRGYA

FASGLAAISTVLELLDKDSHLVAVDDVYGGTYRLLENVRRRSAGLQVSWVKPDDLAGIEAAIRPDTRMIW

VETPTNPLLKLADLSAIAAIARRHNLISVADNTFASPAIHRPLEHGFDIVVHSATKYLNGHSDVVAGLAV

VGDNSGLAEKLGYLQNAVGGVLDPFSSFLTLRGIRTLALRMERHSANALQLAEWLEQQPAVERVWFPWLA

SHPHHQLARQQMALPGGMISVVVKGDEGYAERIISKLRWFTLAESLGGVESLVSQPFSMTHASIPLEKRL

ANGITPQLIRLSVGIEDPNDLIADWQQALRAE

>lcl|NZ\_FO834906.1\_prot\_WP\_171819465.1\_702 [locus\_tag=BN49\_RS04755] [protein=pyridoxal-phosphate dependent enzyme] [protein\_id=WP\_171819465.1] [location=complement(719064..720440)] [gbkey=CDS]

MVMSLFHSVSDLIGHTPLLQLHKLDTGPCSLFLKLENQNPGGSIKDRVALSMIHEAERQGKLAPGGTIIE

ATAGNTGLGLALIAAQKNYRLILVVPDKMSREKIFHLRALGATVLLTRSDVNKGHPAYYQDYARRLADET

PGAFYIDQFNNDANPLAHATSTAPELYQQLEGDIDAIVVGVGSGGTLGGLQAWFAEHSPKTEFILADPAG

SILADQVDTGRYGETGSWLVEGIGEDFIPPLARLEGVHTAYRVSDCEAFHTARQLLQVEGVLAGSSTGTL

LSAALRYCRTQSRPKRVVTFACDSGNKYLSKMFNDDWMRQQGLIARPEQGDLSDFIALRHDEGATVTAAP

DDTLAAVFTRMRLYDISQLPVLEDGRVVGIVDEWDLIRHVQGDRQRFSLPVSEAMSRHVETLDKRAPESE

LQAILDRGLVAVIADNTRFLGLVTRSDVLTAWRNRVAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004150912.1\_703 [locus\_tag=BN49\_RS04760] [protein=DUF1778 domain-containing protein] [protein\_id=WP\_004150912.1] [location=721085..721378] [gbkey=CDS]

MPAANSMSIKRETLNLRIKPAERDLIDRAAKARGKNRTDFVLEAARAAAEEALIEQRIIMADPQAYQEFL

ARLDQAPAPNAALRKTMQTPAPWEQEE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042357.1\_704 [locus\_tag=BN49\_RS04765] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_046042357.1] [location=721375..721860] [gbkey=CDS]

MILAPESLHAGHILTPFCCGIDSMDHWLKQRAMKNQVTGASRTFVCCDDAKVMAYYSLASSAVTTNTAPG

RFRRNMPDPIPVVVLGRLAVDKSLHGKGVGRALVRDAGLRVIQVAETIGIRGMLVHALSDEARDFYLRVG

FEPSPMDPMMLMVTLRDLVNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004188553.1\_705 [locus\_tag=BN49\_RS04770] [protein=hypothetical protein] [protein\_id=WP\_004188553.1] [location=722564..723157] [gbkey=CDS]

MPSILARLSVCIILSLFMVSCSGSFDKTIDYQDAKQMPGYGYIVMDFRLANEMAYGNGYIPGKTNYTISY

KNKGDIFFVDIQHADFRNRILKAYIPYMKGYTLIGIGRSYWYPFFRCDKCDNEPQLKFLYINIVKSVDEA

WCSETTYKNLRSFNAMDGCSQMVGVEESRKVTGDVLITPELKSDFQGMFTPYLKPGR

>lcl|NZ\_FO834906.1\_prot\_706 [locus\_tag=BN49\_RS04775] [protein=transposase] [pseudo=true] [partial=3'] [location=723254..>723470] [gbkey=CDS]

MKKTRYTEEQIAFALKQAETGICVGEVCRKMGISEAIFIIRREIRCSGRN\*T\*IASSAATGG\*KSAAEKA

CG

>lcl|NZ\_FO834906.1\_prot\_WP\_002916694.1\_707 [locus\_tag=BN49\_RS04785] [protein=DUF554 domain-containing protein] [protein\_id=WP\_002916694.1] [location=complement(723985..724698)] [gbkey=CDS]

MVTGPFINASAVLVGGVLGALLSQRLPERIRTAMTSIFGLASLGIGILLVIKCANLPVMVLSTLVGTLLG

EICNMEKGINTLVSKLQQLMSAKGKKKASAHESYIQSYVAIIVLFCASGTGVFGAMREGMTGDASILIAK

AFLDFFTATIFACTLGIAVAAISVPMLLIQLTLAACAAIIMPLTTPMMLADFSAVGGMLLVATGLRICGI

KMFAVVNMLPALVLAMPISAAWTLFFA

>lcl|NZ\_FO834906.1\_prot\_WP\_004197024.1\_708 [locus\_tag=BN49\_RS04790] [protein=ornithine decarboxylase] [protein\_id=WP\_004197024.1] [location=725118..727256] [gbkey=CDS]

MKSMHIAASCELVTRLSTHRRVVALDSTDFTDVAAVVISAADSRSGILTLLRRSGFNLPVYLLSETAVDK

PEGVQAVIAGKDQEWLELEAAACDYEARLLPPFFNTLTQYVEMDNSTFACPGHQHGAFFKKHPAGRQFYD

FFGENVFRADMCNADVKLGDLLIHEGSAKHAQKFAAKVFNADKTYFVLNGTSAANKVVTNALLTRGDLVL

FDRNNHKSNHHGALIQAGATPVYLEAARNPFGFIGGIDERCFDEHYLRDLIREAAPEKANASRPFRLAVI

QLGTYDGTVYNARQVVDKIGHLCDYILFDSAWVGYEQFIPMMADCSPLLLELTPDDPGIFVTQSVHKQQA

GFSQTSQIHKKDNHLRGQARFCPHKRLNNAFMLHASTSPFYPLFAALDVNAKIHEGESGRRLWAECVALG

IEARKAIIANCKMIQPFIPPTVAGRPWQDHPTEAIARERRFFSFEPGARWHGFEGYADDQYFVDPCKLLL

TTPGIDAESGEYSEFGIPATILAHYLRENGIVPEKCDLNSILFLLTPAESAEKMAQLVAMLGQFEQHIEA

DTPLADVLPTIYNKYPVRYRDYTLRELCQEMHDLYVSFDVKSLQKEMFRKRSFPRVVMNPQDANHEFIRG

NVELVRLSEAEGRVAAEGALPYPPGVLCVVPGEVWGGAVLRYFLALEEGVNMLPGFSPELQGVYSETDPD

GIKRLYGYVLKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004144787.1\_709 [locus\_tag=BN49\_RS04795] [protein=nucleoside permease] [protein\_id=WP\_004144787.1] [location=complement(727300..728553)] [gbkey=CDS]

MNLKLQLKILSFLQFCLWGSWLTTLGSYMFVTLKFDGAAIGAVYSSLGIAAVLMPTLLGIVADKWISAKW

VYAICHLVGALTLYLAAQVTTPGEMFLVILLNSLAYMPTLGLINTISYYRLQSAGLDIVTDFPPIRIWGT

IGFILAMWGVSFSGFELSHMQLYIGATLSVLLTLFTLTLPHIPVANAQRNQSWTEMLGLNAFALFKNKRM

AIFFIFSMMLGAELQITNMFGNTFLHSFDKDPLFAGSFIVEHASVLMSISQISETLFILTIPFFLSRYGI

KNVMLISIVAWMLRFGLFAFGDPTPFGTVLLVLSMIVYGCAFDFFNISGSVFVEKEVRPEIRASAQGMFL

MMTNGFGCILGGMVSGKVVEHFTVEGITDWQSVWLIFAGYSLVLAFAFVALFKYKHVRQPTAAQQSV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529070.1\_710 [gene=mltC] [locus\_tag=BN49\_RS04800] [protein=membrane-bound lytic murein transglycosylase MltC] [protein\_id=WP\_016529070.1] [location=complement(728745..729827)] [gbkey=CDS]

MKKYLALALIAPLLVSCSSSNKNGAEYNEAWVKDTNGFDILMGQFAHNIENIWGYNEVLLAGPKDYVKYT

DQYQTRSHINFDEGTITVETIAGTDPRGRLRQAIVKTLLMGDDPNSIDLYSDVDDIQISKEPFLYGQVVD

NTGASIRWEWRAARFADYLLQTRLKSRNNGLRVVYSITINLVPNHLDKRAHKYLGMVRQASRKYGVDESL

ILAIMQTESSFNPYAVSHADAMGLMQVVQHSAGRDVFRSQGKSGLPSRSYLFDPANNIDTGTAYLAMLNN

VYLAGIDNPTSRRYAVITAYNGGAGSVLRVFSSDKVQAANIINSMAPGDVYQTLTTRHPSAESRRYLYKV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004105744.1\_711 [locus\_tag=BN49\_RS04805] [protein=oxidative damage protection protein] [protein\_id=WP\_004105744.1] [location=complement(729877..730152)] [gbkey=CDS]

MSRTIFCTFLQREADGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLSMMNPEHRKLLEQEM

VQFLFEGKDVHIEGYTPPEKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_021314145.1\_712 [gene=mutY] [locus\_tag=BN49\_RS04810] [protein=A/G-specific adenine glycosylase] [protein\_id=WP\_021314145.1] [location=complement(730181..731239)] [gbkey=CDS]

MTFLATQFSAQVLDWYDKYGRKTLPWQIAKTPYKVWLSEVMLQQTQVTTVIPYFERFMARFPTVVDLANA

PLDEVLHLWTGLGYYARARNLHKAAQQVATLHGGEFPRTFDEVAALPGVGRSTAGAILSLSLGQHYPILD

GNVKRVLARCYAVSGWPGKKEVEKRLWDISEEVTPAEGVDRFNQAMMDLGAMVCTRSKPKCELCPLSNGC

VAYANHSWAEYPGKKPKQTLPERTGYFLLMQHGDEVFLSQRPPVGLWGGLFCFPQFADEAELREWLAQRQ

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PV

>lcl|NZ\_FO834906.1\_prot\_WP\_002916627.1\_713 [gene=trmB] [locus\_tag=BN49\_RS04815] [protein=tRNA (guanosine(46)-N7)-methyltransferase TrmB] [protein\_id=WP\_002916627.1] [location=731376..732095] [gbkey=CDS]

MKNDVISPEFDENGRPLRRIRSFVRRQGRLTKGQQHALDNIWPVMGVEFNDAPLDFAALFGRDAPVTLEI

GFGMGASLVAMAKAKPEQNFLGIEVHSPGVGACLASAEEEGVQNLRVMCHDAVEVLHTMIPDNSLNMVQL

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PESRPVTKFEQRGHRLGHGVWDLMFERVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002916620.1\_714 [locus\_tag=BN49\_RS04820] [protein=YggL family protein] [protein\_id=WP\_002916620.1] [location=732095..732421] [gbkey=CDS]

MAKNRSRRLRKKMHIDEFQELGFSVAWRFPEGTSEEQIDQTVNDLIEEVIEPNKLAFDGSGYLSWEGLIC

MQEIGKCTEEHQAIVRKWLEARKLEDVRTSELFDVWWD

>lcl|NZ\_FO834906.1\_prot\_WP\_002916619.1\_715 [locus\_tag=BN49\_RS04825] [protein=DUF2884 domain-containing protein] [protein\_id=WP\_002916619.1] [location=732472..733191] [gbkey=CDS]

MMRKTLLAVALSVTALSAHADYQCSVTPRDDVILSPQQVQVKGENGDLVIKPDGNLTFNGKAYALSAAQR

EQAQDYQASLRSSLPWIDEGARSRVEKSRKALDKIITEQVGANSSMHGRLTKLDAQLKEQMNRIIERRSD

GLTFHYKAIDQVRADGQQLVNQAMGGILQDSINEMGAKAVLKGGGNPLQGILGSLGGLQTAIQEEWKNQE

ADFQQFGKDVCSRVVSLEDSRKALVGSLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004181281.1\_716 [locus\_tag=BN49\_RS04830] [protein=ABC transporter permease] [protein\_id=WP\_004181281.1] [location=complement(733238..734485)] [gbkey=CDS]

MNSKTASHTALDRSDERVRHDEGLFGALRAQITRIKTGDLGTAPVIAGLIVISLVFTFLNPVYIAPNNLV

NLLFDCATVGFISLGIVCVLMLGEIDLSVGSMSGLASAIVGVLWVNAGWPLAGAIAVALACGVAVGLVYA

LLYTRVGMPSFVATLAGLLALLGMQLYILGPSGSINLPYTSPLVRFGQLLVMPGWFSHLMALLPGLAILI

FGLKKRSRRLAANLSAEGVSSLVARAIALTIIFEAAVLYLNQGRGIPWIFGLFVACVMILNYALKRTKWG

RSMFAVGGNREAARRSGINVRAIYVSAFVLCTTLATFGGILAASRLASASQQAGTGDVNLNAIAAAVIGG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004181271.1\_717 [locus\_tag=BN49\_RS04835] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_004181271.1] [location=complement(734490..735299)] [gbkey=CDS]

MPQQQHNSAAGRPILQLRNVSKHFGAVSALTDIELEVHAGEVVALVGDNGAGKSTLVKILAGVHQPTSGT

IEFDGNPVTLDSPGKALEYGIATVFQDLALCENLDVVANLFLGHEISPFQLDEVAMEVKAWTLLQELAAR

IPSVREPVASLSGGQRQTVAIARSLLLNPKIIMLDEPTAALGVAQTAEVLNLIERVRERGLGVIIISHNM

EDVRAVADRIVVLRLGRNKGIFTPDASNQDLVAAITGATENAVSRRVERKSQPTTSGAM

>lcl|NZ\_FO834906.1\_prot\_WP\_016529067.1\_718 [locus\_tag=BN49\_RS04840] [protein=sugar ABC transporter substrate-binding protein] [protein\_id=WP\_016529067.1] [location=complement(735359..736405)] [gbkey=CDS]

MNYRNIFITLAALSGTVTASAWSAESATVAFLMPDQASTRYEQHDFPGFKAEMSKLCADCKVIYQNANAN

ASLQQQQFNSVIAQGAKVIVLDPVDSSAAAALVENAQAQGVKVIAYDRPVPDKPADFYVSFDNEGIGYAI

AKSLTDHLKASGVPQDAGVLQINGSPTDAATGLIRDGIHRGLKESGYKTLAEFDTPEWAPPKAQEWTAGQ

VTRFGDKIKGVVAANDGTGGGAIAAFKAAGVQPLPPVTGNDATIAALQLIIAGDQYNTISKPSEIVAAAA

AKVAVDFIQGKKPQASTTLYNTPSQLFTPEVVTAKNIKAEIFDKKIQTWDQVCSGEYAAACQKLGISK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529066.1\_719 [gene=hemW] [locus\_tag=BN49\_RS04845] [protein=radical SAM family heme chaperone HemW] [protein\_id=WP\_016529066.1] [location=complement(736698..737837)] [gbkey=CDS]

MANLPPLSLYIHIPWCVQKCPYCDFNSHALKGEVPHDDYVQHLLNDLQADAHYAQGREIGTIFIGGGTPS

LLSGPAMQTLLDGVRACLPLAAGAEITMEANPGTVEADRFVDYQRAGVNRISIGVQSFSEPKLQRLGRIH

GPEEAKRAARLASGLGLRSFNLDLMHGLPDQSLEEALDDLRQAIALNPPHLSWYQLTIEPNTLFGSRPPV

LPDDDALWDIFEQGHQLLSAAGYQQYETSAYAKPGFQCQHNLNYWRFGDYLGIGCGAHGKITFPDGRILR

TAKTRHPRGYMEGRYLERQHDVEEADKPFEFFMNRFRLLEAAPRAEFSLYTGLDEQVIRQQIDAAIAEGY

LLEDAQNWQITEHGKLFLNSLLELFLSEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916615.1\_720 [locus\_tag=BN49\_RS04850] [protein=XTP/dITP diphosphatase] [protein\_id=WP\_002916615.1] [location=complement(737830..738423)] [gbkey=CDS]

MQKVVLATGNAGKVRELASLLEDFGLDIVAQTELGVDSAEETGLTFIENAILKARHAAQITGLPAIADDS

GLAVDALGGAPGIYSARYSGVDASDQQNLEKLLDALKDVPDDQRQAQFHCVLVYLRHAEDPTPLVCHGSW

PGVITRQAAGHGGFGYDPIFFVPSEGKTAAELSREEKSAISHRGQALKLLLEALRNG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529065.1\_721 [gene=yggU] [locus\_tag=BN49\_RS04855] [protein=DUF167 family protein YggU] [protein\_id=WP\_016529065.1] [location=complement(738436..738726)] [gbkey=CDS]

MSAVETCADGLVLTLYIQPKASRDSIVGVHGDELKVAITAPPVDGQANAHLVKFLAKQFRVAKSQVLIEK

GELGRHKQVKIIAPQQIPTAVAALTE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916613.1\_722 [locus\_tag=BN49\_RS04860] [protein=YggT family protein] [protein\_id=WP\_002916613.1] [location=complement(738723..739289)] [gbkey=CDS]

MKTLTFLLSTVIELYTMVVLLRVWMQWARCDFYNPFSQFVVKATQPIVGPLRRIIPAMGPIDSASLLVAF

ILCVIKAIVLFMVITFQPIIWISALLILLKTIGSLIFWVLLLMAIMSWVSQGRSPVEYVLMQLADPLLRP

IRNLLPSMGGIDFSPMVLVLLLYVINMGIAEVLQATGNVLLPGLWMAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529064.1\_723 [locus\_tag=BN49\_RS04865] [protein=YggS family pyridoxal phosphate-dependent enzyme] [protein\_id=WP\_016529064.1] [location=complement(739310..740011)] [gbkey=CDS]

MNDIAHNLAQVRDKISGAAARCGRAPEEVTLLAVSKTKPASAIEEALAAGQRAFGENYVQEGVEKINHFQ

QAGVSGLQWHFIGPLQSNKSRLVAEHFDWCHTVDRLKIATRLNEQRPAHLPPLKVLIQINISDEQSKSGI

PLEALDGLAAEIAELPHLELRGLMAIPAPESEYVRQFAVARQMAVAFARLKTRYPTVDTLSLGMSDDMEA

AIAAGSTMVRIGTAIFGARDYSK

>lcl|NZ\_FO834906.1\_prot\_WP\_004149811.1\_724 [locus\_tag=BN49\_RS04870] [protein=type IV pilus twitching motility protein PilT] [protein\_id=WP\_004149811.1] [location=740028..741008] [gbkey=CDS]

MKLEEIVALSVKHNVSDLHLCNSAAPRWRRQGRLEPAPFPAPDIANLLNDWLDAAQLLHWQEHGQIDFAL

NLACGARLRASAFAHTRGISLVLRLLPEQCPRLDMLGAPPALSELLAEESGLLLVTGATGSGKSTTLAAM

VGHLNQHLDGHILTLEDPVEFIHHSERCLIQQREVGRHCPSFAAALRVALRQDPDVILLGELRDSETIRL

ALTAAETGHLVMATLHTRGAAPAVERLIDVFPAEEKDQVRSQLAGSLCAVLAQKLLPARQGGRVALYELL

VNTPAVANLIREGKVHQLPGVMQTGMQAGMLTFTQSFQQRVAAGAL

>lcl|NZ\_FO834906.1\_prot\_WP\_009308631.1\_725 [gene=csgD] [locus\_tag=BN49\_RS04880] [protein=transcriptional regulator CsgD] [protein\_id=WP\_009308631.1] [location=741356..742009] [gbkey=CDS]

MINLNGNSSSSRQVTFITHPSIQSKAFASYLSETLMAPVVLQNINKPLAQRLAKDSVILFDIAVSNKKLN

GVWRDIIRLQADNPRLLIINSAQKYELYEMAQWPALYGVFRHDDDESRLIEGIKAVLNGEQTAELSVMHP

AMYAADHASTPVENSPLTERECEILNELRCGATNLDIARALFISENTVRTHLYNVFRKLSVKNRTQAVSW

ANEHLRH

>lcl|NZ\_FO834906.1\_prot\_WP\_002916605.1\_726 [gene=ruvX] [locus\_tag=BN49\_RS04885] [protein=Holliday junction resolvase RuvX] [protein\_id=WP\_002916605.1] [location=complement(742062..742478)] [gbkey=CDS]

MSGTFLGFDFGTKSIGVAVGQRITATARPLPALKAQDGKPDWNVIEKLLKEWQPEAVIVGLPLNMDGTEQ

PLTARARNFANKIHGRFGVAILLHDERLSTVEARAGLFEHGGYRALNKGSVDSASAVVILESYFEQSF

>lcl|NZ\_FO834906.1\_prot\_WP\_002916603.1\_727 [locus\_tag=BN49\_RS04890] [protein=YqgE/AlgH family protein] [protein\_id=WP\_002916603.1] [location=complement(742478..743041)] [gbkey=CDS]

MNLQHHFLIAMPALQDPIFRRSVVYICEYNDEGAMGIIINKPLENLQVEGILEKLKIVPEPRNPEIRLDK

PVMLGGPLAEDRGFILHTPPSDFSSSIRISDNTVITTSRDVLETLGTDRQPGNVLVALGYSSWEKGQLEQ

EILDNAWLTAPADQNILFRTPIADRWREAAKLIGIDIVTMPGVAGHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002916600.1\_728 [gene=gshB] [locus\_tag=BN49\_RS04895] [protein=glutathione synthase] [protein\_id=WP\_002916600.1] [location=complement(743216..744166)] [gbkey=CDS]

MIKLGIVMDPIATINIKKDTSFAMLLEAQRRGYELHYMEMNDLYLINGEARARTRTLSVEQNYDKWYDFT

GEQDLPLADLDVILMRKDPPFDTEFIYATYILERAEEKGTLIVNKPQSLRDCNEKLFTAWFSELTPETLV

TRNKAQLKAFWEKHGDIIMKPLDGMGGASIFRVKAGDPNLGVIAETLTELGSRYCMAQNYLPAIKDGDKR

VLVVDGEPVPYCLARIPQGGETRGNLAAGGRGEARPLTESDWEIARRVGPTLKAKGLIFVGLDIIGDRLT

EINVTSPTCVREIEAAFPDISITGMLMDAIERRIDK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530642.1\_729 [gene=rsmE] [locus\_tag=BN49\_RS04900] [protein=16S rRNA (uracil(1498)-N(3))-methyltransferase] [protein\_id=WP\_016530642.1] [location=complement(744187..744918)] [gbkey=CDS]

MRIPRIHHPERLIVGSQFALSDDAANHVGRVLRMTTGQHLQLFDGSNQVFDAVITEAGKKNVTVEVLSGE

PDDRESPLHIHLGQVMSRGEKMEFTIQKSIELGVSLITPLFSERCGVKLDAERLQKKIQQWQKIAIAACE

QSGRNVIPEIRPAMQLEAWCAEQDSGLKLNLHPRASASINTLPLPVERVRLLIGPEGGLSAEEIAMTAQY

QFTDILLGPRVLRTETTALTAITALQVRFGDLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002916589.1\_730 [gene=endA] [locus\_tag=BN49\_RS04905] [protein=deoxyribonuclease I] [protein\_id=WP\_002916589.1] [location=complement(745010..745717)] [gbkey=CDS]

MSRMHVLAVAVLSAAVSGPLAAAGINSFSQAKAAGVKVNADVPGDFYCGCKIDWQGKKGVIDLESCGYKV

RKNENRASRVEWEHVVPAWQFGHQRQCWQEGGRKNCAKDPEYRKMESDMHNLQPAVGEVNGDRGNFMYSQ

WNGGEGQYGQCTMKVDFKDKIAEPPARARGAIARTYFYMRDRYQLNLSRQQTQLFTAWNKQYPVTAWECE

RDERIAKVQGNHNPYVQQACQAQKS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530641.1\_731 [locus\_tag=BN49\_RS04910] [protein=SprT family zinc-dependent metalloprotease] [protein\_id=WP\_016530641.1] [location=complement(745779..746312)] [gbkey=CDS]

MKTPRIPIAIQQAVMRSLREHLANANRKLERRYAEPTLVYQQRGTSAGTAWLEKNEIRLNPVLLLENQRE

FIDEVVPHELAHLLVWQHFGRVAPHGKEWKWMMESVLGVPARRTHRFELASVRQNTFPYRCRCQQHQLTV

RRHNRVVRGEATYRCVRCGDLLVAEKQPSELIRNFLI

>lcl|NZ\_FO834906.1\_prot\_WP\_002916587.1\_732 [locus\_tag=BN49\_RS04915] [protein=sugar porter family MFS transporter] [protein\_id=WP\_002916587.1] [location=complement(746390..747784)] [gbkey=CDS]

MPDNKKQGRSNKTMTFFVCFLAALAGLLFGLDIGVIAGALPFIANEFQISAHTQEWVVSSMMFGAAVGAV

GSGWLSFKLGRKKSLMIGAILFVAGSLFSAAAPNVEILLVSRVLLGLAVGVASYTAPLYLSEIAPEKIRG

SMISMYQLMITIGILGAYLSDTAFSYSGAWRWMLGVIIIPAVLLLIGVIFLPDSPRWFAAKRRFVDAERV

LLRLRDTSAEAKRELDEIRESLKVKQSGWSLFKDNSNFRRAVFLGILLQVMQQFTGMNVIMYYAPKIFEL

AGYANTTEQMWGTVIVGLTNVLATFIAIGLVDRWGRKPTLILGFIVMAAGMGVLGTMMHIGIHSSTAQYI

AVLMLLMFIVGFAMSAGPLIWVLCSEIQPLKGRDFGITCSTATNWIANMIVGATFLTMLNSLGSANTFWV

YGGLNVLFILLTLWLIPETKNVSLEHIERNLMQGRPLREIGARD

>lcl|NZ\_FO834906.1\_prot\_WP\_004149807.1\_733 [gene=metK] [locus\_tag=BN49\_RS04920] [protein=methionine adenosyltransferase] [protein\_id=WP\_004149807.1] [location=complement(748167..749321)] [gbkey=CDS]

MAKHLFTSESVSEGHPDKIADQISDAVLDAILEQDPKARVACETYVKTGMVLVGGEITTSAWVDIEEITR

NTVREIGYVHSDMGFDANSCAVLSAIGKQSPDINQGVDRADPLEQGAGDQGLMFGYATNETDVLMPAPVT

YAHRLVQRQAEVRKNGTLPWLRPDAKSQVTFQYDDGKIVGIDAVVLSTQHAEDIDQKSLQEAVMEEIIKP

ILPTEWLNASTKFFINPTGRFVIGGPMGDCGLTGRKIIVDTYGGMARHGGGAFSGKDPSKVDRSAAYAAR

YVAKNIVAAGLADRCEIQVSYAIGVAEPTSIMVETFGTEKVPSEQLTLLVREFFDLRPYGLIQMLDLLHP

IYKETAAYGHFGREHFPWEKTDKAALLREAAGLK

>lcl|NZ\_FO834906.1\_prot\_WP\_223168724.1\_734 [locus\_tag=BN49\_RS30860] [protein=protein YqgC] [protein\_id=WP\_223168724.1] [location=complement(749519..749869)] [gbkey=CDS]

MHERDAGCGVLTRDRTTRRIKRKTLVHYLVSPPHRPATGSATSQSYTYRATGATPLRDSVNTDCLTRLEV

APQGHAPCAFLMSRARRFIPRSGVKSKIKMCLFARLSGNFARRVFP

>lcl|NZ\_FO834906.1\_prot\_WP\_002916578.1\_735 [gene=yqgB] [locus\_tag=BN49\_RS30220] [protein=acid stress response protein YqgB] [protein\_id=WP\_002916578.1] [location=750023..750154] [gbkey=CDS]

MNKKPVAQSQNQQIVLGFRTVHGLLSHLWTAIVVNCLTLIIKN

>lcl|NZ\_FO834906.1\_prot\_WP\_004149805.1\_736 [gene=speA] [locus\_tag=BN49\_RS04930] [protein=biosynthetic arginine decarboxylase] [protein\_id=WP\_004149805.1] [location=750163..752139] [gbkey=CDS]

MSDDMSMVSPSSAGEHGVLRSMQEVAMSSQEASKMLRTYNIAWWGNNYYDVNELGHISVCPDPDVPEARV

DLAELVKAREAQGQRLPALFCFPQILQHRLRSINAAFKRARESYGYNGDYFLVYPIKVNQHRRVIESLIH

SGEPLGLEAGSKAELMAVLAHAGMTRSVIVCNGYKDREYIRLALVGEKMGHKVYLVIEKMSEIAIVLEEA

ERLNVVPRLGVRARLASQGSGKWQSSGGEKSKFGLAATQVLQLVEILREAGHLESLQLLHFHLGSQMANI

RDIATGVRESARFYVELHKLGVNIQCFDVGGGLGVDYEGTRSQSDCSVNYGLNEYANNIIWAIGDACEEN

GLPHPTVITESGRAVTAHHTVLVSNIIGVERNEYTEATPPAEDAARPLQSMWETWLEMHETGNRRSLREW

LHDSQMDLHDIHIGYSSGTFNLQERAWAEQLYLNMCHEVQKQLDPSNRAHRPIIDELQERMADKIYVNFS

LFQSMPDAWGIDQLFPVMPLEGLNKSPERRAVLLDITCDSDGAIDHYVDGDGIATTMPMPEYDPENPPML

GFFMVGAYQEILGNMHNLFGDTEAVDVFVFPDGSVEVELSDEGDTVADMLQYVQLDPNTLLTQFRDQVKN

TGLDDALQQQFLEEFEAGLYGYTYLEDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916572.1\_737 [gene=speB] [locus\_tag=BN49\_RS04935] [protein=agmatinase] [protein\_id=WP\_002916572.1] [location=752373..753293] [gbkey=CDS]

MSTLGHQYDNSLVSNAFGFLRLPMNFMPYESDADWVITGVPFDMATSGRAGGRHGPAAIRQVSTNLAWEH

NRFPWNFDMRERLNVVDCGDLVYAFGDAREMSEKLQAHAEKLLAAGKRMLSFGGDHFVTLPLLRAHAKHF

GKMALVHFDAHTDTYANGCEFDHGTMFYTAPNEGLIDPNHSVQIGIRTEFDKDNGFTVLDAGQVNDRSVD

DVIAQVKQIVGDMPVYLTFDIDCLDPAFAPGTGTPVIGGLTSDRAIKLVRGLKDLNIVGMDVVEVAPAYD

QSEITALAAATLALEMLYIQAAKKGE

>lcl|NZ\_FO834906.1\_prot\_738 [locus\_tag=BN49\_RS28650] [protein=OprD family porin] [pseudo=true] [partial=3'] [location=complement(<753353..753592)] [gbkey=CDS]

MGLAPTGPAQALFKTASRFVRQLEIFRVYTKRDYRDGLPDKAEWGQGIIATFKSGFTQGPVGFGVDCIAQ

YAVRLDGGRG

>lcl|NZ\_FO834906.1\_prot\_739 [locus\_tag=BN49\_RS31370] [protein=OprD family porin] [pseudo=true] [partial=3'] [location=complement(<753637..753720)] [gbkey=CDS]

MFASQQSNSQGFIEDSHLELFLRNAYTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151780.1\_740 [locus\_tag=BN49\_RS04945] [protein=M48 family metallopeptidase] [protein\_id=WP\_004151780.1] [location=complement(753754..754512)] [gbkey=CDS]

MKIRSTVLALGIAATLTGCQNMDSNGLLSSGAEAFQAYSLSDAQVKTLSDQACKEMDAKAKIAPANSEYS

QRLNKIAAALGDNINGQPVNYKVYETKDVNAFAMANGCIRVYSGLMDLMNDNEVEAVIGHEMGHVALGHV

KKGMQVALGTNAVRAAAASAGGIVGSLSQSQLGDLGEKLVNSQFSQRQESEADDYSYDLLRKRGINPSGL

ATSFEKLAKLEAGRQSSMFDDHPASEARAQHIRDRMKADGIK

>lcl|NZ\_FO834906.1\_prot\_741 [gene=tkt] [locus\_tag=BN49\_RS04950] [protein=transketolase] [pseudo=true] [location=754791..756785] [gbkey=CDS]

MSSRKELANAIRALSMDAVQKAKSGHPGAPMGMADIAEVLWRDFLNHNPNNPAWADRDRFVLSNGHGSML

IYSLLHLTGYDLPIEELKNFRQLHSKTPGHPEVGYTAGVETTTGPLGQGIANAVGMAIAEKTLAAQFNRP

GHDIVDHYTYAFMGDGCMMEGISHEVCSLAGTLKLGKLVAFYDDNGISIDGHVEGWFTDDTAKRFEAYGW

HVVRGVDGHDADAIKRAVEEARAVTDKPSLLMCKTIIGFGSPNKAGTHDSHGAPLGDAEIALTREALGWK

HAPFDIPSDIYAQWDAKEAGQAKEAAWNEKFAAYAKAFPQEAAEFTRRMKGEMPSDFDAKANEFIAKLQA

NPAKIASP\*ALQNAIEAFGPLLPGIPRRLRRSRAVQPDPVVWALSPINEDAAGNYIHYGVREFGMTAIAN

GIALHGGFLPYTSTFLMFVEYARNAVRMAALMKQRQVMVYTHDSIGLGEDGPTHQPVEQVASLRVTPNMS

TWRPCDQVESAIAWKYGVERQDGPTALILSRQNLAQQERTAEQLANVARGGYVLKDCAGQPELIFIATGS

EVELAVAAWDKLTAEGVKARVVSMPSTDAFDKQDAAYRESVLPKAVTARVAVEAGIADYWFKYVGLNGAI

VGMTTFGESAPAEQLFEEFGFTVDNVVAKAKALL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916512.1\_742 [gene=epd] [locus\_tag=BN49\_RS04955] [protein=erythrose-4-phosphate dehydrogenase] [protein\_id=WP\_002916512.1] [location=757171..758199] [gbkey=CDS]

MTIRIAINGFGRIGRNVVRALYESGRRAEITVVAINELADAAGIAHLLKYDTSHGRFAWDVRQEREQLFV

GDDAIRLLHEPTIAALPWRELAVDVVLDCTGVYGSREHGEAHLQAGAKKVLFSHPGGNDLDATVVYGVNQ

DELRAGHRIVSNASCTTNCIIPIIKLLDDAYGIESGTVTTIHSAMHDQQVIDAYHPDLRRTRAASQSIIP

VDTKLAAGITRIFPQFNDRFEAIAVRVPTINVTAIDLSVTVKKPVKACEVNQLLQKAAQGAFHGIVDYTE

LPLVSTDFNHDPHSAIVDGTQTRVSGAHLIKTLVWCDNEWGFANRMLDTTLAMAAIGFRFDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002916508.1\_743 [gene=pgk] [locus\_tag=BN49\_RS04960] [protein=phosphoglycerate kinase] [protein\_id=WP\_002916508.1] [location=758239..759402] [gbkey=CDS]

MSVIKMTDLDLAGKRVFIRADLNVPVKDGKVTSDARIRASLPTIELALKQGAKVMVTSHLGRPTEGEYNE

EFSLLPVVNYLKDKLSNPVRLVKDYLDGVEVAAGELVVLENVRFNKGEKKDDEELSKKYAALCDVFVMDA

FGTAHRAQASTHGIGKFADVACAGPLLAAELDALGKALKEPARPMVAIVGGSKVSTKLTVLDSLSKIADQ

LIVGGGIANTFVAAQGHNVGKSLYEADLVDEAKRLLGTCDIPVPTDVRVATEFSETATATLKSVNDIKDD

EQILDLGDVSAQKLAEILKNAKTILWNGPVGVFEFPNFRKGTEIVANAIADSEGFSIAGGGDTLAAIDLF

GIADKISYISTGGGAFLEFVEGKVLPAVAMLEERAKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004144748.1\_744 [gene=fbaA] [locus\_tag=BN49\_RS04965] [protein=class II fructose-bisphosphate aldolase] [protein\_id=WP\_004144748.1] [location=759500..760579] [gbkey=CDS]

MSKIFDFVKPGVITGDDVQKVFQVAKENNFALPAVNCVGTDSINAVLEAAAKVRSPVIVQFSNGGAAFIA

GKGVKTDVPQGAAILGAISGAHHVHQMAEHYGVPVILHTDHCAKKLLPWIDGLLDAGEKHFAATGKPLFS

SHMIDLSEESLHENIEICSKYLARMAKMGMTLEIELGCTGGEEDGVDNSHMDASALYTQPEDVDYAYTEL

SKISPRFTIAASFGNVHGVYKPGNVVLTPTILRDSQEYVSKKHNLPHNSLNFVFHGGSGSSAQEIKDSVS

YGVVKMNIDTDTQWATWDGILQYYKANEAYLQGQLGNPKGEDQPNKKYYDPRVWLRAAQTSMVTRLEQAF

KELNAIDVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916504.1\_745 [locus\_tag=BN49\_RS04970] [protein=small-conductance mechanosensitive channel MscS] [protein\_id=WP\_002916504.1] [location=760770..761627] [gbkey=CDS]

MEDLNVVDSINHAGTWLARNQELLLSYAVNIVAAIAILIVGMIVARVVSNTVNRLMLARKIDATVADFLS

ALVRYAVIAFTLIAALGRVGVQTASVIAVLGAAGLAVGLALQGSLSNLAAGVLLVMFRPFRAGEYVDLGG

VAGTVLNVQIFSTTLRTADGKVVVVPNGKIIAGNIINFSREPARRNEFIIGVAYDADIDKVKQLLTSIIE

SDDRILRDREMTVRLNELGASSVNFVVRVWSKSSDLQNVYWDILERIKREFDANGISFPYPQMDVHVVRL

PEKAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004144747.1\_746 [gene=argO] [locus\_tag=BN49\_RS04980] [protein=arginine exporter ArgO] [protein\_id=WP\_004144747.1] [location=761779..762414] [gbkey=CDS]

MFTYYFQGLALGAAMILPLGPQNAFVMNQGIRRQYHLMIALLCAVSDLLLICAGIFGGSALLMQSPWLLA

LVTWGGVAFLLWYGFGALKTAFSQSLELANAEVMQQGRWKIIITMLAVTWLNPHVYLDTFVVLGSLGGQL

AVEPKRWFALGTISASFLWFFGLALLAAWLAPRLRTARAQRIINIVVGAVMWFIAFQLAREGVSHIQALL

N

>lcl|NZ\_FO834906.1\_prot\_WP\_016530384.1\_747 [locus\_tag=BN49\_RS04985] [protein=oxidative stress defense protein] [protein\_id=WP\_016530384.1] [location=762504..763271] [gbkey=CDS]

MKLKVLALAATLGLTTMAAQASELPDGPHIVTSGTASVAAVPDIATLAIEVNVSAKDAASAKKQADDRVA

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RSVSLGVAQPDAYKDKARKAAIDDAVHQAQELAAGFHSKLGPVYSVRYHVSNYQPSPMVRMMKAADAAPV

SAQETYEQATIQFDDQVDVVFELQPAQAAAPANPAKPAETPKPAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002916497.1\_748 [gene=argP] [locus\_tag=BN49\_RS04990] [protein=DNA-binding transcriptional regulator ArgP] [protein\_id=WP\_002916497.1] [location=complement(763325..764218)] [gbkey=CDS]

MKRPDYRTLQALDAVIRERGFERAAQKLCITQSAVSQRIKQLENMFGQPLLVRTVPPRPTEQGQKLLALL

RQVELLEEEWLGDEQTGSTPLLLSLAVNADSLATWLLPALANVLSDSPIRLNLQVEDETRTQERLRRGEV

VGAVSIQPQALPSCLVDQLGALDYLFVASKEFAQRYFPNGVTRSALLKAPVVAFDHLDDMHQAFLQQNFD

LPPGSVPCHIVNSSEAFVQLARQGTTCCMIPHLQIEKELNSGELIDLTPGLFQRRMLYWHRFAPESRMMR

RVTDALIDYGHKVLRQD

>lcl|NZ\_FO834906.1\_prot\_WP\_002916495.1\_749 [gene=rpiA] [locus\_tag=BN49\_RS04995] [protein=ribose-5-phosphate isomerase RpiA] [protein\_id=WP\_002916495.1] [location=764386..765045] [gbkey=CDS]

MTQDELKKAVGWAALQYVQPGTIVGVGTGSTAAHFIDALGTMKGQIEGAVSSSDASTEKLKSLGITVFDL

NSVDRLGIYVDGADEINGHMQMIKGGGAALTREKIIASVADKFICIADASKQVDILGKFPLPVEVIPMAR

SAVARQLVKLGGRPEYRQGVVTDNGNVILDVHGLEILDAIALENAINGIPGVVTVGLFANRGADVALIGT

ADGVKTIVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002916493.1\_750 [gene=serA] [locus\_tag=BN49\_RS05005] [protein=phosphoglycerate dehydrogenase] [protein\_id=WP\_002916493.1] [location=765315..766547] [gbkey=CDS]

MAKVSLEKDKIKFLLVEGVHQKAIDSLRAAGYTNIEFHKGALDSEQLKASIRDAHFIGLRSRTHLTEEIF

AAAEKLVAVGCFCIGTNQVDLNAAAKRGIPVFNAPFSNTRSVAELVIGELLLMLRGVPEANAKAHRGVWN

KQAVGSFEARGKKLGIIGYGHIGTQLGILAESLGMHVFFYDIENKLPLGNATQVQHLSDLLNMSDVVSLH

VPENASTKNMMGAEELALMKPGALLINASRGTVVDIPALCDALASKHLAGAAIDVFPTEPATNSDPFTSP

LCEFDNVILTPHIGGSTQEAQENIGLEVAGKLAKYSDNGSTLSAVNFPEVSLPLHGGRRLLHIHENRPGV

LTAINQIFAAQSINIAAQYLQTSPQMGYVVIDIEAEEDVAQQALQAMKAIPGTIRARLLF

>lcl|NZ\_FO834906.1\_prot\_WP\_004144746.1\_751 [locus\_tag=BN49\_RS05010] [protein=5-formyltetrahydrofolate cyclo-ligase] [protein\_id=WP\_004144746.1] [location=complement(766631..767227)] [gbkey=CDS]

MTIQPDTLLSRQHIRQQIRDRRRALSPEQQRLFAQQAAERMMAWPPIVLAHNVALFLSFDGELDTQPLID

QLWRAGKRVYLPVLHPFSPGNLLFLHYHPQSQLIVNRLKIREPKLDVRDVLPLAELDVLVTPLVAFDVSG

QRLGMGGGFYDRTLQNWQQYRLQPVGYAHDCQQVDSLPSEEWDIPLPAVITPGKTWCW

>lcl|NZ\_FO834906.1\_prot\_WP\_016531067.1\_752 [gene=zapA] [locus\_tag=BN49\_RS05015] [protein=cell division protein ZapA] [protein\_id=WP\_016531067.1] [location=complement(767551..767880)] [gbkey=CDS]

MSAQPVDLQIFGRSLRVNCPPEQRDALNQAAEDLNQRLQDLKERTRVTNTEQLVFIAALNISYELTQEKA

KTRDYASSMAQRIRMLQQTIEQALLEQGRISEKPGSKFE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916486.1\_753 [locus\_tag=BN49\_RS05020] [protein=YecA family protein] [protein\_id=WP\_002916486.1] [location=768047..768625] [gbkey=CDS]

MSIQNEMPGYNDVDQLLNQQGVGLTPAEMHGLISGLLCGGNTDSSWQPLVHDLTNEGLAFGHELAQALRN

MHSAISDSLDDDGFLFQLYLPEGDAVSVFDRADALAGWVNHFLLGLGVSQPKLDKVKDETGEAIDDLRNI

AQLGYDEDEDQEELEMSLEEIIEYVRVAALLCHDTFARQQPTAPEVRKPTLH

>lcl|NZ\_FO834906.1\_prot\_WP\_016531068.1\_754 [gene=pepP] [locus\_tag=BN49\_RS05025] [protein=Xaa-Pro aminopeptidase] [protein\_id=WP\_016531068.1] [location=768649..769965] [gbkey=CDS]

MTQQEFLSRRQTLLAQMQPGSAALIFAAPEAVRSADSEYPYRQNSDFWYFTGFNEPEALLVLIKSDETHN

HSVLFNRVRDLTAEIWFGRRLGQEAAPAKLGVDRALAFSEINQQLYQLLNGLDAIYFAQGEYAYADEIVF

NALEKLRKGSRQNLQAPNSVIDWRPIVHEMRLFKSAEELAVMRRAGEITALAHTRAMEKCRPSMFEYQLE

GEILHEFNRHGARFPSYNTIVGGGENGCILHYTENESELRDGDLVLIDAGCEYRGYAGDITRTFPVNGKF

TQPQREIYDIVLESLETALKLYRPGTSICQVNQEVVRIMITGLVRLGILKGEIDELIANNAHRPYFMHGL

SHWLGLDVHDVGNYDTDRSRVLEPGMVLTVEPGLYIATDADVPAQYRGIGIRIEDDIVITEDGNENLTAG

VVKKADEIEALMAAARQS

>lcl|NZ\_FO834906.1\_prot\_WP\_002916482.1\_755 [gene=ubiH] [locus\_tag=BN49\_RS05030] [protein=2-octaprenyl-6-methoxyphenyl hydroxylase] [protein\_id=WP\_002916482.1] [location=769962..771140] [gbkey=CDS]

MSVLIVGGGMTGATLALAISRLTGGALPVHLIEAQDPHSSRHPGFDDRAIALAAGTCQQLARIGIWQRLA

ERATPIQRVHVSDRGHAGFVNLAAADYGLSALGQVVELHDVGQRLFGLLREAPGVTLHCPAKVEAVSRSQ

ESVSLTLEGGEIINGKLLVAADGSRSALGARCGISWQQQPYEQIAIIANVSTALPHEGRAFERFTEHGPL

AMLPMSQGRCSLVWCHPQSRRDEVQSWSDERFCQELQQAFGWRLGRITHAGKRSVYPLALTTASRAVSHR

LALVGNAAQTLHPIAGQGFNLGLRDVMSLAELLADAHLSGEDVGHYPLLCRYQARRAGDKAATIGVTDGL

VHLFANRWAPLVAGRNVGLMAMELFTPARDALAQRTLGWVPR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530364.1\_756 [gene=ubiI] [locus\_tag=BN49\_RS05035] [protein=FAD-dependent 2-octaprenylphenol hydroxylase] [protein\_id=WP\_016530364.1] [location=771151..772353] [gbkey=CDS]

MQSVDVAIVGGGMVGLAVACGLQGSGLRVAVLEKAEPRPLAADAPPALRVSAINAASEKLLTKLDVWREI

VAQRASCYHGMEVWDKDSFGHISFDDQSMGFSHLGYIIENAVVHHALWQKAQRCADVTLLAPAELQQVAW

GENEAFLSLQDGSMLTARLVIGADGANSWLRNKADIPLTFWDYHHHALVATIRTAEPHQAVARQAFHGDG

ILAFLPLSDPHLCSIVWSLSPGEAQRMQQADETTFNQALNIAFDNRLGLCQLASEREVFPLTGRYARQFA

AHRLALVGDAAHTIHPLAGQGVNLGFMDAAELIDELKRLHAQGKDIGQHLYLRRYERSRKHSAALMLAGM

QGFREMFSGSHPAKKLLRDVGLKLADTLPGVKPQLIRQAMGLNDLPAWLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530363.1\_757 [gene=gcvT] [locus\_tag=BN49\_RS05040] [protein=glycine cleavage system aminomethyltransferase GcvT] [protein\_id=WP\_016530363.1] [location=772776..773870] [gbkey=CDS]

MAQQTPLYEQHTLCGARMVDFHGWMMPLHYGSQIDEHHAVRGDAGMFDVSHMTIVDFHGSRIREFLRYLL

ANDVAKLTTPGKALYTGMLTASAGVIDDLIVYFLSEDYFRLVVNSATREKDLAWISEQAEPYGLEITVRD

DLSLIAVQGPQAKAKAATLFTDAQRQAVEGMKPFFGVQAGDLFIATTGYTGEAGYEIAMPNEQAADFWRG

LLDAGVKPCGLGARDTLRLEAGMNLYGQEMDEGVSPLAANMGWTIAWEPADRNFIGREALEMQREKDTEQ

LVGLVMTEKGVLRGGLPVRFTDSDGNQKEGIITSGTFSPTLGYSIALARVPAGIGDTAVVQIRNREMPVK

VTKPGFVRNGKAIV

>lcl|NZ\_FO834906.1\_prot\_WP\_002916479.1\_758 [gene=gcvH] [locus\_tag=BN49\_RS05045] [protein=glycine cleavage system protein GcvH] [protein\_id=WP\_002916479.1] [location=773895..774284] [gbkey=CDS]

MSNVPAELKYSKEHEWLRKEADGTYTVGITEHAQELLGDMVFVDLPEVGATVEAGADCAVAESVKAASDI

YAPISGEIVAVNEELNDSPELVNSDPYTDGWIFKIKASDEAQVAALLDAAAYEALLEDE

>lcl|NZ\_FO834906.1\_prot\_WP\_004900541.1\_759 [gene=gcvP] [locus\_tag=BN49\_RS05050] [protein=aminomethyl-transferring glycine dehydrogenase] [protein\_id=WP\_004900541.1] [location=774491..777364] [gbkey=CDS]

MTQTLSQLENRDAFIERHIGPDAQQQQEMLKTVGADSLNALIGQIVPQDIQLATPPQVGDATTEFAALAE

LKAIASRNKRFKSYIGMGYTAVQLPPVIQRNMLENPGWYTAYTPYQPEVSQGRLESLLNFQQVTLDLTGL

DIASASLLDEATAAAEAMAMAKRVSKLKSANRFFVAADVHPQTLDVVRTRAETFGFDVIVDDADKVLDHQ

DVFGVLLQQVGTTGEIHDYSKLIAELKARKVIVSVAADFMALVLLTAPGKQGADIVFGSAQRFGVPMGYG

GPHAAFFAAKDEFKRSMPGRIIGVSKDAAGNTALRMAMQTREQHIRREKANSNICTSQVLLANIASLYAV

FHGPAGLKRIAGRIHRLTDILADGLQKKGLKLRHAHYFDTLCVEVADKAAVLARAEDLQINLRSDIHGAV

GITLDEATTREDVLNLFRAIVGDDHGLDIDTLDKDVALDSRSIPAAMLRDDAILTHPVFNRYHSETEMMR

YMHALERKDLALNQAMIPLGSCTMKLNAAAEMIPITWPEFAELHPFCPVEQAEGYQQMIAQLSDWLVKLT

GYDAVCMQPNSGAQGEYAGLLAIRHYHESRNEGHRDICLIPSSAHGTNPASAQMAGMQVVVVACDKNGNI

DLADLREKAEQAGANLSCIMVTYPSTHGVYEETIREVCEIVHQFGGQVYLDGANMNAQVGITSPGFIGAD

VSHLNLHKTFCIPHGGGGPGMGPIGVKAHLAPFVPGHSVVQIEGMLTRQGAVSAAPFGSASILPISWMYI

RMMGAEGLKQASQNAILNANYIATRLKDAYPVLYTGRDGRVAHECILDIRPLKEETGISELDIAKRLIDF

GFHAPTMSFPVAGTLMVEPTESESKVELDRFIDAMLAIRAEIDRVKAGEWPLEDNPLVNAPHTQGELVGE

WNHPYSRELAVFPAGLHNKYWPTVKRLDDVYGDRNLFCSCVPMSEYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004174442.1\_760 [locus\_tag=BN49\_RS05055] [protein=SDR family oxidoreductase] [protein\_id=WP\_004174442.1] [location=777427..778170] [gbkey=CDS]

MGIALISGASRGIGRATALLLAQEGYTVAVNYHHNINAATEVVNTIVASGGKATALRADISDEAQVMAMF

EAIDRMGEPLTALVNNAGILFTQCTVESLSAERINRVLATNVTGYFLCCREAVKRMSHRHGGKGGAIVNV

SSAASRLGAPGEYVDYAASKGAVDTLTTGLALEVAAQGIRVNGVRPGLIYTEMHASGGEPGRVDRVKGSL

PMQRGGQPEEVAQAIAWLLSDKASYVTGSFLELAGGK

>lcl|NZ\_FO834906.1\_prot\_WP\_009308618.1\_761 [locus\_tag=BN49\_RS05060] [protein=protein disulfide oxidoreductase] [protein\_id=WP\_009308618.1] [location=complement(778291..778794)] [gbkey=CDS]

MASKIRRWLRELAVWLLIGAAVSLAVDYFRQPALPQNVSATSLQTLDGRTLDLNAMSQQKPLLLYVWATW

CGVCRYTTPSVASLAADGGNVLTVALRSGDNAALEKWLTRKKLALPTVNDPSGQLARQWDIQVTPTLVVI

SQGEVKSVTTGWTSSWGMRLRLWLASW

>lcl|NZ\_FO834906.1\_prot\_WP\_009308617.1\_762 [locus\_tag=BN49\_RS05065] [protein=thioredoxin domain-containing protein] [protein\_id=WP\_009308617.1] [location=complement(778784..779395)] [gbkey=CDS]

MRAITALLLLCVSAFSFAAPAEEPQSNGNDQLAQLLFNDPNSPRTGAKEPKLTIVSFTDYNCPYCKQFDP

LLEKIVHDNPDIQLIVKLLPFKGQSSVNAAKIALSTWRQQPDKFWALHQRLMAKKGYHDDASIAAAQKKT

ATDSVNIDDKTMDSLKMNLILSQVLNIQGTPATIIGDQMVAGAIPAEDLEGLVKEQLAKARGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042370.1\_763 [locus\_tag=BN49\_RS05070] [protein=protein-disulfide reductase DsbD family protein] [protein\_id=WP\_046042370.1] [location=complement(779397..781406)] [gbkey=CDS]

MYMVFRRLLVCLLWLWLPVSQAADSGWLRAADNQHASVRLRAQTESNGDTRLLLDVALEKGWKTYWRSPG

EGGIAPAIAWHTPLEVNWRWPTPQRFDVAGISTQGYHGDVSFPMTLRGKIPPTLSGVLTLSTCSNVCILT

DYPFSLDMTTPAGERFNYDFTRAMGTLPLRDGLTSQLTASYVSGKLTVTARRDAGWQQPALFIDSMEDVD

FGKPSFTTRGDTLTATVPVTDSWGEAAPDLRGKTLSLVLADSGQAQESQVAVAAGSAAPGLALGWVLLMA

LAGGLILNVMPCVLPVLAMKLGSLVQTEGRERGAVRRQFLASVFGIVVSFLALALMMTALRLGNQALGWG

IQFQNPWFIGAMALVMVLFSASLLGLFEIRLSSSASTFLATRGGNGLRGHFWQGAFATLLATPCTAPFLG

TAVSVALVAPLPLLWGIFFAMGIGMSLPWLLIVAWPGLAQRLPRPGRWMNHLRVVLGLMMLGSALWLVSL

LTIHIGRTPVLTLLVMLAIALLVATAWRYRWRTALRAGALAIVVAGAVAFVAQQDGQGPRRDRVNWQPLS

EQAIASALAEHKRVFIDVTADWCVTCKANKYNVLLRDDVQQALLAPDVIALRGDWSRPSADISQFLTARG

SAAVPFNQIYGPELPQGQILPALLDREHLLATLSAAKGK

>lcl|NZ\_FO834906.1\_prot\_WP\_004900527.1\_764 [locus\_tag=BN49\_RS05075] [protein=hypothetical protein] [protein\_id=WP\_004900527.1] [location=complement(781456..781815)] [gbkey=CDS]

MIKRQRKAILFVLLACLVVLTCTAQRMAGMHALVMNLTADSPSLQKNQDQAEAPVTPCELSAKSLMAVPP

MLFEGALLAITLLLAVLAAIPPRIERQWPPRVISSPRLRVHLRLCVFRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916322.1\_765 [gene=bglA] [locus\_tag=BN49\_RS05080] [protein=6-phospho-beta-glucosidase BglA] [protein\_id=WP\_002916322.1] [location=complement(781940..783373)] [gbkey=CDS]

MKKLTLPKDFLWGGAVAAHQVEGGWDQGGKGPSICDVLTGGAHGVPREITHQVEAGKYYPNHEAVDFYGR

YKEDIKLFAEMGFKCFRTSIAWTRIFPQGDETQPNEEGLKFYDDMFDELLKYNIEPVITLSHFEMPLHLV

QQYGGWTNRKVVDFFVRFAEVVFERYKHKVKYWMTFNEINNQRNWRAPLFGYCCSGVVYTEHDNPEETMY

QVLHHQFVASALAVKAARRINPDMQVGCMLAMVALYPYSCKPEDVMFAQESMRERYVFTDVQLRGYYPSY

VLNEWERRGFNIRMEDGDAQILREGTCAYLGFSYYMTNAVKAEGGTGDAISGFEGSVPNPHVKASDWGWQ

IDPVGLRYSLCELYERYQKPLFIVENGFGAYDKVEADGSINDDYRIDYLRAHIEEMIKAVTYDGVDLLGY

TPWGCIDCVSFTTGQYSKRYGFIYVNKHDDGTGDMSRSRKKSFNWYKEVIASNGENL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916321.1\_766 [locus\_tag=BN49\_RS05085] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_002916321.1] [location=complement(783492..784220)] [gbkey=CDS]

MFSHAAVASLNNLEMMVYHYVIKNRDKVMYMTIRELAEAAGVSTTTVLRFCRKLQCEGYSEFRVRFKLYL

EQNEPQQANIGASEIMSFFKSVNNDEFDELLEQAVDIILASERIIFVGAGTSGALAKYGARFFSNVGKFS

NHIDDPYFPVTNDMARNALAIVLSVSGETEEILRFASQFSLHHCKVMSITSHEHSRLAKLADFNLSWHVP

QTRIGGVYDITTQIPVIYILESLGRKLARKIS

>lcl|NZ\_FO834906.1\_prot\_WP\_004144734.1\_767 [gene=yqfB] [locus\_tag=BN49\_RS05090] [protein=N(4)-acetylcytidine aminohydrolase] [protein\_id=WP\_004144734.1] [location=784270..784581] [gbkey=CDS]

MQANDITFFQRFQDDILAGRKTITIRDAAESHFKPGDVLRVGRYEDDGYFCTIAVTATSTVTLDTLTEQH

AQQENMTLGQLRQVISDIYPGESQFYVIEFKTL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916317.1\_768 [locus\_tag=BN49\_RS05095] [protein=hemolysin III family protein] [protein\_id=WP\_002916317.1] [location=784745..785404] [gbkey=CDS]

MVRKPLITQGYSLAEEVANSISHGIGLVFGIVGLVLLLVQAADTNASATAIASYSLYGGSMIMLFLASTL

YHAIPHQRAKQWLKKFDHCAIYLLIAGTYTPFLLVGLNSPLAKGLMIVIWSLALLGILFKLTIAHRFKIL

SLVTYLTMGWLSLIVVYQLAVKLAVGGVTLLAVGGVVYSLGVIFYVCKRIPYNHAIWHGFVLGGSVCHFL

AIYLYIGQS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530681.1\_769 [gene=ygfZ] [locus\_tag=BN49\_RS05100] [protein=tRNA-modifying protein YgfZ] [protein\_id=WP\_016530681.1] [location=complement(785503..786486)] [gbkey=CDS]

MAFTPFPPRQPSSSARLPLTLMTLDDWALATISGPDSEKYLQGQITADVSHLTDAQHLLAAHCDAKGKMW

SNLRVFRREGGFAWIERRSLRDAQLTELKKYAVFSKVTIAANDDLVLLGVAGFQARAALAPLFAALPDAA

TPVVSEGATNLLWFEHPGERFLLVTDVDTANRVTDALRGEAQFNNSQQWLALNIEAGLPVIDSANSGQFI

PQATNLQALGGISFKKGCYTGQEMVARAKFRGANKRALWTLSGTASRVPEAGEDLELKMGDNWRRTGTVL

AAVQLDDGSLMVQVVMNNDMEPDSVFRVRDDAGSLSIKPLPYSLEED

>lcl|NZ\_FO834906.1\_prot\_WP\_002916312.1\_770 [gene=sdhE] [locus\_tag=BN49\_RS05105] [protein=FAD assembly factor SdhE] [protein\_id=WP\_002916312.1] [location=786732..786998] [gbkey=CDS]

MDINNKARIHWACRRGMRELDISIMPFFEYEYDTLSDADKQLFIRLLENDDPDLFNWLMNHGKPADAELQ

RMVTLIQTRNRERGPVAI

>lcl|NZ\_FO834906.1\_prot\_WP\_002916310.1\_771 [locus\_tag=BN49\_RS05110] [protein=protein YgfX] [protein\_id=WP\_002916310.1] [location=786979..787389] [gbkey=CDS]

MVLWQSDLRISWRAQWFSLLLHGVVAALVLLVPWPLSYTPIWLLLLSLVVFDCVRSQRRIHARRGEIKLL

TDSRLRWQNAEWEILGTPWVINSGMLLRLRHVDTRRGQHLWLAADSMDAGEWRDLRRLVLQKPAQE

>lcl|NZ\_FO834906.1\_prot\_WP\_004144730.1\_772 [gene=fldB] [locus\_tag=BN49\_RS05115] [protein=flavodoxin FldB] [protein\_id=WP\_004144730.1] [location=complement(787396..787917)] [gbkey=CDS]

MNIGLFYGSSTCYTEMAAEKIRDIIGPELVTLHNLKDDSPALMSQYDVLILGIPTWDFGEIQEDWEAVWD

QLDTLNLEGKIVALYGMGDQLGYGEWFLDALGMLHDKLATKGVKFVGYWPTEGYEFTSPKPVIADGQLFV

GLALDETNQYDLSDERIQSWCEQILGEMAEHFS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042376.1\_773 [gene=xerD] [locus\_tag=BN49\_RS05120] [protein=site-specific tyrosine recombinase XerD] [protein\_id=WP\_046042376.1] [location=788018..788914] [gbkey=CDS]

MKQDLALIEQFLDALWLERNLAENTLSAYRRDLTMLVEWLHHRGLSLASVGSDDLQALLAVRQSGGYKAT

STARLLSAVRRFFQHLYREKIRPDDPSALLASPKLPQRLPKDLSEAQVERLLQAPLVEQPLELRDKAMLE

VLYATGLRVSELVGLTMSDISLRQGVLRVVGKGNKERLVPLGEEAVLWVENYLEYGRPWLLNGVASDVLF

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HVATERLRQLHQQHHPRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174456.1\_774 [gene=dsbC] [locus\_tag=BN49\_RS05125] [protein=bifunctional protein-disulfide isomerase/oxidoreductase DsbC] [protein\_id=WP\_004174456.1] [location=788937..789650] [gbkey=CDS]

MKKGLLMFTLLAASLSGTAHADSAAIKQSLAKLGVQSTDIQPSPVSGMSTVLTDSGVLYVTDDGKHIIQG

PMYDVSGAQPVNVTNQLLLGKLNALSNEMIVYKAPKEQHVITVFTDITCGYCHKLHEQMSDYNALGITVR

YLAFPRQGLQSQAEQDMKAIWCAKDRNKALDDAMNGKGVQPASCSVDIAKHYTLGVQMGVNGTPAMVLSN

GMVLPGYQGPKELKAFLDEHKKQTSGN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530103.1\_775 [gene=recJ] [locus\_tag=BN49\_RS05130] [protein=single-stranded-DNA-specific exonuclease RecJ] [protein\_id=WP\_016530103.1] [location=789656..791389] [gbkey=CDS]

MKQQIQLRRREAVDGVELPADLPPLLQRLYASRGVRSAQELERSVKGMLPWTQLTGVEKAVEMLHDAFQK

GLHIVVVGDFDADGATSTALSVLALRALGYGNVSYLVPNRFEDGYGLSPEVVDQAHARGAQMIMTVDNGI

SSHAGVDHAHALGIPVLVTDHHLPGETLPAAEAIVNPNLRDCDFPSKSLAGVGVAFYLMLALRTFLRDKG

WFDARGIPAPNLGELLDLVALGTVADVVPLDANNRILTWQGLSRIRAGKCRPGIKALLEIANRDPQKLAA

SDLGFALGPRLNAAGRLDDMSVGVALLLCDNIGEARVLANELDALNQTRKEIEQGMQAEALTLCQQLERS

ADTLPGGLAMYHPQWHQGVVGILASRIKERFHRPVIAFAPTGDGTLKGSGRSIQGLHMRDALERLDTLYP

GLILKFGGHAMAAGLSLEEARFEEFQQRFGELVTEWLDPALLQGEVVSDGPLAAAEMSMEVAQMLRDAGP

WGQMFPEPLFDGRFRLLQQRLVGERHLKVMVEPVDGGPLLDGIAFNVDTSIWPDNGVREVQLAYKLDINE

FRGNRSLQLIIDHLWPN

>lcl|NZ\_FO834906.1\_prot\_WP\_095858446.1\_776 [gene=prfB] [locus\_tag=BN49\_RS05135] [protein=peptide chain release factor 2] [exception=ribosomal slippage] [protein\_id=WP\_095858446.1] [location=join(791475..791549,791551..792573)] [gbkey=CDS]

MFEINPVKNRIQDLTERSDVLRGYLDYDAKKERLEEVNAELEQPDVWNEPERAQALGKERSSLEAIVDTL

DQMSQGLEDVAGLLDLAVEADDEETFNEAVAELDTLEEKLAQLEFRRMFSGEYDSADCYLDIQAGSGGTE

AQDWASMLMRMYLRWAEARGFKTEIIEESEGEVAGIKSVTIKIIGDYAYGWLRTETGVHRLVRKSPFDSG

GRRHTSFSSAFVYPEVEDDIDIEINPADLRIDVYRASGAGGQHVNRTESAVRITHIPTGLVTQCQNDRSQ

HKNKDQAMKQMKAKLYELEMQKKNAEKQAMEDNKSDIGWGSQIRSYVLDDSRIKDLRTGVETRNTQAVLD

GSLDQFIEASLKAGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916299.1\_777 [gene=lysS] [locus\_tag=BN49\_RS05140] [protein=lysine--tRNA ligase] [protein\_id=WP\_002916299.1] [location=792583..794100] [gbkey=CDS]

MSEQQAQGADAAIDLNNELKTRREKLAALREQGVAFPNDFRRDHTSDQLHADFDGKENEELEALNVEVAV

AGRMMTRRIMGKASFVTLQDVGGRIQLYVARDDLAEGVYNDQFKKWDLGDIIAARGKLFKTKTGELSIHC

TELRLLTKALRPLPDKFHGLQDQEARYRQRYLDLISNDESRKTFKVRSQILAGIRQFMVGRGFMEVETPM

MQVIPGGASARPFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMEL

YMAYADYKDLIELTESLFRTLAQDILGNTEVPYGDQVFDFGKPFEKLTMREAIKKYRPETEMADLDNFDS

AKAIAESIGIKVEKSWGLGRIVTEIFEEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGG

REIGNGFSELNDAEDQAQRFQDQVDAKAAGDDEAMFYDEDYVTALEHGLPPTAGLGIGIDRMVMLFTNSH

TIRDVILFPAMRPQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002916298.1\_778 [gene=idi] [locus\_tag=BN49\_RS05145] [protein=isopentenyl-diphosphate Delta-isomerase] [protein\_id=WP\_002916298.1] [location=complement(794335..794889)] [gbkey=CDS]

MAGEHVILLDEQDQPAGMLEKYAAHTFDTPLHLAFSCWLFNQQGQLLVTRRSLGKKAWPGVWTNSVCGHP

QQGETFEQAVTRRCRFELGVEISDIAPVHPAFRYRAVAPNGIVENEVCPVYAARVVSEVQPNDDEVMDYQ

WVDLATMLSALAATPWAFSPWMVLEAENRDARQALTDFVARLRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004157874.1\_779 [locus\_tag=BN49\_RS05155] [protein=amidase activator ActS] [protein\_id=WP\_004157874.1] [location=795206..795919] [gbkey=CDS]

MMKRFYMTLMLAASLVLAGCSSTSDSGGTYTVKRGDTLYGISRTTGTSVRDLARLNNISPPYTIEVGQKL

KLNGSSSTKTTKKKSSSTRTAAVTPSSAVPQSSWPPVGQRCWRWPTSGKVVLPYSTADGGNKGIDIAGTR

GQPVYAAGAGKVVYVGNQLRGYGNLIMIKHSEDYITAYAHNDKLMVNNGQSVKAGQQIATMGSTDADSVR

LHFQIRYRATAIDPLRYLPPQGSKPKC

>lcl|NZ\_FO834906.1\_prot\_WP\_042941128.1\_780 [locus\_tag=BN49\_RS05165] [protein=hypothetical protein] [protein\_id=WP\_042941128.1] [location=796702..797142] [gbkey=CDS]

MDLRGYSFKQHLSDLLLPNNEFYSTVNPAYLNSGGVYVLRSFNDAGQALTIPRVLDDDRDGILYIGMAKL

FCHRTGDLARSFSSQYRQSKHQTGQRYWSDERYQQRYPYEHLKMFMWISDHPATLEQSFFQSYLARFGET

PPLNRI

>lcl|NZ\_FO834906.1\_prot\_WP\_016530105.1\_781 [locus\_tag=BN49\_RS05170] [protein=hypothetical protein] [protein\_id=WP\_016530105.1] [location=complement(797528..797752)] [gbkey=CDS]

MDQELIKKLGLEPTHTFNQTSFVNKTKGRLDIDVIMYDEFDKSGVRVAEVTIHDTTERYPPFSREIYLES

RVKV

>lcl|NZ\_FO834906.1\_prot\_WP\_071609135.1\_782 [locus\_tag=BN49\_RS28660] [protein=hypothetical protein] [protein\_id=WP\_071609135.1] [location=complement(797823..798089)] [gbkey=CDS]

MPICKQAHRYNSIFINLPYDQGGEGRHKCCGCAYDQGYCAGLARTGQVWVDLTALPDSQAGTVRHKSPQA

AFAEGYRDGVRDSYKQAI

>lcl|NZ\_FO834906.1\_prot\_WP\_023327926.1\_783 [locus\_tag=BN49\_RS05175] [protein=recombinase family protein] [protein\_id=WP\_023327926.1] [location=798766..799335] [gbkey=CDS]

MSRTFAYCRVSTNEQTTENQIMAIRQAGYDILDSRVVSETVSGGVQAMQRRAFANMVDHKLEEGDTLVVL

KLDRLGRDNIDVQQTITMLIERGIKVVSLDLPVRDLSSAEGKLMLQMFSSFAEFEKSRIIERTKEGLERA

KQEGKILGRPVATETRRRVQEAREQGLSQSKAAQSLGLGIATIKRYWNI

>lcl|NZ\_FO834906.1\_prot\_WP\_129015075.1\_784 [locus\_tag=BN49\_RS30225] [protein=hypothetical protein] [protein\_id=WP\_129015075.1] [location=799813..800151] [gbkey=CDS]

MNNYLFCNWHGTYFHGSFINNNSAFTAFCNHQSAAYWDNEGKCIKHLIPQNVGVYARLPLNKDDNIEDVF

SDSKFILCFEGDLLNDYLDCNEVLGLYLFGKINAVQKIYRTR

>lcl|NZ\_FO834906.1\_prot\_WP\_042940720.1\_785 [locus\_tag=BN49\_RS05180] [protein=hypothetical protein] [protein\_id=WP\_042940720.1] [location=801210..801389] [gbkey=CDS]

MKYFTIEQVVEALKTGAARRHQIYDNFAQARYRGFTERASLFKTALEIFDQWKRENKTS

>lcl|NZ\_FO834906.1\_prot\_WP\_162571991.1\_786 [locus\_tag=BN49\_RS30865] [protein=hypothetical protein] [protein\_id=WP\_162571991.1] [location=801386..801562] [gbkey=CDS]

MNVTFDQETYKDLIYEANLQGLAAPALVARIIRQYIKNQTGPYEGANQPEDLNGKNKR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529417.1\_787 [locus\_tag=BN49\_RS05185] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016529417.1] [location=801543..801956] [gbkey=CDS]

MGKTKDNYFKSHYDIFKINTINGKKFSISAKSIYSYLKSFSDAGLKVFPSHNEIADTFGITRNAAIKQIE

KLIELGLIERETRPGNCNEYHILTIQIENTAGRTYSENRGTRYEVVGDFGNKSGIVLIEEDNDDLPW

>lcl|NZ\_FO834906.1\_prot\_WP\_016529416.1\_788 [locus\_tag=BN49\_RS05190] [protein=hypothetical protein] [protein\_id=WP\_016529416.1] [location=801972..802724] [gbkey=CDS]

MGKKKTFEVSINNLPAALKRLDLPAEQVQVIEDYKKQFPFLLEEGENVLVSLDQLWEALDTPYYTRPGTI

PESSGSVKSRSIQQEKQYKRNKFNQWVESVLKEIDGEPFSRMVPTGKTKRKETFVTIEDAKIIAMMAPGE

QGRKIRRYFVTVEKVCKILWQYNLQRNQIEDKSKEVYKLRLAQTGYKGFDVAAKDKVRFNSLVKQIAGAR

NVRETDLENYHHIQHEVFNAMKRGCTDSQILAFYLGDEAA

>lcl|NZ\_FO834906.1\_prot\_789 [locus\_tag=BN49\_RS05195] [protein=IS3 family transposase] [pseudo=true] [location=complement(802931..804164)] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQPAISLA\*AIPGGKSYCCGCRRTGRS

CL\*TCCRHEAD\*RTPAPARQKNDGK\*TP\*RSR\*IWASKKVDSARALIARGWGVSFVSRCLRVSRAQLHVI

LRRTDDWKDGRRSRHTDDTDVLRRIHHVIGKLPTYGYRRGWALLRRQTEPDGMPAINAKRVYRIMRQNAL

FA\*AKTRCTAIETGTYRQSGCERK\*SAMVL\*RV\*VPL\*\*RRKTAGHVRAGLL\*P\*GTALGGHNGWLRQ\*N

STGRHARSSGTPLWQRASGVSSGVADG\*WFMLPGE\*NTSVRQDVGT\*TEEHGSAESGE\*RNSRELRENDK

A\*LHKYHAQTRRVNGSKEPCRGVRAL\*RMASA\*CAGLSLATGISAAAGQ\*WVK\*\*QVSGNI

>lcl|NZ\_FO834906.1\_prot\_WP\_129015076.1\_790 [locus\_tag=BN49\_RS05205] [protein=hypothetical protein] [protein\_id=WP\_129015076.1] [location=804228..804482] [gbkey=CDS]

MSGDSGGQSTPEEQETINSMDGVTWKPRQRYAGFKFNREPLKFECLFDNINEYEGWLEFNRLENEQYQGY

DVDIIDAAYNGITD

>lcl|NZ\_FO834906.1\_prot\_WP\_016531927.1\_791 [locus\_tag=BN49\_RS05210] [protein=hypothetical protein] [protein\_id=WP\_016531927.1] [location=804509..804784] [gbkey=CDS]

MINFEQHKNIVEDFVEQHYPLAHSLMVDSYIDPEAYYSNYQMLLEAMSKLPEHPEFFLEWLLEDDAALYI

NLMELVVITRTIHNVFEQVSP

>lcl|NZ\_FO834906.1\_prot\_WP\_016530284.1\_792 [locus\_tag=BN49\_RS05215] [protein=hypothetical protein] [protein\_id=WP\_016530284.1] [location=805242..805466] [gbkey=CDS]

MVAIHKGVKTFDGKIPVTLLVDDVETANELIKLAKTANVPVVEQEEDLNKSKNKTTQDKLKQIIKNKGVP

NGTN

>lcl|NZ\_FO834906.1\_prot\_WP\_117262243.1\_793 [locus\_tag=BN49\_RS30230] [protein=hypothetical protein] [protein\_id=WP\_117262243.1] [location=805453..805803] [gbkey=CDS]

MALIKFPQPNLSVCDVLSRELNGYSRKVKVFPKIPDCVPGTVIDDSGEIVGSASTSANVVLEYKDADTTP

VAVLVANTNIHIKDFSLVCDDVAKAKELLSADPSVYFSTGNDLPTT

>lcl|NZ\_FO834906.1\_prot\_WP\_016530283.1\_794 [locus\_tag=BN49\_RS05220] [protein=major capsid protein] [protein\_id=WP\_016530283.1] [location=805844..806884] [gbkey=CDS]

MFSYDAYKMVDLAPIFEVAPSEGYLLQNLNIFDKSSSDGIYVMLDRLIEDNKTLLNQPKKRYSFEHDSTA

RTPANSFPVELLHLHREDTVSAADFQKAGRKPGTDVQETMLDIVADYTLKHAKAYKRYVESAYGDALFRG

LVQTPYTQEAPVIDYADSFDAPMMADTITLSNGSTDALEVFNGFLDKISNATDGLWTDVRRVVCFASASF

YNSLRFHASMKSAYQYVDPFNEMNIVYQRKEVLPNVQTFTLPGLSIDVIKVTDPLLTPFIADGTAVMLPV

FQSNTNVYQHLYGPASVDTNLAAAGITQEYFSYQYEKERGEVEIVSEASVLPVNHGTNFSLVITAN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530282.1\_795 [locus\_tag=BN49\_RS05225] [protein=hypothetical protein] [protein\_id=WP\_016530282.1] [location=807249..809075] [gbkey=CDS]

MSGTQITASTLVNKIVYRTDLNSLKKARNDMKKLQQEFSKSNNQVAKVKQQADKQIHQAQIKQQRDIDKQ

QKQTAKQQAADTKAKQNEQKKLAAAQSRAAKIQMQQQAKTAKISENARLAERKALFDIGRLQGLNGTERF

QAIKHAQGLIDSYKNQTITLRDLNQQLSQYLTTQRSIARNNSKQAKQSGKGKKSGSSGWVARNASAILPV

DQLLGPTAAAFLGQQTYQIISGTLAGAIERNQGRKMISSMGLNPLEADAAIQETLKRTGFNMSYEKISDI

SKDVQDKIGQLSLGEWKTDKKTGQSTYSGGGEMGDWLQMMVSRGGYTQQGALKTLQNVKGPVELAVLLEG

LRKSAKLTDSEFTALAEVINDFSYLAKSVDASGQNVIDTMNTMVNSGLALNSQQQKSIDNLSQMSIVFDN

ARNSLGDQFAASFSKGLEDLGINTQNLSSEMGTLVPLVKDLGTGTAQTVKVFKDLLDVLSIITEWKNRLL

GTDKPAEQNIFQQGATFVGESLLPPGVLDMAGKVKAWLTPEGNSVAAQAQSGALINQMMVQTPAMSYQPV

IPDLKADFNLTVNPSPEFGMMVEAVADKRIEWAFDDQNFQINQSILGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530281.1\_796 [locus\_tag=BN49\_RS05230] [protein=tyrosine-type recombinase/integrase] [protein\_id=WP\_016530281.1] [location=complement(809135..810331)] [gbkey=CDS]

MSIKSQSYLYPTPEGVWMFQIFVPKYMRHIFGGKKLYRKSTGTKDLATAKHFRNHMLIEWKALKEQYCPD

TEERRINNAILELRAQTVMKSPLQAIPTLIEIRDRYADQYKDRRSFSTLAKSARSVEVFLKHLECADIKI

TKIRRSQVALFAMRHIEKKADQTVQNWLTCLGSLYEFARRVHDDIPPDNPFHGHNLEARRTIESYQPFTT

KQLVTLVENAEEELQGVILIGLYSGMRLDEIASLKRDDIVEIEGIRCFNITKSKTKAGVRLVPIHSKALP

IVDRWLSLKSGEYLLPTANRIQRADGKKGPFYSQAFTRLRNKVIPAATNRQCYHSLRGHFITCLDRKGIE

ETRVGTLTGQIEKKAKTEAFRTYSAGPLMRELKQIIELVSYSEIEKGH

>lcl|NZ\_FO834906.1\_prot\_WP\_042941239.1\_797 [locus\_tag=BN49\_RS05235] [protein=MFS transporter] [protein\_id=WP\_042941239.1] [location=complement(810594..811982)] [gbkey=CDS]

MTLFSSQPGDEGLPGPARARVMAAIMTTTLMGVFDGTMINIALPSMAQEMQVPASIAVWFANGYLLAAAM

TLAIFAALAARLGYRPVFLAGLTTFTLTSLGCALANKPEVLIGMRVLQGIGGAATLSIAPAILRSVFPGR

LLGRILGFHALLIASSSAIGPVLGGTILHTLSWQWLFAINILPGTLALLLAVRALPRDAIRMQAPFDTVG

AILSALLLGSTIMAANSLQNAISQFGSLCWMALAALSGMAFIWQIRRTGHPLLPPSMFKNERFTLAAFTS

MVAFVSQGITFIALPFLFQSEYGYSPVVSALLFTPWPLGIVLIAPHAGRWADTISAPAISTLGLVIFVVG

LILLATLPARPSMWDICLRSLVCGIGFGCFQSPNNREMLSNVIREHASYASGVLSIMRTFGQCLGAAAVA

VLLAADERSIHVALWSAAAASAVSVVVSASRLRKIAHPAETG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530279.1\_798 [locus\_tag=BN49\_RS05240] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530279.1] [location=812112..813041] [gbkey=CDS]

MSDPDFNLLVALDILLSEASVAGAARRLNLSTSAMSRTLSRLRDVTGDPILVRAGRNMVLTPWAEATRDR

ARRAVHDARAVLQPSTETFSAQNLARLFTIRANDGFVVAFGPALIAAVADAAPDVCIRFAPKPEKTSRYL

REGLVDLEIGVQSNMGPEIRLQRLFEDRFVGVVRKGHPLAKQAEIGVDDYVAWGHVVASPEGALHGSVDD

ALAELGTKRKIASVVPGFPTALSVALESDLIAMIPALYLLNQQVTDQVHVFELPFKSRRITVSQMWHPRM

ERDPGHRWLREQILAICGVGRSVMTKEPV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530278.1\_799 [locus\_tag=BN49\_RS05245] [protein=carboxymuconolactone decarboxylase family protein] [protein\_id=WP\_016530278.1] [location=complement(813405..814208)] [gbkey=CDS]

MKNVIAAAALSLVLSDFAYAHEQRDEAMMKITPSTLADADIQAVSPALARFGREAISNDLWQRDALSARD

RSIVTVAMLIARNQPGELKHYIAVALDSGVTPAEVSEIITHLAFYAGWPNAMSAVSVAKTIFEARGVTAE

ALPAASPTLLPLNEQVEKQRADTVEKNVGPISPGLVKFTADPLFLDLWQRPALTPRDRSLVTVSALIAAG

QSAQIGYHLNRAMDNGLSAEEAGEVVAQAAFYAGWPNAFTAAPVVGEVLRARESKAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916289.1\_800 [locus\_tag=BN49\_RS05250] [protein=aldo/keto reductase] [protein\_id=WP\_002916289.1] [location=complement(814241..815260)] [gbkey=CDS]

MQYTRLGKSDLLVSRICMGCMGFGDPSTGQHRWTLDETASRDIIRHALEQGINFYDTAIAYQNGSSERYV

GRALREMAKREEVVLATKFLPRTAAQIAEGISGKQAIARSLDQSLRNLGMDYIDLYIYHIWDYNTPVIDV

LEALHTAVTAGKVRAIGISNCYAWQLAKVNALAEREGLTSFVSVQSHYNLIMREDERELFGLCAEEGIAM

TPYSALASGRLSRLEGHTRRAVEDDYARGKYDGTAEQDRIIIARVAELAERHQVSMTEISLAWLLTKVTA

PVIGATQKHHVDGAVNAVALQLSPEDIRYLEEAYQPHVLTGVMAQNTPQAKDHHQVWTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004181226.1\_801 [locus\_tag=BN49\_RS05255] [protein=NAD(P)H-dependent oxidoreductase] [protein\_id=WP\_004181226.1] [location=complement(815281..815838)] [gbkey=CDS]

MAHILVVSGHPDLNHSIANATILDELATALPDAEIRRLDWLYPDGKFNIAAEQESLLQADVIVWQFPFSW

YGLPGLMKQWLDEVFVHGFAHGSTAKLGGKKLILSFTTGAPQALYTADGFFGHAIEEYLLPFETTARLCN

LELLAPVYTCGISYADRDADKIAQQKTLAREHAARLIARLNTLVE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530277.1\_802 [locus\_tag=BN49\_RS05260] [protein=hypothetical protein] [protein\_id=WP\_016530277.1] [location=complement(815859..816155)] [gbkey=CDS]

MRILCLDIPAPGATLEHYAPHLTAEALHAWGLYKSGFIRDIYFRQDRPGVAIFLECDTVEEANNVMAEFP

LAKSGLLTFECIPLGSFISWENLFSAEF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530276.1\_803 [locus\_tag=BN49\_RS05265] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530276.1] [location=816294..817193] [gbkey=CDS]

MNNALYNQIRIFQSIAHEGNISAAARKLEITPPSVSNALRLLEEHIGHPLFVRPTRRIELTETGQQLLEQ

TAAAVETLEKSLEIIRDQNQEPSGAVRITLSRFAYLLILKPAMAAFCQQYPGIQLEISVYDGTVNIIEER

FDLGIRFGDILEGGVVARPLMKPFREGLYASSAYLAEYGVPAMPADLHHHRLIGYRFITNNRILPLILND

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GRTKRVKALIDFLIMHAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_023317269.1\_804 [locus\_tag=BN49\_RS28670] [protein=hypothetical protein] [protein\_id=WP\_023317269.1] [location=817365..817640] [gbkey=CDS]

MGRRFIVCIFALVAFSTSAAHGVHGGHNGQSVSAGADGGNGSNGGDIDNSSGRAGCPGGTDPDKHGHFYL

PGTSEPCNPGPQDAEKVGSSR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042393.1\_805 [locus\_tag=BN49\_RS05275] [protein=DUF1349 domain-containing protein] [protein\_id=WP\_046042393.1] [location=complement(817644..818216)] [gbkey=CDS]

MQPYFHWINEPAEWRRDADGLTVVTNKHTDFWRHTWYGFERFSGHLYAAEVAGDFTLQAKICADFTTLYD

QAGLMMMADEQTWLKAGIEFNDDAPAIGSVLTLTHSDWATGLFHGDPRTFWLRLTRKGDALRLQYSTDGE

RWPLLRLGYFPPGPVKAGVMCCSPERGGLAVAFQDIQLSPPLDKALHDLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002916282.1\_806 [locus\_tag=BN49\_RS05280] [protein=YciI family protein] [protein\_id=WP\_002916282.1] [location=complement(818247..818540)] [gbkey=CDS]

MSTIYVVVLTYIKPLEEVDRAIPAHIEWLKKGYADGLFLASGRRIPRTGGVILAKCDSRETLQARLSQDP

FQQLGLARTEIIPFEASMASPALQSLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916281.1\_807 [locus\_tag=BN49\_RS05285] [protein=metalloregulator ArsR/SmtB family transcription factor] [protein\_id=WP\_002916281.1] [location=818759..819088] [gbkey=CDS]

MSLLPLQLFKNLADETRLGIVLLLKARGELCVCDLCTALAQSQPKISRHLAMLRESGLLLDRKQGKWVHY

RLSPQMPAWAAQVIEQAWLSQQEDVRLMISRLAGGPGCR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530274.1\_808 [locus\_tag=BN49\_RS05290] [protein=arsenic transporter] [protein\_id=WP\_016530274.1] [location=819140..820432] [gbkey=CDS]

MLLAGTIFILTLVLVIWQPRGLGIGWSAAFGAALALATGGVQVADIPVVWHIVWNATATFIAVIIISLLL

DESGFFEWAALHVSRRGRGRGRLLFTWIILLGAAVAALFANDGAALILTPIVIAMLRALGFSKGTMLAFV

MAAGFIADTASLPLVVSNLVNIVSADFFAIGFREYASVMVPVDLAAILTTLAMLHLFFRKDIPPAWDMAL

LKAPATAIKDPATFRTGWGVLLLLLAGFFVLEPLGIPVSAIAALGAGILFAVAKRGRVINTGKVLRGAPW

QIVIFSLGMYLVVYGLRNAGLTDYLTTVLNMLAERGLWAATLGTGILSAFLSSIMNNMPSVLVGALSIDG

STATGTIKEAMIYANVIGCDLGPKITPIGSLATLLWLHVLAQKHITIGWGYYFRCGITMTLPVLLVTLAA

LALRLSFNQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002916278.1\_809 [gene=arsC] [locus\_tag=BN49\_RS05295] [protein=glutaredoxin-dependent arsenate reductase] [protein\_id=WP\_002916278.1] [location=820442..820864] [gbkey=CDS]

MSITIYHNPDCGTSRNTLALIRNSGAEPTVIYYLETPPSGDELRQLLAAMGIPVRALLRKNVEPYDALGL

AEDRFTDDQIIDFMLQHPILINRPIVTTPQGTRLCRPSEVVLEILTAPQKGAFVKEDGEPVIDAAGQRVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002916277.1\_810 [locus\_tag=BN49\_RS05300] [protein=peptide MFS transporter] [protein\_id=WP\_002916277.1] [location=821337..822890] [gbkey=CDS]

MHSSVNKNESRTFFGHPYPLGSLFFTEMWERFSFYGIRPLLILFMAATVYDGGMGLARENASAIVGIFAG

SMYLAALPGGWLADNWLGQQRAVWYGSILIALGHLSIALSAWLGNDLFFIGLMFIVLGSGLFKTCISVMV

GTLYKKGDARRDGGFSLFYMGINIGSFIAPLISGWLIKSHGWHWGFGIGGIGMLVALIIFRVFAVPSMKR

YDAEVGLDSTWNSPVAKKNGVGAWLLALALGVAVLVTLISLGTIVINPVAVASVLVYVIAASVALYFIWL

FVFAGLNRKERARLLVCFILLVSAAFFWSAFEQKPTSFNLFANDYTNRMIGDFEIPAVWFQSINALFIIL

LAPVFSWAWPALARKNVRPGSMTKFVIGILCAAAGFGLMMLAAQNVLSNGGAGVSPLWLVGSILMLTLGE

LCLSPIGLATMTLLAPERMRGQMMGLWFCASALGNLAAGLIGGHVKADQLSLLPDLFARCSIALLICAAV

LAVLIVPVRRMLENSRSSAAQKSLSNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002916274.1\_811 [locus\_tag=BN49\_RS05305] [protein=DUF1889 family protein] [protein\_id=WP\_002916274.1] [location=823075..823374] [gbkey=CDS]

MPAVIDKALDFIGGMNTSEPVPQSMDESTAKGILKYLKELGVPATPADVAARGQQQGWSAGFTDKVAEWA

ERVAAGERLVIKHPEFFSTYMREELRALV

>lcl|NZ\_FO834906.1\_prot\_WP\_002916272.1\_812 [locus\_tag=BN49\_RS05310] [protein=MdtP family multidrug efflux transporter outer membrane subunit] [protein\_id=WP\_002916272.1] [location=complement(823437..824885)] [gbkey=CDS]

MMILPFSARLRGTLFTLTLTLLSGCALIQDEPAQVAIVNPQQAQLAQVIHLANSDWPAARWWEAYDDPQL

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WYTLNTVGVGAQLNIDLWGADRARVAAAIGEKNARLAETAGIELDIASSVAQLYFAMQATFQKIALLQEL

EGIARFSVEAHEHRTRRGLEDSVDVANAQAEQLAARQQIISAEGMLTQYRETLRALIGADAQSMPAIHPV

ALPALQETLPPSLSFELLARRPDLQALRGYVTASLSQVDAAKAAFYPHFDIKAFWGYNALSVGDLFKSSF

QQINLLPGLYLPIFDGGRLNANLQSVRTASNILIKQYNQAVLDAVRDVAISSSQLNDLNQQRALQQLKVT

AAQTTTDSARAHYQRGLLSRYAAEEARRAVLAQQLLLLDIEAQRLSTDITLIKALGGGYRGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_032438974.1\_813 [gene=mdtO] [locus\_tag=BN49\_RS05315] [protein=multidrug efflux transporter permease subunit MdtO] [protein\_id=WP\_032438974.1] [location=complement(824882..826819)] [gbkey=CDS]

MFPLAHFLRQELRDAPGRASYTLRLTLSCAVLITLFMTLQIPFLAVALIVVFYVSQPNVLMIKLVSVVFF

VTVTVALGGVLLIIKWTYDYPLIRLAASVALFFCALYLMRVLGKLGLAFFVVALAVIYAQTFPSMTSQSE

ILVRLLLWLWVAINTAILVTLLVNACFQQAFPGNQFKARLAGMLHEVARRLAAPDAEAPPTFGETAAQFN

QLQSLFAQASRATPEIAADPQAWRSRLAATLRCYQLTALLQADEADSDDRQQLSQAVLQLKNALSEGPFD

GAIPPLTLSGRGVNRAVLQEMATTLQRLAQGEPVALPQGEVEKAPLLAPDAWRNPAYLHFALKTLLATLI

CYVFYTAADWQGLHTIMLSCVIVAQPGLGATMQKTWLRIGGALLASLLALLLIVFVQPWTDSLTGLLAMS

LPVLALAAWIAAGSERIAYAGIQIGFTFALAFLSWFAPLTNLTELRDRVLGILLGVLVSSIVHLYLWPDS

EAPQLKTRLAALYRRLADCLAAPKEAVPLAPLLVAFTDSEALLHRVRAEPLGTYAHPWPQAKGWPMRATL

AQAEEIARLSEGYRLNATPGDPTLARCAEQLRRYAERIEQEATAPGEQLTAELTNPFGPALAAALAALPD

WGPTPIATEQQAKTS

>lcl|NZ\_FO834906.1\_prot\_WP\_004174502.1\_814 [gene=mdtN] [locus\_tag=BN49\_RS05320] [protein=multidrug transporter subunit MdtN] [protein\_id=WP\_004174502.1] [location=complement(826832..827857)] [gbkey=CDS]

MTTSRTSLLRKKWPLLALVLAAILALILVIWQLQTSPETNDAYVYADTIDVVPEVSGRIVEMPIRDNQRV

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EPLVPQGFASQEDLDQARTAEKAARAELEATLLQAKQASAAVTGVDAMVAQRAGVLAQIALAELHLEFTE

VRAPFNGVVVALKTTVGQYASALKPVFTLLDDDRWYVIANFRETDLNNVRPGVAARITVMTNHNRTFNGV

VDSVGSGVLPEGGSVIEGLPLIQKSINWVHVSQRFPVKIAVSDPDPELFRMGASASAVLQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002916204.1\_815 [locus\_tag=BN49\_RS05325] [protein=YtcA family lipoprotein] [protein\_id=WP\_002916204.1] [location=complement(827864..828136)] [gbkey=CDS]

MNHIATIARPARLLLVLPLSGCSLSPEIPVLGAAFPGWFFCLLGGAFLLIPCHILITRKGWQPRFSPLVF

SYVALMFLFATLLWFLFFVH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530761.1\_816 [locus\_tag=BN49\_RS05330] [protein=(4Fe-4S)-binding protein] [protein\_id=WP\_016530761.1] [location=828342..828572] [gbkey=CDS]

MDKELLEAGYWAYTGEKIDVYFNTAICQHSGNCVRGSAKLFNLKRKPWIIPNEVDVATVVNVIDTCPSGA

LQYRHK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530762.1\_817 [locus\_tag=BN49\_RS05335] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_016530762.1] [location=828584..828856] [gbkey=CDS]

MEILEGHNKFYVNNAQGNQVAEIVFVPTGEHLSIIEHTDVDPSLKGQGVGKQLVAKVVEKMRQEQRKIIP

LCPFAKHEFDNTREYDDIRA

>lcl|NZ\_FO834906.1\_prot\_WP\_023287976.1\_818 [locus\_tag=BN49\_RS05340] [protein=EAL domain-containing protein] [protein\_id=WP\_023287976.1] [location=complement(828899..830311)] [gbkey=CDS]

MMTDYILSPCSLAARGLSQLMLNAAKRPAELPVEGVSLRELAAVKRIVVYLPDDPLWMLTTLRQAARLLD

EALPPLPMLILSRSPAIWLWQTLLYQVSHPDRLRNIHTAPADLSCAELAHRLENAPRLERLASEAALIHG

KRVVGLTHAELKVILALLQGQTIGEQAQRLGLSQKTLYTQRLAGVKKLVECHPHLAPRFPRTLLPRSPAN

ALTAFEQEWVQAIHDRQVFPVFQPIVDSRSQLQGVEILIRWRHRGQVLHPQTFLPHFRADYTWLLLTAFV

LQEAVQNINEYPGAFYFSVNIPSSLADSDSLLRMVEAARQQLRQPEGVARLVLEYAETIDFRHQSRSAAH

VAQLQRAGVRVMLDDCFSQGSVIFPARRLHFNAYKLDMSIVNDAQHDPKALALIKSLAYYCQLSGSRCVA

EGVDSLAKFTQLKSLGIDRFQGYLFSPPMRREHLPDLIRRFSHQRDPAKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151788.1\_819 [locus\_tag=BN49\_RS05345] [protein=fimbrial protein] [protein\_id=WP\_004151788.1] [location=complement(830308..831213)] [gbkey=CDS]

MKKIIPLFTTLLLLGWSMNAWSFACKTATGATIPIGGGSANVYVNLTPAVNVGQNLVVDLSTQIFCHNDY

PETITDYVTLQRGSAYGGVLSSFSGTVKYNGTSYPFPTTTETARVIYDSRTDKPWPAVLYLTPVSTAGGV

AITAGSLIAVLILHQTNNYNSDSFQFIWNIYANNDVVVPTGGCDVSARDVTVTLPDYPGSMAVPLTVHCA

QSQQLGYYLSGTTADSANAIFTNTASASPAQGIGVQLTRNGSAVPANSTVSLGTVGTSPVNLGLTATYAR

TTGQVTAGNVQSIIGITFVYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_073901412.1\_820 [locus\_tag=BN49\_RS05350] [protein=type 1 fimbrial protein] [protein\_id=WP\_073901412.1] [location=complement(831231..831716)] [gbkey=CDS]

MGWLLAGLLTASASLRAADVTLTVNGKVVARPCTVSTVNATVELGDLYTFSLIGAGSASAWHSVALDLSN

CPVGTSRVKATFSGTADSTGYYKNQGTAGNIQLELQNEDGTTLNNGSSQSVQVDETSQSARFPLQVRALS

VNGGATQGTIQAVINVTYTYA

>lcl|NZ\_FO834906.1\_prot\_WP\_004185520.1\_821 [locus\_tag=BN49\_RS05355] [protein=type 1 fimbrial protein] [protein\_id=WP\_004185520.1] [location=complement(831744..832271)] [gbkey=CDS]

MRTLQYLLGALFTLGAPAALAADSTIAISGYVRDNACAVAGESKDFTVDLQDNAAKQFYAVGATTPPVPF

RIVLSPCGTSVTAVKVGFTGVADSVNTSLLKLDAGTSAAAGMGVEILDQQQSRLPVNAPSSTMTWTTLTP

GQTNILNFYARLMATQVPVTAGHVNATATFTLEFQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530766.1\_822 [locus\_tag=BN49\_RS05360] [protein=fimbrial biogenesis usher protein] [protein\_id=WP\_016530766.1] [location=complement(832282..834888)] [gbkey=CDS]

MSHRKYGLDHLGCRTARRLVSPALALWLCSQPFAARADLYFNPRFLADDPAAVADLSGFEKGQEVPPGTY

RVDIYLNNGFMTTRDVTFQADAQGHGLSPCLTRGQLASMGVDTGRVPGMATLDSTACVPLTTLISEATTR

FDVGQQRLYLTVPQAFMGNHARGYIPPELWDNGITAGLINYNFTGNNAHNTTGGSSRYAYLNLQSGLNIG

AWRLRDNSTWSYSSGGSTSSNENRWQHVNSWLERDITPLRSRLTLGDSYTNGDVFDGINFRGAQLASDDN

MLPDSQKGFAPVIHGIARGTAQVSIRQNGYEIYQSTVPPGPFTIDDLYAAGNGGDLQVTIKEADGSRQVF

SVPWSTVPVLQREGHTRFALTAGEYRSGNSQQETPDFFQGTAMHGLPAGWTLYGGTQLADRYRAFNLGVG

KNMGYFGALSLDITQANATLADDSEHQGQSVRFLYNKSLDETGTNLQLVGYRYSTRGYYNFADTTYRRMS

GYSVETQDGVIQVKPKFTDYYNLAYSKRGKVQLSVTQQLGRTATLYLSGSHQTYWGTDDADEQLQAGLNA

AVDDINWSLSYSLTKNAWQQGRDQMLAINIPFSHWLRSDSRSVWRHASASYSLSHDLNGRMTNLAGLYGT

LLEDNNLSYSVQTGYAGGGNGDNGSTGYTALNYRGGYGNANVGYSRSDGFKQLYYGVSGGVLAHANGITL

SQPLNDTVVLVKAPGAGGVKVENQTGVRTDWRGYAVLPYATEYRENRIALDTNTLADNVDLDDAVVSVVP

THGAIVRANFNAQVGMKILMTLTHRGKPVPFGALATGDSNQSGSIVADNGQVYLSGMALAGKVRVKWGDG

PDAQCLTDYRLPPESQQQALSQLSVACR

>lcl|NZ\_FO834906.1\_prot\_WP\_002916192.1\_823 [locus\_tag=BN49\_RS05365] [protein=fimbria/pilus periplasmic chaperone] [protein\_id=WP\_002916192.1] [location=complement(834970..835695)] [gbkey=CDS]

MSRQGDNVRKTATMAHGLLAGCVLFAASIFSASAQAGVALGATRVIYPAGQKQVQLAVTNNDDNSTWLIQ

SWVENADGQRDGRFVITPPLFAMQGKKENTLRIIDATNNQLPQDRESLFWMNVKAIPSMDKSKLSDNTLQ

LAIISRIKLYYRPGKLALPPDQAAEKLTFSRSGSSLTLTNPTPYYLTVTELNAGTRILENALVPPMGKTS

VKLPADAGNTITYRTINDYGALTPKMNGVLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530767.1\_824 [locus\_tag=BN49\_RS05370] [protein=type 1 fimbrial protein] [protein\_id=WP\_016530767.1] [location=complement(835724..836260)] [gbkey=CDS]

MQGMKSGLLLLLPPLALAGNHWNVTLPGGSMRFQGLIMASSCRVESGDRQMTVNLGQISSNRFHAVGEDS

NPIPFAIHLQDCSTAVSQHVGVTFHGVADGKNPDVLSVGEGPGIASGIGIALFDSQGQQLPLNRPADRWI

SLYRGPTTLNFVAKYRATGRQVTGGAANAQAWFSLTYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530768.1\_825 [gene=fimA] [locus\_tag=BN49\_RS05375] [protein=type 1 fimbrial major subunit FimA] [protein\_id=WP\_016530768.1] [location=complement(836331..836879)] [gbkey=CDS]

MKIKTLAMIVVSALSLSSTAALADTTTVNGGTVHFKGEVVNAACAVDAGSIDQTVQLGQVRSAKLATAGS

TSSAVGFNIQLDDCDTTVATKASVTFAGTAIDSSNTTVLALQNSAAGSATNVGVQILDNTGTPLALDGAT

FSAATTLNDGPNIIPFQARYYATGAATAGIANADATFKVQYE

>lcl|NZ\_FO834906.1\_prot\_WP\_002916189.1\_826 [gene=fimE] [locus\_tag=BN49\_RS05380] [protein=type 1 fimbria switch DNA invertase FimE] [protein\_id=WP\_002916189.1] [location=complement(837361..837969)] [gbkey=CDS]

MNRRRFLTAKEVQAMMQAARQGPTGERDYCLILLAFRHGMRISELLDLHYHDLDLHEGRVNVRRLKNGFS

TIHPLRFDEREAIERWSLVRAGWKAADKTDALFISRRGTALSRQQAYRIIRSAGENAGTVTHTHPHMLRH

ACGYELAERGTDTRLIQDYLGHRNIRHTVRYTASNAARFAGIWERNNLLEEKDQKTKNEITD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151951.1\_827 [gene=fimB] [locus\_tag=BN49\_RS05385] [protein=type 1 fimbria switch DNA invertase FimB] [protein\_id=WP\_004151951.1] [location=complement(838434..839039)] [gbkey=CDS]

MTNNADIKKRNFLTQNEIESLLKAADTGPYAARNYCLTLLCFIHGLRASEICRLRISDIDLAARCVYIHR

LKKGFSTTHPLLDKEIYALKRWLAIRSSWPQAASEWLFLSRKGNPLSRQQFYQIIASSGGLAGLPLEIHP

HMLRHSCGFALANMGIDTRLIQDYLGHRNIRHTVWYTASNAGRFYGIWDNPRDKQRSSLIQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530769.1\_828 [locus\_tag=BN49\_RS05395] [protein=nickel/cobalt transporter] [protein\_id=WP\_016530769.1] [location=840257..841213] [gbkey=CDS]

MTTPIALRDWRLLAAGCGGLLLLAAAITLHSHWGDFLQWCLATQITLHRYLVMYLLLLNNHQYSGGIWLL

VGAFLYGVLHAVGPGHGKFIVTTYLSTNQESLTAARVVPFLGSLLQGVTAILFVFILAVGLNLAAGDLSA

SRWYVEKISALTIGVFGAYVIFRALQSLWPAKQVIRRLTPAHQHDASCGCGHHGVGQDLQGADWKTRLGV

VLAIGVRPCSGAIMILLFANALGIVSWGIAAVMSMALGTALSILGLSLLVHYARHRTVKRLVTNHRPRPW

LVPLVKILGGLALILFAVGLFFSVVPISANGDFIAAGC

>lcl|NZ\_FO834906.1\_prot\_WP\_002916184.1\_829 [locus\_tag=BN49\_RS05400] [protein=MarR family transcriptional regulator] [protein\_id=WP\_002916184.1] [location=complement(841210..841716)] [gbkey=CDS]

MDKSPPIDAVDRILAQWQRERPDLDCSPMGPIGRLKRCAMLLEPQVEVAFTRHDLVRWEFDMLATLRRAG

APFVLSPTQLFSTLMITSGTMTHRLKALEKRGFITRLPNPEDARSMLVALTSAGRERIDAAVETHVDNER

QLLAGLSDGERQQLDQALRVLMRLLETG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530770.1\_830 [locus\_tag=BN49\_RS05405] [protein=DMT family transporter] [protein\_id=WP\_016530770.1] [location=841798..842694] [gbkey=CDS]

MAFLSRNLILDLLLTALAPAIWGTTYIVTSQFLPPDRPFIAALLRVLPAGIALLIWSRRFPQRGEWAKLI

VTGILNIGAFQALLFIAAYRLPGGLAAVIGAIQPLLVMLLAWCVDRQRSPWLAVLSAIAGILGMAMLLLS

PHTVLDPLGIGAAFLGAISMALGTWLSRRWALSLPIVALTGWQLTIGGVVLAPVALIVDPPLHQVTVLQA

AGYLWLCLAGAMLAYGLWFRGIGRLSPVAVSAMSLLSPVTAVVLGWIFLGQKIQGMALMGLIVVLASVLS

IQLALARQAAGAKTKKAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002916131.1\_831 [locus\_tag=BN49\_RS05410] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_002916131.1] [location=complement(842790..842999)] [gbkey=CDS]

MKNVKLLAAAGMLSLVSFASFAHPVSVTADTLDSAEAKIATIAKEQGASYHITEAYTGNQVHMTAELSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002916128.1\_832 [gene=mrkA] [locus\_tag=BN49\_RS05415] [protein=type 3 fimbria major subunit MrkA] [protein\_id=WP\_002916128.1] [location=843705..844313] [gbkey=CDS]

MKKVLLSAAMATAFFGMTAAHAADTTVGGGQVNFFGKVTDVSCTVSVNGQGSDANVYLSPVTLTEVKAAA

ADTYLKPKSFTIDVSNCQAADGTKQDDVSKLGVNWTGGNLLAGATSKQQGYLANTEASGAQNIQLVLSTD

NATALTNKIIPGDSTQPKAKGDASAVADGARFTYYVGYATSAPTTVTTGVVNSYATYEITYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004211921.1\_833 [gene=mrkB] [locus\_tag=BN49\_RS05420] [protein=type 3 fimbria chaperone MrkB] [protein\_id=WP\_004211921.1] [location=844409..845110] [gbkey=CDS]

MKRIALFFCFIFSFAAHANNIIVNGTRFIYPGNEKEITVQLSNNADRPALAQAWLDNGDADATPDTITTP

FIITPPISRVDAKSGQTLRIKLGSSAGLAKDKETLWWLNLLEIPPVVANQKNEGQNVLQLAIRSRFKFIY

RPAGLGNRDAAAEKLTLTASGSGLAINNPTPFYITVSRISRDGGKALNSKTVMLAPQSSQTVALSSAVNR

GETLTVNNINDYGADVAVKVAVK

>lcl|NZ\_FO834906.1\_prot\_WP\_000813718.1\_834 [gene=mrkC] [locus\_tag=BN49\_RS05425] [protein=type 3 fimbria usher protein MrkC] [protein\_id=WP\_000813718.1] [location=845122..847608] [gbkey=CDS]

MKQRSFCPGRLSTAIAIALCCFPPFSSGQENPGTVYQFNDGFIVGSREKVDLSRFSTSAITEGTYSLDVY

TNDEWKGRYDLRIARDKDGRLGVCYTKAMLAQYGIAAEKLNPQLSEQEGYCGSLKSWRNEENVKDNLVQS

SLRLNISVPQIYEDQRLKNYVSPEFWDKGITALNLGWMANAWNSHTSSVGGSDNSSAYLGVNAGLSWDGW

LLKHIGNLNWQQQQGKAHWNSNQTYLQRPIPQLNSIVSGGQIFTNGEFFDTIGLRGVNLSTDDNMFPDGM

RSYAPEIRGVAQSNALVTVRQGSNIIYQTTVPPGPFTLQDVYPSGYGSDLEVSVKEADGSVEVFSVPYAS

VAQLLRPGMTRYALSAGKVDDSALRNKPMLYQATWQHGINNLLTGYTGVTGFDDYQAFLVGTGMNTGIGA

LSFDVTHSRLKSDAHDDSGQSYRATFNRMFTDTQTSIVLAAYRYSTKGYYNLNDALYAVDQEKNSRSNYT

LWRQKNGMTFTVNQNLPDGWGGFYLSGRISDYWNRSGTEKQYQVSYNNSFGRLSWSASAQRVYTPDSSGH

RRDDRISLNFSYPLWFGDNRTANLTSNTSFNNSRFASSQIGINGSLDSENNLNYGVSTTTATGGQHDVAL

NGSYRTPWTTLNGSYSQGEGYRQSGIGASGTMIAHSGGVVLSPESGSTMALIEAKDAAGAMLPGSPGTRV

DSNGYAILPYLRPYRINAVEIDPKGSHDDVAFDRTVAQVVPWEGSVVKVAFGTKVQNNLTLQARQANHEP

LPFAASIFSPDGKEIGVVGQGSMMFISDANAKRAIVKWSGGQCSVDLGQQTTKDSVCR

>lcl|NZ\_FO834906.1\_prot\_WP\_002916123.1\_835 [gene=mrkD] [locus\_tag=BN49\_RS05430] [protein=type 3 fimbria adhesin subunit MrkD] [protein\_id=WP\_002916123.1] [location=847599..848594] [gbkey=CDS]

MSLRKLLTLFIVLMALGTTSSWASCTRLSSPTVMLDMVVGRVVVPPDLPVGSVILTRDWTMSAPGGASYR

CTSGTNRFAAKIVSPGATDLGNKIYSTNVPGIGMRFSRGGATVNIVYPDVFSSRVYNTTNYSLEGSRFTL

QIIKTAATTGSGTLAAGKYTSYDWESGGNPILETYLSANAITVVSPSCSVLSGKNMNVDVGSIRRTDLKG

VGTTAGGKDFNIDLQCSGGLSETGYANISTSFSGTLATSTTATMGALLNEKAGSGMAKGIGIQVLKDGSP

LQFNKKYTVGRLNNQETRYITIPLHARFYQYGPTTSTGEVESHMIFNLTYD

>lcl|NZ\_FO834906.1\_prot\_WP\_002916122.1\_836 [gene=mrkF] [locus\_tag=BN49\_RS05435] [protein=type 3 fimbria minor subunit MrkF] [protein\_id=WP\_002916122.1] [location=848608..849243] [gbkey=CDS]

MKGLPKNTIAWLLFCGSLAAPSAWGFETNYDRGRVDFAGRVTDISCSVALNGGQHAGSGNVWLAPVSLAE

VHDRGAGAFMKPQPFTLALSNCQLRHDGGAASQDEVRRVSVRWVDGFLLTAVGNENAGYLANTLPDGAQN

IYLALSTNDNNTLDKSNKIVPADPQQNQVRLQESAVSGGLFTYYVGYVSPTPKSATSGPITSWATWELVY

N

>lcl|NZ\_FO834906.1\_prot\_WP\_004144002.1\_837 [gene=mkrJ] [locus\_tag=BN49\_RS05440] [protein=phosphodiesterase MrkJ] [protein\_id=WP\_004144002.1] [location=complement(849278..849994)] [gbkey=CDS]

MNTKIFEDNILSRNDIAVRYVFQKMFSPQGTLVAVECLSRFDNLSISPEDFFRHATAAVRERIFLEQLAL

IEKHKAWFLRNHISATINVDDHILNLLRQKDIKAKVAALTCVHFEVTENAENLLHNSLAAWQSPQDTSLW

LDDFGSGYAGINAIRGYHFDYVKIDKDFFWHLMRKESGRQLMDALVTFLSRNHHNVIIEGVESEAHKEWL

QGMEWFAIQGHYWREVSIEQLVADDIAM

>lcl|NZ\_FO834906.1\_prot\_WP\_002916079.1\_838 [gene=mrkI] [locus\_tag=BN49\_RS05445] [protein=transcriptional regulator MrkI] [protein\_id=WP\_002916079.1] [location=complement(850138..850710)] [gbkey=CDS]

MLYTNDNLIGHSIYHYLIDSHENATRLSYADVIHEKHLPLAQTIIFNLINKDISAIRIVDLLNALRLSLL

RCQQPVLMVKSDIVGLCRELINFDNAMIISEKSPLTLFSSIVQRAKGVSELPPRGLRKQLSPRECQILEL

LIANNNNKRIAALLGIAHKTVHSHRIHIMQKLGIDNSRTMNQRIAALHQC

>lcl|NZ\_FO834906.1\_prot\_839 [gene=mrkH] [locus\_tag=BN49\_RS05450] [protein=transcriptional activator MrkH] [pseudo=true] [partial=5'] [location=complement(850728..>850910)] [gbkey=CDS]

LTIDLVVKNVIVITLDNANEESESYYQISCQFKFRHLDDQRRIEKILLDLILEAKRKKRI

>lcl|NZ\_FO834906.1\_prot\_840 [locus\_tag=BN49\_RS28685] [protein=IS3 family transposase] [pseudo=true] [location=850999..852231] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQPAISLA\*AIPGGKSYCCGCRRTGRS

CL\*TCCRHEAD\*RTPAPARQKNDGK\*TP\*RSR\*IWASKKVDSARALIARGWGVSFVSRCLRVSRAQLHVI

LRRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNAL

LLERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSET

VQDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIK

RDYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_841 [gene=mrkH] [locus\_tag=BN49\_RS05460] [protein=transcriptional activator MrkH] [pseudo=true] [partial=3'] [location=complement(<852242..852772)] [gbkey=CDS]

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DGGCALMTKTPNLKFLSHNALLKNAVLMLAEYGEITI

>lcl|NZ\_FO834906.1\_prot\_WP\_016530388.1\_842 [locus\_tag=BN49\_RS05465] [protein=aldo/keto reductase family oxidoreductase] [protein\_id=WP\_016530388.1] [location=complement(853155..854033)] [gbkey=CDS]

MSSVTLSGRGMLGDRQVYRLGYGAMQLAGPGVFGPPKDPEEAVRVLQAAVEAGINHIDTSDFYGPHVTNQ

LIRKALHPYPDDLCIVTKVSARRDEKGNWLPAMSPAELTQAVEDNLRHLGLEVLEVVNLRSMLSPHGPVE

GSLEAPLATLLELKERGLIRHIGLSNVTAKQVADAQKMTPIVCVQNLYNVAHRADDALVDALAAQHIAWV

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RTLDNIATAARR

>lcl|NZ\_FO834906.1\_prot\_WP\_002916058.1\_843 [locus\_tag=BN49\_RS05470] [protein=amino acid permease] [protein\_id=WP\_002916058.1] [location=complement(854152..855381)] [gbkey=CDS]

MSKIWSKEETLWSFALYGTAVGAGTLFLPIQLGSAGAIVLFITALVAWPLTYWPHKALSQFILSANIAPG

TGITGAVNHYYGKKIGNLITGLYFLAFFVVVLIYAVAITNSLAEQVAHRTPMTPGLRALLSLGVVLVLNL

IFLMGRQVTIKVMGFLVFPLIACFLFLSLYLIRDWHPEHLTSQMQFSPQTLHQVWISIPVMVFAFSHTPI

ISTFAIDQQEKHGDLAMGKCKKIMKVAYTIICASVLFFVFSCLLAIPATYIETARDQGVTILSALSMVPG

APGWLAVTGIIVAVVAMSKSFLGTYFGVIEGASEIVKSSLGLLGVRKSRAFNRAMSILLVSAFTFAVCFI

NPNAISMIYAISGPLIAMILFIMPTLSTWLIPALKPYRSVGNAITLVVGLLCVSVMFFG

>lcl|NZ\_FO834906.1\_prot\_WP\_002916056.1\_844 [locus\_tag=BN49\_RS05475] [protein=multidrug/biocide efflux PACE transporter] [protein\_id=WP\_002916056.1] [location=complement(855505..855966)] [gbkey=CDS]

MQQTPHQRKTLTERVIHAITFEGLATLILAPTAAWLMQRSVVEMGGLSILLATLAMVWNIIYNAAFDRLW

PVSRFPRQLKVRALHALGFETGFVIIGVTMVAIVLGVSLLQAFMLEIGFMLFFLPYTMAFNWVWDTLRER

VIRHRRPRQTARG

>lcl|NZ\_FO834906.1\_prot\_WP\_002916055.1\_845 [locus\_tag=BN49\_RS05480] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002916055.1] [location=856069..856938] [gbkey=CDS]

MRYSPEALTAFVEAVDSGSFSAAARRLRKSQSTISTAIANLEADLGVILFDRATRQPTLTPQGEQVLSYV

KAILAASERLDELAVSLSGETEPRLTFVLSDTLHPDVLEDLLVQFDRRFPHTEFECLIGEDEDVIDLLQK

SRAQVGLIEARERYPTDIGSTRLPLQTAMGIYVAPGHPLAAQGKVAWDELRSWRELRLSTFLASATEPAA

GQVWSAPNYLLLLSMAAQGFGWCILPSALVAEFAPQGGLVALDIPGWPRAISVDLLWNKKAPPGAAGSWL

RQHLQRRER

>lcl|NZ\_FO834906.1\_prot\_WP\_002916052.1\_846 [locus\_tag=BN49\_RS05485] [protein=acetyl-CoA C-acetyltransferase] [protein\_id=WP\_002916052.1] [location=857057..858235] [gbkey=CDS]

MKDVVIVGALRTPIGCFQGALSRHSAVELGSVVVKALVEKTGIDPHSVDEVILGQVLTAGTGQNPARQSA

IRGGLPNTVSAITINDVCGSGLKALHLATQAIQCGEADVVIAGGQENMSRAPHVLTDSRTGAQLGNSQLI

DSLVHDGLWDAFNDYHMGVTAENLAREFGISRELQDAWALSSQHKARKAIDSGRFRDEIVPVVTEHNGAA

RTVDTDEQPRVDASAEGLASLQPTFDRLGSVTAGNASSINDGAAAVMMMSEAKALELGLPILARIRAFAS

VGVDPALMGIAPVHATRRCLERAGWRLDDVDLIEANEAFAAQAISVGRVLEWDERRVNVNGGAIALGHPI

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>lcl|NZ\_FO834906.1\_prot\_WP\_004143995.1\_847 [gene=ompK26] [locus\_tag=BN49\_RS05490] [protein=KdgM family porin OmpK26] [protein\_id=WP\_004143995.1] [location=858485..859180] [gbkey=CDS]

MLKRSLVLAALCGMSFAATAVTIDLRHEFIDGGKSDKSNADRVSVSHRFANGLGFTVEAKWRSGGDNGSQ

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VGVNDRSDRQTRFRVGVAYSF

>lcl|NZ\_FO834906.1\_prot\_WP\_002916048.1\_848 [locus\_tag=BN49\_RS05495] [protein=oligogalacturonate lyase family protein] [protein\_id=WP\_002916048.1] [location=complement(859316..860491)] [gbkey=CDS]

MAKGMRVKLNYHVSHDPDTGAEVTRLTPPEVTCHRNYFYQKCFFNDGSHLLFAGEFDGHWNYYLLNIASA

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GIEIAKSDWTPLNDWQIFHDFFHKGPHCRLLRVDLRSGESQVIHEEKIWLGHPIYRPFDDHTVAFCHEGP

HDLVDARMWLVNEDGSHVRKVKAHAPGESCTHEFWVPDGSALIYVSYLKGQQGRTIYRFDPESGVNEALM

TMPACSHLMSNFDGTLLVGDGSGTPVDVKDTGGYSIDNDPWLYVFNVAEKRYFRVARHDTSWATVANSRQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_002916003.1\_849 [gene=kduD] [locus\_tag=BN49\_RS05505] [protein=2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase KduD] [protein\_id=WP\_002916003.1] [location=860977..861738] [gbkey=CDS]

MILDAFSLQGKVAVVSGCDTGLGQGMALGLAEAGCDIVGINIVEPVETIERVTALGRRFLSLTADLRQID

GIPQLLERAVAEFGHIDILVNNAGLIRREDALAFSEKDWDDVMNLNIKSVFFMSQAAAKHFIAQGSGGKI

INIASMLSFQGGIRVPSYTASKSAVMGVTRLLANEWAKHNINVNAIAPGYMATNNTQQLRADEQRSSEIL

DRIPAGRWGLPADLMGPVVFLASSASDYINGYTVAVDGGWLAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002916001.1\_850 [locus\_tag=BN49\_RS05510] [protein=sugar porter family MFS transporter] [protein\_id=WP\_002916001.1] [location=862034..863455] [gbkey=CDS]

MTSISNDSTLSPRTQRDTRRMNWFVSIAAAVAGLLFGLDIGVISGALPFITDHFTLSSQLQEWVVSSMML

GAAIGALFNGWLSFRLGRKYSLMAGAVLFVAGSIGSAFAASVEVLLVARVVLGVAVGIASYTAPLYLSEM

ASENVRGKMISMYQLMVTLGIVLAFLSDTAFSYSGNWRAMLGVLALPAVILIILVVFLPNSPRWLAEKGR

HIEAEEVLRMLRDTSEKARDELNEIRESLKLKQGGWALFKVNRNVRRAVFLGMLLQAMQQFTGMNIIMYY

APRIFKMAGFTTTEQQMIATLVVGLTFMFATFIAVFTVDKAGRKPALKIGFSVMALGTLVLGYCLMQFDN

GTASSGLSWLSVGMTMMCIAGYAMSAAPVVWILCSEIQPLKCRDFGITCSTTTNWVSNMIIGATFLTLLD

AIGAAGTFWLYTALNVAFIGITFWLIPETKNVTLEHIERNLMAGEKLRNIGNR

>lcl|NZ\_FO834906.1\_prot\_WP\_004149647.1\_851 [locus\_tag=BN49\_RS05515] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_004149647.1] [location=complement(863452..864447)] [gbkey=CDS]

MASLKDVAKLANVSLMTVSRALNTPERLKPETLARVQAAIAETNYVPDLSAKKIRGARATPSTIGVLALD

TVTTPFSVEITLSIEETARAHGWNSFVVNMFSDDRPEAVVDLLLSHRPDGIIFTTMGLRQVPLPEKLLTL

PCVLANCESLSQPVASYIPDDEQGQYDAVKALLAAGYRRPLCLHLPASQPATIRRRRGLERACREAGIEP

DHLSHSYMGQGDEHYHDIPAVVLAHIREGKPGFDSVICGNDRIAFMVYQTLLGQGLRIPQDVAVVGYDNM

VGIGDLFLPPLSTVQLPHYDIGRLSALHIIHGDNHRETRKVASPWLPRASH

>lcl|NZ\_FO834906.1\_prot\_WP\_004143987.1\_852 [locus\_tag=BN49\_RS30870] [protein=hypothetical protein] [protein\_id=WP\_004143987.1] [location=864542..864676] [gbkey=CDS]

MLRLIFDRDRIFIMLTLTFVINIIYRSESTCVLFFVNVTIIAFL

>lcl|NZ\_FO834906.1\_prot\_WP\_002916000.1\_853 [locus\_tag=BN49\_RS05525] [protein=MFS transporter] [protein\_id=WP\_002916000.1] [location=864689..865930] [gbkey=CDS]

MMKAPHSHSYPLLSALLFFFFVTWSSSGSLLSIWLHQEVGLKAGDTGIIYAVLSVSALFAQVCYGFIQDK

LGLRKHLLWYITALLILSGPAYLLFGHLLKINVLLGSIFGGIYIGLTFNGGIGVLESYTERVARQSQFEF

GRARMWGSLGWAVATFFAGLLFNINPQLNFLVASCSGLVFFILLARLRVSSAPHAMQEAVSGGKVTLEDA

LRLLTLPRFWALVFFVIGTCIYGVYDQQFPVYFSSQFATLQEGNEMYGYLNSFQVFLEAAGMFCAPWLVN

RIGAKNGLIFAGMVMAMRMVASGLVEGPLLISITKLLHAVELPILLVAIFKYNSLNFDKRLSSTLYLVGF

ACTSSIIASVLSPLAGYSYEKYGFAQSYLIMGLLVFCTTFISIFLLRSGKSSADPLVSQPTAI

>lcl|NZ\_FO834906.1\_prot\_WP\_026005853.1\_854 [locus\_tag=BN49\_RS05530] [protein=glycoside hydrolase family 32 protein] [protein\_id=WP\_026005853.1] [location=865950..867383] [gbkey=CDS]

MTYTISRAEQVLQTQRQALNLRWYPHYHLAARAGWINDPNGLVWFDGWYHAFYQHHPYSTQWGPMHWGHA

RSKDLVHWEHLPVALAPEGPEDKDGCFSGSAVVDGDTLALIYTGHKFHGDPGDEANLYQVQCLATSRDGI

HFERQGMVVDTPPGMHHFRDPKVWREGDSWYMIVGAREGDTGQVRLYRSADLRQWQDAGVLDEAESTMGY

MWECPDFFTLNGKRVLMFSPQGMQAAGFSNRNLFQSGYLIGEWQPGQRFIRHGEFREMDNGHDFYAPQSF

ATPDGRRIVIGWLDMWESPLPEQQDGWAGMLSLPRELSLSADDRLQMRPAKEVESLRGAWFPWPVSTLNN

QQTTMVDNCEAMEVNLRWDCARSSAEQYGLRFGDGLRIYVDAQQQRLVLERHYPQYGLCGTRSVPLTAGA

DLNLRIFFDSSSVEVFVNDGEACLSSRIYPQAPRRELALFAWSGSAALTEAGAWQLE

>lcl|NZ\_FO834906.1\_prot\_WP\_004149644.1\_855 [locus\_tag=BN49\_RS05535] [protein=carbohydrate porin] [protein\_id=WP\_004149644.1] [location=867505..868848] [gbkey=CDS]

MNKIWVGCFLTSLYLPSVMAQAPLSLEERLAQMEQRLKATEARAASAEAEIKTLKGQQQAATVARAAPAS

PRLQLNDNGELKFYGDVEFNLDGASRTGSLTSVKTSANKSWAPGDKERWDINGRILLGFDGRRNGADGQY

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AAAAIESNLVNNAYGYQSQSGRWVDQSNRTGYGLTMSWNTLKSDPQDGAVVNLSTALLDAADETDFSAGI

NALWHRVELGYIYAHNKIDQFNMAGVTSECDGDCAILAPGRYDIHTLHTSWQLPNIMAMPNFNIYLGAYA

SWLDSTAAKSGNPDERYGARVRFKYFF

>lcl|NZ\_FO834906.1\_prot\_WP\_016531527.1\_856 [locus\_tag=BN49\_RS05540] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016531527.1] [location=complement(868908..870194)] [gbkey=CDS]

MKNVLISATLSATLGLSAFSSLAQDVDLRMSWWGGNGRHQVTLKALEEFHKQNPDINVKAEYTGWDGHLS

RLTTQIAGGTEPDVMQTNWNWLPIFSKNGDGFYDLNTLKDEIDLSQFDTKELQSTTVNGKLNGIPISVTA

RVFYFNDEAWKKAGIPFPKTWDELMAAGKTFESKLGKQYYPVVLEHQDVLALLNSYMVQKYNQPAIDEKG

RKFSYSKAQWADFFGMYKKLIDSHVMPDTRYYASFGKSNMYEMKPWIQGEWGGTYMWNSTINKYSDNLKP

PAKLVLGEYPMLPGATDAGLFFKPAQMLSIGKSTKNPQAAAKVINFLLNSKEGVDILGLERGVPLSKAAV

TYLTEDGVIKADDPAVSGLKLAQSLPTALPVSPYFDDPQIVAQFGTTLQYIDYGKKSVEEAAEDFQRQTD

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531528.1\_857 [locus\_tag=BN49\_RS05545] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016531528.1] [location=complement(870211..871338)] [gbkey=CDS]

MAEVIFNKLEKVYSNGFKAVHGIDLKIADGEFMVIVGPSGCAKSTTLRMLAGLETISDGEVRIGDKIVNN

LAPKSRGIAMVFQNYALYPHMTVRENLAFGLKLSKLPKAQIDRQVEEAAKILELEELLDRLPRQLSGGQA

QRVAVGRAIVKKPDVFLFDEPLSNLDAKLRASMRIRISDLHKQLKKSGKPATTVYVTHDQTEAMTMGDRI

CVMKLGHIMQVDTPDNLYHQPKNMFVAGFIGAPEMNIRPSQLVEHGGRLHLTLGDQRLPLNDRLQSKVET

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RKVYFTFDLNKCHIFDAKTEQNLSL

>lcl|NZ\_FO834906.1\_prot\_WP\_002915996.1\_858 [locus\_tag=BN49\_RS05550] [protein=carbohydrate ABC transporter permease] [protein\_id=WP\_002915996.1] [location=complement(871351..872253)] [gbkey=CDS]

MADIQQMAPVMSDADREVARTLRREKVSRVVRYVVLIFVGLLMLYPLAWMFSASFKPNHEIFTTLGLWPA

HATWDGFINGWKTGTEYHFGHYMLNTFKYVIPKVVLTIISSTIVAYGFARFEIPWKKFWFATLITTMLLP

STVLLIPQYLMFREMGMLNSYLPLYLPLAFATQGFFVFMLIQFLRGVPRDMEEAAQIDGCNSIQVLWYVV

VPILKPAIISVALFQFMWSMNDFIGPLIYVYSVDKYPIALALKMSIDVTEGAPWNEILAMASISILPSII

VFFLAQRYFVQGVTSSGIKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915995.1\_859 [locus\_tag=BN49\_RS05555] [protein=sugar ABC transporter permease] [protein\_id=WP\_002915995.1] [location=complement(872246..873136)] [gbkey=CDS]

MNENKLLGLAWISPYIIGLIVFTAFPFVSSFFLSFTEYDLMSPPVFNGIENYRYMLTEDSLFWKSMGVTF

AYVFLTIPLKLAFALGIAFVLNFKLRGIGFFRTAYYIPSILGSSVAIAVLWRALFAIDGLLNSFLAVFGI

DAINWLGEPSLALMSVTLLRVWQFGSAMVIFLAALQNVPQSQYEAAMIDGASKWQMFMKVTVPLITPVIF

FNFIMQTTQAFQEFTGPYVITGGGPTYYTYLFSLYIYDTAFKYFDMGYGAALAWVLFLVVAVFASIAFKS

SKYWVFYSADKGGKNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915993.1\_860 [locus\_tag=BN49\_RS05560] [protein=cupin domain-containing protein] [protein\_id=WP\_002915993.1] [location=complement(873589..873915)] [gbkey=CDS]

MFIFHKDTTLEDLGNGVTRRILAHDGKMMAVEVNFAAGAVGPMHNHPHEQLTYVLSGEFEFTIGEETRVV

SAGDTLYKRPGIMHGCVCLQPGTLLDTFTPIREDFLEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915992.1\_861 [locus\_tag=BN49\_RS05565] [protein=aspartate/glutamate racemase] [protein\_id=WP\_002915992.1] [location=874055..874768] [gbkey=CDS]

MKTIGLLGGMSWESTIPYYRLINEGVKARLGGLHSASLVLHSVDFHDIEACQSAGDWDRAGEILAEAAVG

LQQAGAEGIVLCTNTMHKVADAIAARCQVPFLHIADATGRAIAAKGQRRVALLGTRYTMEQTFYRGRLQE

QFAIETLIPEADDRAQINQIIFDELCLGTFSEASRDYYLQTIAALAEQGAEGVIFGCTEIGLLVPAELSP

LPVFDTAAIHAEDAVNFMLSAGPTPAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915991.1\_862 [locus\_tag=BN49\_RS05570] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002915991.1] [location=complement(874734..875660)] [gbkey=CDS]

MPAVNLRHIEIFHAVMTTGNLTEAARMLHTSQPTVSRELARFEKVLGLQLFERTRGRLQPTVQGLRLFEE

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AQRHDLGLTETLHTPAGTERTPLLTLNEVCVLPAGHPLAAQATLTPADFQGENYISLSRTDSYRQLLDAL

FLEHQVKRRMVVETHSAASICAMVRAGAGISVVNPLTALDYADSGVVVRRFSVEVPFTVSLIRPLHRPRS

ALVDAFVAHLQQSLPQILTPLASVLQRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915990.1\_863 [gene=lysA] [locus\_tag=BN49\_RS05575] [protein=diaminopimelate decarboxylase] [protein\_id=WP\_002915990.1] [location=875798..877060] [gbkey=CDS]

MPHSLYATDTDLTADNLLRLPAEFGCPVWVYDAQIIRRQIAQLSQFDVVRFAQKACSNIHILRLMREQGV

KVDSVSLGEIERALAAGYDPQQNPEDIVFTADLIDDATLDRVKALQIPVNAGSIDMLSQLGEVSPGHRVW

LRVNPGFGHGHSQKTNTGGENSKHGIWYSHLPAALEVMRRYQLQLVGIHMHIGSGVDYGHLEQVCGAMVR

QVVDFGQDLQAISAGGGLSIPYREGEEAIDTAHYYGLWNRAREQIAAHLGHPVKLEIEPGRFLVAESGVL

VSQVRSVKEMGSRHFVLIDAGFNDLMRPAMYGSYHHITALAGDGRDLSAAPQVETVVAGPLCESGDVFTQ

QEGGKVETRLLPAVAPGDYLVLHDTGAYGASMSSNYNSRPLLPEVLFDGGKARLIRRRQTIQELLALELI

>lcl|NZ\_FO834906.1\_prot\_WP\_004229436.1\_864 [locus\_tag=BN49\_RS05580] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_004229436.1] [location=complement(877053..878054)] [gbkey=CDS]

MLDVSIRAGVSKATVSRVLNGTGQVKESTRQQVFKAMEELGYRPNFLARSLANQTSNSIGLVVSTFDGFY

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VINRDVAQARERCVFFEQQEAAFQAVEYLITQGHRDIACITVPMHTPTGQARLQGYRNALIKHGIEWDPS

RVKYGDSTMTRGYELCRELLDEKARFSALFSCNDDMALGASKALHQAGLRIPQDVSLFGFDDAPSAKWLE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004174520.1\_865 [locus\_tag=BN49\_RS05585] [protein=PTS transporter subunit EIIC] [protein\_id=WP\_004174520.1] [location=878354..879691] [gbkey=CDS]

MALQDKLIDALGRFATTFNSYRYIMAIKSAFITLMPVIIVGAFSVLISNMVLDPKNGLASFSSLSFLAAL

KPITSALNYATLNFLNIGAVFLIGIELGRINGIKSLFPGLLAVICFICVTPTTVEMMVDGQMHVVKDVLL

RQFSDTRSLFLGMFIAILSVEIYCWLEGRKGLKIKMPDTVPPNVSASFSALIPAIITTTAIATFGFLFHQ

LTGMYLYDAVYQVVQQPLERVVQSLPGILLLMFVAQLFWVIGIHGNQMIKPIREPLLLGAITVNMSAFEQ

GKEVPNIITMPFWDVYMSIGGSGLTIGLLIAVMIATRRKEMKEIAKLSIGPGLFNINEPVIFGMPIMLNP

ILAIPFIITPLVTGSIGYFATLTGFAGKAVVMVPWTTPPLINAWLSTAGSMGAVVTQLICIVVAVLIYLP

FVKIASRRADAAQRQVDNQQTANPV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174521.1\_866 [locus\_tag=BN49\_RS05590] [protein=glycoside hydrolase family 1 protein] [protein\_id=WP\_004174521.1] [location=879699..881126] [gbkey=CDS]

MTTVRMTIPDDFILGAAASAWQTEGWSGKKPGQDSWPDLWYKNDRHVWHNGYGPAVATDFINRFQEDVQL

MKLAGLTHYRTSINWSRFLTDYENVTVDEEYAAYYDQLFDALLANGITPMICLEHYELPGYLLEKYGGWG

SKTVVELFVRYAEKVFARYHPKVTRWFTFNEPIVVQTRVYLDALRWPYEQNTSTWMQWNYHKVLATASVV

KRFRELGYPGTVGCILNPEVTYPRSRAPHDLRAAEIYDLFYNRMFLDPLVHGVWPPELLALLEQHQVTWE

TSEEDLAVIREHTVDELGINLYYPHRVKAPSRAWHPHTPFHPAWYYEPFELPGRRMNASRGWEIYPQIIF

DMAMRIKNDYRNIPWFVAESGMGVENEGQFRNREGVIDDSYRIRFISEHLWHTLRAREAGANCQGYMLWA

FTDNVSPMNAFKNRYGLIEIDLQNHRARRPKASAHWFRQLGERRELVLDIDDEYR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915985.1\_867 [locus\_tag=BN49\_RS05595] [protein=GntR family transcriptional regulator] [protein\_id=WP\_002915985.1] [location=881194..881967] [gbkey=CDS]

MEKAIVPPEKKPYQEIGDDLRAQIAQGRYPVGSRLPPERHIAETYGVSRTIVREALLMLELQGTVDIRQG

SGVYVMRIPHENDSEEEQLLSSDVGPFEILQARQLLESNIAAFAAKMATRADIDNLKRIIEQEQRAIALN

DTAQDNARLFHLVLAGATQNQMLLATVERIWLQMDSSPLWQQFNVHIASRAWRLKWLGDRQTLLAALRRR

DVMGAWQAMWQHLENVKNSLLELSDEDAPDFDGYLFDSVPIFQGKLV

>lcl|NZ\_FO834906.1\_prot\_WP\_046042444.1\_868 [locus\_tag=BN49\_RS05600] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_046042444.1] [location=881964..882443] [gbkey=CDS]

MTILPLYAAPQFAPQVTDWLWQAFGGETLPRQFFASIVQHSQTAEALPLTFIAVEGEQLLGTIGLWRCDL

ISRQDLFPWLAALFVAPAARGQGLAGKLQRHVIDYARRADFRELYLYSACRDFYERFGWRYIGEGLDYPA

TAVHLYRYDLSPSCGATTE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529841.1\_869 [gene=galR] [locus\_tag=BN49\_RS05605] [protein=HTH-type transcriptional regulator GalR] [protein\_id=WP\_016529841.1] [location=complement(882404..883420)] [gbkey=CDS]

MATIKDVARLAGVSVATVSRVINNSPKASEASRQSVGAAMETLNYHPNANARALAQQSTETVGLVVGDVS

DPFFGAMVKAVEQVAYRTGNFLLIGNGYHNVQKERQAIEQLIRHRCAALVVHAKMIPDEELAGLMKQIPG

MVLINRILPGYETRCVALDDRYGAWLATRHLIQQGHTRIGYLCSNHDISDAEDRLQGYYAALEESGLPCN

DRLVTFAEPDESGGEQAMTELLGRGRHFSAVACYNDSMAAGAMGVLNDNGIDVPREISLIGFDDVLISRY

IRPRLTTVRYPIVTMATQAAELALALAEQRPAPEITHLFSPTLVRRHSVVAPQEGDKS

>lcl|NZ\_FO834906.1\_prot\_870 [locus\_tag=BN49\_RS31260] [protein=hypothetical protein] [pseudo=true] [location=883514..883778] [gbkey=CDS]

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MLLGFFRLLFKGLYRVRLTGDTQALYQQKVLITPNHVSFLDGILLALFLPVRPVFAVYTSISQRWFMRAL

TPIIDFVPLDPTKPMSIKHLVRLIEQGRPVVIFPEGRISVSGSLMKIYDGAAFVAAKSQATIVPLRIEGA

ELTPFSRLKGLVKRRLFPRIQLHLLPPTHLPMPEAPRARDRRKIAGEMLHQIMMEARMAVRPRETLYESL

LAAQDRFGARKPCVEDINFQPDTYRKLLTKTLFVARILEKYSQPGEKIGLMLPNAGISAAVIFGAIARGR

IPAMMNYTAGVKGLSSAIAAAELNTIFTSRTFLDKGKLWHLPEQLTQVRWVFLEDLKGDITLADKLWIFA

HLLAPRLAQVKQQPEDAAMILFTSGSEGNPKGVVHSHKSLLSNVEQIKTIADFTANDRFMSALPLFHSFG

LTVGLLTPLLTGAEVFLYPSPLHYRVVPELVYDRNCTVLFGTSTFLANYARFANPYDFYRLRYVVAGAEK

LQESTKQLWQDKFGLRILEGYGVTECAPVVSINVPMAAKVGTVGRILPGMDARLLAMPGIDQGGRLQLKG

PNIMKGYLRVENPGVLEAPAAENQHGEMEAGWYDTGDIVTFDEQGYVRIQGRAKRFAKIAGEMISLEMVE

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>lcl|NZ\_FO834906.1\_prot\_WP\_002915976.1\_872 [gene=lplT] [locus\_tag=BN49\_RS05620] [protein=lysophospholipid transporter LplT] [protein\_id=WP\_002915976.1] [location=886194..887387] [gbkey=CDS]

MSESVHTNPSLYSKGMLAVICAQFLSAFGDNALLFATLALMKQLYYPEWSQPVLQMLFVGAYILFAPFVG

QFADSFAKGRVMMVANGLKLLGAGCICFGVNPFIGYTLVGIGAAAYSPAKYGILGELTTGDKLVKANGLM

ESSTIAAILLGSMAGGILADWHVLAALIVCALVYGGAVVANLWIPRLPAARPGQSWRFKPMTHSFFSACR

TLWRNGETRFSLMGTSLFWGAGVTLRFLLVIWVPVALGITSNAMPTYLNAMVAVGIVLGAGAAAKLVTLE

TVSRCMPAGILIGIAVIAFAVQQSLLPAFGLLLLLGVFGGFFIVPLNALLQERGKHSVGAGNAIAVQNLG

ENVAMLLMLGLYSLAVSVGVPPVAVGIGFGAVFAVAIAALWVWGRRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002915975.1\_873 [locus\_tag=BN49\_RS05625] [protein=NADP(H)-dependent aldo-keto reductase] [protein\_id=WP\_002915975.1] [location=complement(887490..888530)] [gbkey=CDS]

MQYHRIPHSSLEISTLGLGTMTFGEQNSEADAHQQLDYAVANGINLIDVAEMYPVPPRPETQGLTETYVG

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FGKLGYTWADAAPAVTLLDTLEALTEFQRAGKIRYIGVSNETAFGVMRYLHLADKHDLPRIVTIQNPYSL

LNRSFEVGLAEVSQFEGVELLAYSCLAFGTLTGKYLNGAKPAGARNTLFSRFTRYSSEQSQKAVAAYVDI

AKRHGLDPAQMALAFVRRQPFVASTLLGATTMTQLQANVESLQLELSEEVLAEIEAVHQVYTYPAP

>lcl|NZ\_FO834906.1\_prot\_WP\_016532289.1\_874 [locus\_tag=BN49\_RS05630] [protein=YgdI/YgdR family lipoprotein] [protein\_id=WP\_016532289.1] [location=complement(888751..888969)] [gbkey=CDS]

MKKWAVLISAVGLAFSVSGCSSDYVMATEDGRMILTDGKPTVDDDTGLISYEDQQGNKMQINRDDVSQII

KR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915973.1\_875 [locus\_tag=BN49\_RS05635] [protein=TerC family protein] [protein\_id=WP\_002915973.1] [location=complement(889093..889806)] [gbkey=CDS]

MLFAWITDPNAWLALGTLTLLEIVLGIDNIIFLSLVVAKLPTAQRAHARRIGLMGAMVMRLALLASIAWV

VKLTNPLFTVFGQEISFRDLILLLGGLFLIWKASKEIHESIEGEEEGLKTNVHSFLGAIVQIMLLDIIFS

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>lcl|NZ\_FO834906.1\_prot\_WP\_032440299.1\_876 [gene=mutH] [locus\_tag=BN49\_RS05640] [protein=DNA mismatch repair endonuclease MutH] [protein\_id=WP\_032440299.1] [location=complement(889870..890565)] [gbkey=CDS]

MPAIAPLDSPPQSQEQLLAQARQLAGYSLGELAALAGIPIPRDLKRDKGWTGILLELWLGASAGSKPEQD

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FYLKKNFTAALLARHFLLQHD

>lcl|NZ\_FO834906.1\_prot\_WP\_004218186.1\_877 [locus\_tag=BN49\_RS30875] [protein=hypothetical protein] [protein\_id=WP\_004218186.1] [location=complement(890651..890794)] [gbkey=CDS]

MSLFPSYPTFLWITWCKILFIVSDQFWKTRLHRFHKPHDEFKKPYKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002915936.1\_878 [gene=rppH] [locus\_tag=BN49\_RS05650] [protein=RNA pyrophosphohydrolase] [protein\_id=WP\_002915936.1] [location=891248..891778] [gbkey=CDS]

MIDDDGYRPNVGIVICNRQGQVMWARRYGQHSWQFPQGGINPGESAEQAMYRELFEEVGLSRKDVRILAS

TRNWLRYKLPKRLVRWDTKPVCIGQKQKWFLLQLIGNDADINMQTSSTPEFDGWRWVSYWYPVRQVVSFK

RDVYRRVMKEFASVTMSLAESAPKPQNAPAYRRKRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915935.1\_879 [gene=ptsP] [locus\_tag=BN49\_RS05655] [protein=phosphoenolpyruvate--protein phosphotransferase] [protein\_id=WP\_002915935.1] [location=891791..894037] [gbkey=CDS]

MLTRLREIVEKVASAPRLNEALDILVTDVCQAMETEVCSVYLADNDRRCYYLMATRGLKKPRGRTVALAF

DEGLVGLVGRLAEPINLADAQKHPSFKYIPAVKEDRFRAFLGVPIIQRRQLLGVLVVQQRELRQFDESEE

SFLVTLATQMAAILSQSQLNALFGQYRQTRIRALPASSGVAIAEGWMDVSLPLMEQVYEASTLDTASERE

RLTGALEEAANEFRRYSKRYAAGAQKETAAIFDLYSHLLSDARLRRELFAEVDKGAVAEWAVKKIIEKFA

EQFAALSDGYLKERAGDLRTLGQRLLFHLDDSIQGPNTWPARIILVADELSATTLAEVPQDRLAGVVVRD

GAANSHAAIMVRALGIPTVMGADIQPSLLHGHTLIVDGYRGELLVDPEPVLLQEYQRLISEENELSRLAE

DDLQRASELKSGERVKVMLNAGLSPEHEEKLGSFVDGIGLYRTEIPFMLQSGFPSEEEQVAQYQGMLQMF

NSKPVTLRTLDIGADKQLPYMPISEENPCLGWRGIRITLDQPEIFLIQVRAMLRANAATGNLSILLPMVT

SLEEVDEARRLIDRASREVEEMIGYAIPRPRLGVMLEVPSMVFMLPQLASRIDFISVGTNDLTQYLLAVD

RNNTRVASMYDSLHPAVLRALAMIAHDAERFGIDLRLCGEMAGDPMCVTILIGLGYRHLSMNGRSVARVK

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531632.1\_880 [gene=lgt] [locus\_tag=BN49\_RS05660] [protein=prolipoprotein diacylglyceryl transferase] [protein\_id=WP\_016531632.1] [location=894283..895158] [gbkey=CDS]

MNSGYLHFPEFDPVIFSLGPASLHWYGLMYLVGFVFAMWLATRRANRPGSGWTKNEVENLLYAGFLGVFL

GGRIGYVLFYNLPVFLADPLYLFRVWDGGMSFHGGLIGVILVMIIFARRTKRTFFQVSDFIAPLIPFGLG

AGRLGNFINGELWGRVDPSFHYTMIFPGSRAEDLALLPTHPEWQSLFDTYGALPRHASQLYELALEGVVL

FLILNLFIRKPRPTGSVSGLFLIGYGLFRIIVEFFRQPDAQFTGGWVQYISMGQILSIPMVLAGIIMMVW

AYRHRPQPQNS

>lcl|NZ\_FO834906.1\_prot\_WP\_004174525.1\_881 [gene=thyA] [locus\_tag=BN49\_RS05665] [protein=thymidylate synthase] [protein\_id=WP\_004174525.1] [location=895165..895959] [gbkey=CDS]

MKQYLDLMQKVLTEGTPKNDRTGTGTISIFGHQMRFNLQEGFPLVTTKRCHLRSIIHELLWFLQGDTNIA

YLHENNVTIWDEWADENGDLGPVYGKQWRSWPAPDGRHIDQITTVMNQLKNDPDSRRIIVSAWNVGELDK

MALAPCHAFFQFYVADGKLSCQLYQRSCDVFLGLPFNIASYALLVHMVAQQCDLQVGDFVWTGGDTHLYS

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>lcl|NZ\_FO834906.1\_prot\_WP\_040188384.1\_882 [locus\_tag=BN49\_RS05670] [protein=prepilin peptidase-dependent protein] [protein\_id=WP\_040188384.1] [location=896146..896697] [gbkey=CDS]

MQTFFAYLAGKAIFRHRVRTNRRGILNAMNREHGYTLMETLVTLTLMMILSVGGLYGWQRWQQQQRLWQT

AVQVRDFLVFLRDDANAYNRDRVLRVGQDEAGWCLSAQGEGADCTAGSAFTLRPRWPGITLVGVTPGLGF

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>lcl|NZ\_FO834906.1\_prot\_WP\_064754486.1\_883 [locus\_tag=BN49\_RS05675] [protein=prepilin peptidase-dependent protein] [protein\_id=WP\_064754486.1] [location=896694..897251] [gbkey=CDS]

MNSRGFSLAEALIAMAIGSLLLMGACRFLPALQRHILRQGEQLALENELWQRVHAVGKHLQRAGYCRGAC

GGAGLELAAGGECLIVRWDANSNGRWETSPAAAAESTGFRLRDGALETLRGASDCRGGGWEKITNPAAIV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004181182.1\_884 [locus\_tag=BN49\_RS05680] [protein=DUF2509 family protein] [protein\_id=WP\_004181182.1] [location=897248..897655] [gbkey=CDS]

MIRQRGMSSLLMVLLLLTLGSLLLEGLNLQQRALLAQTASETQAIRDTAIAHSALQWGKQQVWSAQVALA

CREQAPQGWRACLRIFGDGSLVLSSASGEVQVWQSGEVRGGQVRFSAHGWSDFCPLREASLCQMP

>lcl|NZ\_FO834906.1\_prot\_WP\_002915888.1\_885 [locus\_tag=BN49\_RS05685] [protein=prepilin-type N-terminal cleavage/methylation domain-containing protein] [protein\_id=WP\_002915888.1] [location=897640..897963] [gbkey=CDS]

MSNALKRQRGFSLPETVLAMALMVLTVTALGGYQRGMAQGIVQLNQTRQLWRDAWRYSQLSAPPSPARGQ

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DMFVRVLKDIPGESAFSKQSMSWKLMTLLPQHLEEDDFILLRQYLSDDGDKRKLFQLAARVADLYDQYLV

YRPEWLMRWEAGQRVEGLGDAQQWQAPLWQALVSYTAELGQPQWHRANLYQRFISTLEKADEPPAGLPSR

VFICGISALPPVYLQALQALGKHVDVYVLFTNPCRYYWGDIKDPAFLAKLLSRQRRHHREARALPLFRDT

EQAPGLFNDAGEQDVGNPLLASWGKLGRDYIYLLAGLERYEELDAFVDIAPDNLLHNLQSDILELRNAAV

AGQSAEAFAHSRDKRPLTLDDRSLSIHVCHSPQREVEVLHDRLLAMLEADPTLTPRDIIVMVADIDSYSP

YIQAVFGAASGDRWLPWAISDRRARESHPVLQAFITLLSLPDSRFASEDVLALLDVPVLAARFNITEEGL

RYLRQWVNESGVRWGMDDDNVRELDLPATGQHTWRFGLTRMLLGYAMDSSEGEWQSVLPYDESSGLIAEL

VGNLASLLMQLNLWRRGLAQQRPLAEWLPVCRDLLNDFFLPDSETEAALALIEQQWLAVIDSGLEAQYGE

QVPLTLLRDELAQRLDQQRISQRFLAGPVNICTLMPMRSIPFKVVCLLGMNDGVYPRTLPPLGFDLMSQK

PQRGDRSRRDDDRYLFLEALMSAEQTLYISYIGRSIQDNSERFPSVLVQELVDYIGQSHCLAGDEELDCD

ASEARVKAHITHLHTRMPFDVANFQEDENKSYAREWLAAAGQQGEAHSDFIQPLTAPPIDSLPFDQLLRF

WQHPVRAFFQQRLRVNFRAEEDDIPDDEPFTLEGLSRYQLNQQLLNTLIEEQDVSAMFRRFRAAGELPYG

AFGELVWETQRLEMQALAERVMAERQQAQSMEIDLQCGGVNLTGWLQQVQPDGLLRWRPSLLSVSQGMQL

WLEHLVYCASGGTGESRLFVRKEGEWRFPALAPAEAQAYLNELVDGYLLGMSQPLLLLPESGGAWLKACY

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RSTQI

>lcl|NZ\_FO834906.1\_prot\_WP\_016531296.1\_887 [gene=ptrA] [locus\_tag=BN49\_RS05695] [protein=pitrilysin] [protein\_id=WP\_016531296.1] [location=901474..904359] [gbkey=CDS]

MPRSLWFKVFVVLAALWAPFSQADTGWQPIQETIRKSEKDTRQYQAIRLDNDMVVLLVSDPQAVKSLSAL

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AVDRLADAIAAPLLDKKYADRERNAVNAELTMARTRDGMRMAQVSAETINPAHPAAHFSGGNLETLSDKP

GSPVLDALHTFRDSWYSANLMKAVIYSNKPLPALARMAADTFGRVPNRQISRPEITVPVVTDAQKGIIIH

YVPAMPRKVLRVEFRIDNNSDRFRSKTDELVTYLIGNRSPGTLSDWLQKQGLAEGIRADSDPVVNGNSGV

LAISATLTDKGLAHRDEVTAAIFSYLDLLRTQGIDKRYFDELAHVLALDFRYPSINRDMDYVEWLADTMI

RVPVEHALDVVNIADQYDPQAIKDRLAMMTPQNARIWYISPQEPHNKTAYFVDAPYQVDKISEQTFADWQ

HKSQAIQLQLPALNPYIPDDFTLIKSDKAWPHPQLILDEPTLRVVYAPSQYFASEPKADISLVLRNPQAM

DSARRQVMFALNDYLAGIALDQLSNQAAVGGISFSTGANNGLMVNANGYTQHLPALFSDLLQGYFSYTPT

EEQLEQAKSWYAQMMDSAEKGKAYDQAIMPIQMVSQVPYFQREVRRALLPSITLKEVLDYRANLKTRGRP

ELMVIGNMTADAATTLARQIQQQLGADGNEWCRNKDVVVNRQQLAIFNKAGNSTDSALAAVFAPPNVDEF

SSTAASTLLGQIIQPWFYNQLRTEEQLGYAVFAFPMNVGRQWGMGFLLQSSDKQPAFLWQRFQAFFPTAE

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042464.1\_888 [gene=recB] [locus\_tag=BN49\_RS05700] [protein=exodeoxyribonuclease V subunit beta] [protein\_id=WP\_046042464.1] [location=904356..907892] [gbkey=CDS]

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ELRGRIRSNIHELRIACLRGESDNPLYSALLAEIADKDDAAKTLLLAERQMDEAAVFTIHGFCQRMLSLN

AFESGMLFEQQLIEDESRLRYQACADFWRRHCYPLTRDIAAVIHDVWKGPRDLLKSLDRWLQGEAPQLKS

PPAPNETLAERHQQIIARIDSLKQQWREQVGEIEGVLENSGLDRRKFNRGNQGKWMEKVNAWAQEETLSY

QLPDALEKFAQSFLLERTKAGGEPPVHPLFSAVESLLASSLTLTDLVLARAMVEIRDAVAREKRRRGELG

FDDMLSRLDEALRGDSGETLASAIRQRFPVAMIDEFQDTDPQQYRIFRRIWRRQPETALLLIGDPKQAIY

AFRGADIFTYMKARGDVAAHYTLDTNWRSSPGMVGSVNRLFSLSDNPFMFHEIPFLPVKAAAKNKGLRFT

VDAADVPAMNVWLMPGDTVGSGDYQTFMAQLCATQIRDWLSAGQRGRALLWRGETSRPVQASDITVLVRN

RLEAAQVREALQTLGIPSVYLSNRDSVFETLEAQELLWLLQAVLAPERENTLRSALATSMFGLTALDIEN

LNQDEQAWDALVEEFSEYRQIWRQRGVMPMLRALMTARHIAENLLATRGGERRLTDILHISELLQEAASQ

LESEHALVRWLAQHIAEPDSNAASQQMRLESDKHLVQIVTIHKSKGLEYPLVWLPFIARFRKQDQAFYHD

RETFAAVLDLGQDEASLELAEAERLAEDLRLLYVALTRAVWHCSLGVAPLSSRKSGNSDFHLSALGRLLQ

AGEAMDAAGLAARLADFCHGDIALQRPGELDLTPWQAPAATIPRLSARELQRRIADDWRVTSYSGLQQHG

FSGGQDLLPRLDVDAAGVGEVVEEPQLTPHQFPRGAAPGTFLHSLFEELDFTQPVPEGWMAEKLQLSGFD

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DFRQVRGMLKGFIDLVFRHEGRYYLLDYKSNWLGEDREAYTRPAMEQAMRAHRYDLQYQLYSLALHRYLR

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LASTLNALFPATGETDWQKVAAAVALTRRISVISGGPGTGKTTTVAKLLAALIQIEDSPRCRIRLAAPTG

KAAARLTESLGAALRKLPLTDAQKALIPTEASTLHRLLGAQPGSQRMRYHAGNPLHLDVLVVDEASMIDL

PMMSRLIDALPAHGRVIFLGDRDQLASVEAGAVLGDICAWASSGYTAARAQELTRLTGSPVPAGEGAIAG

ALRDSLCLLQKSYRFGSHSGIGSLARAVNAGARAEVKATLRQPFDDIALHPLSTTEEYEAMLGAAQQGYE

RYLQLRRERAEPQAMLAAFSEFQLLCALREGPYGVSGVNERLEQRLNRQRAIALPRHSRWYDGRPIMISR

NDSALGLFNGDIGIALERNGELRVWFLMPDGAIKSVQPSRLPEHDTAWAMTVHKSQGSEFEHAALILPAR

SVPLVTRELVYTAITRAKRRLSLYADEQVLSQAIVTRTERRSGLAEIFAGREAP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531904.1\_890 [locus\_tag=BN49\_RS05710] [protein=hypothetical protein] [protein\_id=WP\_016531904.1] [location=complement(909791..910111)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004149616.1\_891 [gene=argA] [locus\_tag=BN49\_RS05715] [protein=amino-acid N-acetyltransferase] [protein\_id=WP\_004149616.1] [location=complement(910341..911672)] [gbkey=CDS]

MVKERRTELVEGFRHSVPYINAHRGKTFVIMLGGEAIEHENFSNIVNDIGLLHSLGIRLVVVYGARPQID

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VDDGVDYCHSGRIRRIDEEAIHRQLDSGAIVLMGPVAVSVTGESFNLTSEEIATQLAIKLKAEKMIGFCS

SQGVYNQAGEIVSELFPNEAQARVEELEADEDYNSGTVRFLRGAVKACRSGVRRCHLISYQENGALLQEL

FSRDGIGTQIVMESAEQIRRATINDIGGILELISPLEQQGILVRRSREQLEMEIDKFTIIQRDNTTIACA

ALYPFPEEKIGEMACVAVHPDYRSSSRGEVLLERIAAQARQMGLSKLFVLTTRSIHWFQERGFTPVDIDL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004174538.1\_892 [gene=amiC] [locus\_tag=BN49\_RS05720] [protein=N-acetylmuramoyl-L-alanine amidase AmiC] [protein\_id=WP\_004174538.1] [location=911900..913153] [gbkey=CDS]

MSGNNSGLSRRRLLQGAGAMWLMSVSPVGLAAAARVVAVRVWPASTYTRVTVESNHVLKYRQFALSNPER

VVVDLEGVNLNSVLKGMGGQIRADDPFIKSARVGQFDPQTVRMVFELKQNVKPQLFALAPVAGFKERLVM

DLYPANATDVQDPLLALLEDYNKGDLERQVPPAQSGPQPGKAGRDRPIVIMLDPGHGGEDSGAVGKYRTR

EKDVVLQIARRLRALIDKEGNMKAYMTRNEDVFIPLKVRVAKAQKQRADLFVSIHADAFTSRQPSGSSVF

ALSTKGATSTAAKYLAQTQNASDLIGGVSKSGDRYVDHTMFDMVQSLTIADSLKFGKAVLEKMGNINNLH

KNRVEQAGFAVLKAPDIPSILVETAFISNVEEERKLKTAKFQQEVAESILAGIKAYFADGATLARRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004185485.1\_893 [gene=cobD] [locus\_tag=BN49\_RS05725] [protein=threonine-phosphate decarboxylase CobD] [protein\_id=WP\_004185485.1] [location=913171..914247] [gbkey=CDS]

MALLKSAHGGNIREAAALLGIAPGELLDFSANINPLGMPASLRQAIVDNPGCAERYPDVEYQQLHQALAA

HHQLPAAHILAGNGETESIFTLVHGLKPRRAMIVIPGFAEYRRALQTVDCEVVEYALRERDGWQLTDAIL

DALTPALDCLFLCTPNNPTGLLPERGLLEAIAQRCRALNISLILDEAFLDFIPDQPGFIPLLAQHPHVWV

LRSLTKFYAIPGLRLGYLLNADAQAVARLRARQMPWSINAYAALAGEIILQDRAYQRATWQWLQEEGARF

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AALRRVLA

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MAVAQCPASCGELIQGWILGSEKLVSCPVDWYSTVEVETGVPRKDERPLSRAMVDQLLAHWGYPPALSQQ

IRITLHSTIPVAKGMASSTADIAATAVATAHHLGHLLDEPTLARLCVALEPTDSTLFRQLTLFDHNTAAT

QIACPPPPALDLLVLESPLTLRTTDYHQLPREPGLLANASRLQLAWEKVQQACHCGNPQLLGEAATISAI

ASQQLLPKPGFDALLDLVESAGLYGLNVAHSGSVVGLLLDRRRHDVEFLQWRLADSDIAAHWPQQHLLAM

VPGGVILQ

>lcl|NZ\_FO834906.1\_prot\_WP\_032104157.1\_895 [locus\_tag=BN49\_RS05735] [protein=acetate/propionate family kinase] [protein\_id=WP\_032104157.1] [location=complement(915209..916423)] [gbkey=CDS]

MTYKIMAINAGSSSLKFQLLNMPQGALLCQGLIERIGLPEARFTLKTSAQKWQETLPIADHHEAVTLLLE

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PAVAVFDTAFHQTLAPEAWLYPLPWRYYAELGIRRYGFHGTSHHYVSSALAEKLGVPLSALRVVSCHLGN

GCSVCAIKGGQSVNTSMGFTPQSGVMMGTRSGDIDPSILPWLVEKEGKSAQQLNQLLNNESGLLGVSGVS

SDYRDVEQAADAGNERAALALSLFAERIRATIGSYIMQMGGLDALIFTGGIGENSARARATICRNLHFLG

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>lcl|NZ\_FO834906.1\_prot\_WP\_002915858.1\_896 [gene=pduV] [locus\_tag=BN49\_RS05740] [protein=propanediol utilization protein PduV] [protein\_id=WP\_002915858.1] [location=complement(916420..916860)] [gbkey=CDS]

MKRLMLIGPSQCGKTSLTQVLRGETLRYQKTQAIVWTPAAIDTPGEYLENRCLYSALLTSACEADVIALV

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NAEEYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002915850.1\_897 [gene=pduU] [locus\_tag=BN49\_RS05745] [protein=propanediol utilization microcompartment protein PduU] [protein\_id=WP\_002915850.1] [location=complement(916865..917215)] [gbkey=CDS]

MEPQTPTERMIQEYVPGKQVTLAHLIANPGKDLFKKLGLPDAVSAIGILTITPSEASIIACDIATKSGAV

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042470.1\_898 [gene=pduT] [locus\_tag=BN49\_RS05750] [protein=propanediol utilization microcompartment protein PduT] [protein\_id=WP\_046042470.1] [location=complement(917254..917769)] [gbkey=CDS]

MTQAIGILELTSIARGMELGDVMLKSANVQLLLCRTLCPGKFLLMLGGDVGAVQQAIAAGTARAGEMLVD

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>lcl|NZ\_FO834906.1\_prot\_WP\_023285520.1\_899 [locus\_tag=BN49\_RS05755] [protein=SLBB domain-containing protein] [protein\_id=WP\_023285520.1] [location=complement(917772..919124)] [gbkey=CDS]

MSEAIVPLSSIDAAEIRERVRAAGVVGAGGAGFPTHIKLQARVDTVLVNAAECEPMLKVDQQLMAQQADR

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INGGPMMGSLITSLETPVTKTTGGLLVLPGNHPLIQRRRQDERTLLAIARTVCEQCRLCTDLCPRHLIGH

ELSPHLLVRAVNYRQAATPSLLLSALTCSECNVCESVACPVGISPMRINRLLKRELRAKNLRYDGPLRPA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531326.1\_900 [gene=pduQ] [locus\_tag=BN49\_RS05760] [protein=1-propanol dehydrogenase PduQ] [protein\_id=WP\_016531326.1] [location=complement(919121..920233)] [gbkey=CDS]

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KYPLFHEALCPDMAIIDPTLVVSVPPTITAHTGLDALTHALEAWVSPQATDFTDALAEKAVRLVFRALPV

AIHQGDCIATRSKMHNASTLAGMAFSQAGLGLNHAIAHQLGGQFHLPHGLANALLLTAVIRFNAGEPRAA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531325.1\_901 [gene=pduP] [locus\_tag=BN49\_RS05765] [protein=CoA-acylating propionaldehyde dehydrogenase PduP] [protein\_id=WP\_016531325.1] [location=complement(920245..921633)] [gbkey=CDS]

MNTAELETLIRTILSEKLAPTPPAPQQEQGIFCDVGSAIDAAHQAFLRYQQCPLKTRSAIISALRETLAP

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ETIINNSISMLAAGNSVYFSPHPGAKKVSLKLIARIEEIAYRCSGIRNLVVTVAEPTFEATQQMMSHPLI

AVLAITGGPGIVAMGMKSGKKMIGAGAGNPPCIVDETADLVKAAEDIISGAAFDYNLPCIAEKSLIVVAS

VADRLIQQMQDFDALLLSRLEADTLRAACLPDGAANKKLVGKSPAALLAAAGLAVPPRPPRLLIAEVEAN

DPWVTCEQLMPVLPIVRVADFDSALALALRVEEGLHHTAIMHSQNVSRLNLAARTLQTSIFVKNGPSYAG

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042475.1\_902 [gene=pduO] [locus\_tag=BN49\_RS05770] [protein=two-domain cob(I)yrinic acid a,c-diamide adenosyltransferase PduO] [protein\_id=WP\_046042475.1] [location=complement(921630..922646)] [gbkey=CDS]

MAIYTRTGDAGSTSLFTGQRVSKTHPRVEAYGTLDELNAMLSLCVCAVAEEEQRTLLEALQQHIFWFSVE

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AEVTIRQILLRYLNRLSDCLYALARSEDHAAHQRRLVTEIAARYLAASRSPAPDAPKAQAGSLSFHELHQ

LIRQAIEHARQLQVPVVISIVDAHGTETVTWRMPDALLVSSELAPKKAWTAVAMKTATHELATTVQPGAA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002915814.1\_903 [locus\_tag=BN49\_RS05775] [protein=ethanolamine utilization protein EutN] [protein\_id=WP\_002915814.1] [location=complement(922657..922932)] [gbkey=CDS]

MHLARVTGAVVSTQKSPSLNGKKLLLVRRVSADDDRPILPTSGDEVAVDSVGAGVGELVLLCSGSSARHV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004900288.1\_904 [gene=pduM] [locus\_tag=BN49\_RS05780] [protein=microcompartment protein PduM] [protein\_id=WP\_004900288.1] [location=complement(922936..923427)] [gbkey=CDS]

MNHAMLQRIVEEVAARLRHRALSTATLSVAQLGEADIRSLLCQHASLRIVQVDLPLLEQLAGQRALAAAG

CALHEAMAWGVRVQLTLLPALLPALAVKKLARLPLTFSDPLGQPVRLHAASVLTYADVARFSGGYLVLRR

RPIITALAREAAVARHVQLIKQE

>lcl|NZ\_FO834906.1\_prot\_WP\_002915810.1\_905 [locus\_tag=BN49\_RS05785] [protein=phosphate propanoyltransferase] [protein\_id=WP\_002915810.1] [location=complement(923424..924056)] [gbkey=CDS]

MDKQQLASTVNKVLDEMRQRPIPIGISSRHIHLAAADYARLFPAQPIQPKKALLQPGQYAAEQTVTLVGP

KGRLNNVRLLGPLRQTSQVEISRTDARILGIAAPLRMSGNLQGTPGIRLISPFAELELSGGTIVAQRHIH

MSPLDALILRVSHGDSVAVAIEGSDRRLIFDNVAVRVAPDMRLEMHIDTDEANAAGADAAQAWATLVTKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002915808.1\_906 [locus\_tag=BN49\_RS05790] [protein=BMC domain-containing protein] [protein\_id=WP\_002915808.1] [location=complement(924056..924502)] [gbkey=CDS]

MKQSLGLLEVSGLALAITCADAMAKAAAITLLALEKTNGSGWMVVKIAGDVASVQAAVMTGAELAERQQG

LVAQKVIARPGEGLLPARVQAPSPAPDVAVTEENTALTDAPSHSTERVTCNLCLDPHCPRQKGDPRSQCL

HAGKRGDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915806.1\_907 [gene=pduJ] [locus\_tag=BN49\_RS05795] [protein=propanediol utilization microcompartment protein PduJ] [protein\_id=WP\_002915806.1] [location=complement(924524..924799)] [gbkey=CDS]

MNNALGLVETKGLVGAIEAADAMVKSANVQLIGYEKIGSGLITVMVRGDVGAVKAAVDAGSAAASVVGEV

KSSHVIPRPHSDVEAILPKSV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174562.1\_908 [locus\_tag=BN49\_RS05800] [protein=glycerol dehydratase reactivase beta/small subunit family protein] [protein\_id=WP\_004174562.1] [location=complement(924818..925168)] [gbkey=CDS]

MESSVVAPAIVIAVTDECSEQWRDVLLGIEEEGIPFVLQPQTGGDLIHHAWQAAQRSPLQVGIACDRERL

IVHYKNLPASTPLFSLMYHQNRLARRNTGNNAARLVKGIPFRDRNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149610.1\_909 [locus\_tag=BN49\_RS05805] [protein=diol dehydratase reactivase subunit alpha] [protein\_id=WP\_004149610.1] [location=complement(925158..926990)] [gbkey=CDS]

MRYIAGIDIGNSSTEVALATVDDAGVLNIRHSALAETTGIKGTLRNVFGIQEALTQAAKAAGIQLSDISL

IRINEATPVIGDVAMETITETIITESTMIGHNPKTPGGVGLGVGITITPEALLSCSAGTPYILVVSSAFD

FADVAAMVNAATAAGYQITGIILQQDDGVLVNNRLQQPLPVIDEVQHIDRIPLGMLAAVEVALPGKIIET

LSNPYGIATVFDLNAEETKNIVPMARALIGNRSAVVVKTPSGDVKARAIPAGNLLLIAQGRSVQVDVAAG

AEAIMKAVDGCGKLDNVAGEAGTNIGGMLEHVRQTMAELTNKPAQEIRIQDLLAVDTAVPVSVTGGLAGE

FSLEQAVGIASMVKSDRLQMALIAREIEHKLQIAVQVGGAEAEAAILGALTTPGTTRPLAILDLGAGSTD

ASIINAQGEISATHLAGAGDMVTMIIARELGLEDRYLAEEIKKYPLAKVESLFHLRHEDGSVQFFPSALP

PTVFARVCVVKPDELVPLPGDLPLEKVRAIRRSAKSRVFVTNALRALRQVSPTGNIRDIPFVVLVGGSSL

DFEIPQLVTDALAHYRLVAGRGNIRGCEGPRNAVASGLLLSWQKGGTHGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002915750.1\_910 [gene=pduE] [locus\_tag=BN49\_RS05810] [protein=propanediol dehydratase small subunit PduE] [protein\_id=WP\_002915750.1] [location=complement(927003..927527)] [gbkey=CDS]

MNTDAIESMVRDVLSRMNSLQDGITPAPAAPTNDTVRQPKVSDYPLATRHPEWVKTATNKTLDDLTLENV

LSDRVTAQDMRITPETLRMQAAIAQDAGRDRLAMNFERAAELTAVPDDRILEIYNALRPYRSTQAELLAI

ADDLEHRYQARLCAAFVREAAGLYIERKKLKGDD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529665.1\_911 [gene=pduD] [locus\_tag=BN49\_RS05815] [protein=propanediol dehydratase medium subunit PduD] [protein\_id=WP\_016529665.1] [location=complement(927542..928231)] [gbkey=CDS]

MEINETLLRQIIEEVLVEMKSGADKPVSFSAPAASVASAAPVAVAPVSGDSFLTEIGEAKPGTQQDEVII

AVGPAFGLAQTANIVGIPHKNILREVIAGIEEEGIKARVIRCFKSSDVAFVAVEGNRLSGSGISIGIQSK

GTTVIHQRGLPPLSNQELFPQAPLLTLETYRQIGKNAARYAKRESPQPVPTLNDQMARPKYQAKSAILHI

KETKYVVTGKNPQELRVAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529664.1\_912 [gene=pduC] [locus\_tag=BN49\_RS05820] [protein=propanediol dehydratase large subunit PduC] [protein\_id=WP\_016529664.1] [location=complement(928242..929906)] [gbkey=CDS]

MRSKRFEALAKRPVNQDGFVKEWIEEGFIAMESPNDPKPSIRIVNGAVTELDGKPVEQFDLIDHFIARYG

INLARAEEVMAMDSVKLANMLCDPNVKRSDIVPLTTAMTPAKIVEVVSHMNVVEMMMAMQKMRARRTPSQ

QAHVTNIKDNPVQIAADAAEGAWRGFDEQETTVAVARYTPFNAIALLVGSQVGRPGVLTQCSLEEATELK

LGMLGHTCYAETISVYGTEPVFTDGDDTPWSKGFLASSYASRGLKMRFTSGSGSEVQMGYAEGKSMLYLE

ARCIYITKAAGVQGLQNGSVSCIGVPSAVPSGIRAVLAENLICSALDLECASSNDQTFTHSDMRRTARLL

MQFLPGTDFISSGYSAVPNYDNMFAGSNEDAEDFDDYNVIQRDLKVDGGLRPVREEDVIAIRNKAARALQ

AVFAGMGLPPITDEEVEAATYAHGSKDMPERNIVEDIKFAQEIINKNRNGLEVVKALAKGGFPDVAQDML

NIQKAKLTGDYLHTSAIIVGEGQVLSAVNDVNDYAGPATGYRLQGERWEEIKNIPGALDPNELG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915739.1\_913 [gene=pduB] [locus\_tag=BN49\_RS05825] [protein=propanediol utilization microcompartment protein PduB] [protein\_id=WP\_002915739.1] [location=complement(929925..930737)] [gbkey=CDS]

MSSNELVEQIMAQVIARVATPEQQALPDTPHPTGETAMAEKSCSLTEFVGTAIGDTLGLVIANVDAALLE

AMKLEKRYRSIGILGARTGAGPHIMAADEAVKATNTEVVSIELPRDTKGGAGHGSLIVLGGNDVSDVKRG

IEVALKELDRTFGDVYGNEAGHIELQYTARASYALEKAFGAPLGRACGIIVGAPASVGVLMADTALKSAN

VEVVAYSSPAHGTSFSNEAILVISGDSGAVRQAVISAREIGKTVLATLGAEPKNDRPSYI

>lcl|NZ\_FO834906.1\_prot\_WP\_002915737.1\_914 [gene=pduA] [locus\_tag=BN49\_RS05830] [protein=propanediol utilization microcompartment protein PduA] [protein\_id=WP\_002915737.1] [location=complement(930734..931018)] [gbkey=CDS]

MQQEALGMVETKGLTAAIEAADAMVKSANVLLVGYERIGSGLVTVIVRGDVGAVKAATDAGAAAARHVGE

VKAVHVIPRPHTDVEKILPKGNSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_009485655.1\_915 [gene=pduF] [locus\_tag=BN49\_RS05835] [protein=propanediol diffusion facilitator PduF] [protein\_id=WP\_009485655.1] [location=931538..932347] [gbkey=CDS]

MNGSLRAQCIAEFLGTGLFLFFGICCLSALKLTGASLGLWEICIIWGLGISLAVYLTAGISGGHLNPAVT

VALWLFACFPGRKVVPYIVAQVAGAFGGAVLAWILYSTLFTQFETVHHMVRGSLESLQLASIFSTYPAPE

LSIWHAALVEVVITSMLMGMIMALTDDGNGVPKGPLAPLLIGILVAVIGASTGPLTGFAMNPARDFGPKL

FTWFAGWGNIAMTGGRNIPYFIVPIIAPLLGACLGAAIYRFLIANNLPCHTCVEEENTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004181164.1\_916 [gene=pocR] [locus\_tag=BN49\_RS05840] [protein=regulatory protein PocR] [protein\_id=WP\_004181164.1] [location=932551..933462] [gbkey=CDS]

MISASTLNSELINKIAQDFAQATSLAVVVVNIHGDEISELFNFTPFCQLMRQHPEHSGRCRMSDRCGGLE

ASKKDQLCIYRCHAGLTDFSIPLVIAGHLVGFVLCGQVRLSNDVELVDILNVDDRWQDDPALVQAFRDVP

EMDYSRVIASADLLKLIVENCLKKQLNFVVIKDNPSQNDPAQASRAPSPHDGKMKKALRYIDAHLSDELR

LEDVAAHVYLSPYYFSKLFKKYQGIGFNAWVNQQRMASAKELLCHSDWSIASIARNLGFSQTSYFCKVFR

QTYQVTPQAFRQQINAGSQTESF

>lcl|NZ\_FO834906.1\_prot\_WP\_046042482.1\_917 [locus\_tag=BN49\_RS05845] [protein=cobyrinate a,c-diamide synthase] [protein\_id=WP\_046042482.1] [location=934015..935391] [gbkey=CDS]

MATRRAFILAGTGSGCGKTTVTLGLLSLLQQRGMRVQPCKVGPDYLDTAWHTAISGIASRNLDSFMLPAP

ILNALFTEQLQQADIAVIEGVMGLYDGYGTDPNYCSSAAMAKQLGCPVILLVDGKAVSTSIAATVMGFQH

FDPALDIAGVIVNRVNSDAHFQLLKSAIERYCQVPVLGYVPRVEGVALPERHLGLVTARESVVNQQAWRD

FASLLGRTLDIDRLLALSELAAMPIGEWGEQLAADAGEGLTLALADDEAFNFYYPDNLALLARCGVKMVR

FSPLRDRQLPACQMIWLGGGYPELHAAGLSANHEMLTQLRAAHRRGVAIYAECGGLMYLGTTLEVTSGER

YTMADIIPGHSRMGTRLTRFGYCEAQAQQQTLLAAPGEWLRGHEFHYSDFSPATPAVLACRKQRDGKTLQ

QWQGGWQYGSAFASYLHVHFAQRPTMLNHWLRAARRAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002915724.1\_918 [gene=cbiB] [locus\_tag=BN49\_RS05850] [protein=adenosylcobinamide-phosphate synthase CbiB] [protein\_id=WP\_002915724.1] [location=935388..936347] [gbkey=CDS]

MTLLAWCVAWILDVVIGDPPHWPHPVRWIGRLIAVSQRVVRRVCHSDRALRIGGGVMWLVVIGLTWGVAW

GVLALAHGIHPWLGWLVEVWMIFTALAGRCLAQSAMAVARPLQAGDLAESRHKLSWIVGRDTSQLQPAQI

NRAVVETVAENTVDGIIAPLFFLLLGGAPLAMAYKAVNTLDSMVGYKHEKYRAIGMVSARLDDVANFLPA

RLSWLLLSLAAVLCREDGARALRTGWRDRYQHSSPNCAWPEATVAGALGIRLGGPNDYFGQRVEKPWIGD

AVRDIAVDDISRTIRLMWVASSLALALFIGVRYWLVGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915711.1\_919 [locus\_tag=BN49\_RS05855] [protein=cobalt-precorrin-8 methylmutase] [protein\_id=WP\_002915711.1] [location=936358..936993] [gbkey=CDS]

MQYIQQPQAIEAKSFDIISEIIAETRPDYRFASPLHEAIIKRVIHTTADFDWLDILWFSPDALIALSEAL

SRPCTLYTDTTMALSGINKTLLARFGGECRCYISDPRVVREAQSRGMTRSMAAVDIAVQEPGEKVFVFGN

APTALFRLLEHRETAIGGVVGVPVGFVGAAESKAALSESGLPAIAALGRKGGSNVAAAIVNALLYHLREA

Q

>lcl|NZ\_FO834906.1\_prot\_WP\_016531683.1\_920 [gene=cbiD] [locus\_tag=BN49\_RS05860] [protein=cobalt-precorrin-5B (C(1))-methyltransferase CbiD] [protein\_id=WP\_016531683.1] [location=936990..938129] [gbkey=CDS]

MSDQTFDAPVWHHGKALRKGYTTGSCATAAAKVAALMVMRQHLIHQVSIVTPSGVTLCLNVESPHVEGQQ

AVAAIRKDGGDDVDATHGMLIFARVTLNDSGEISLQGGEGIGTVTRKGIGLPTGSPAINRTPRHTIETAV

REAIGPTRGAQVEIFAPEGALRAQKTYNARLGILGGISIIGTTGIVTPMSEESWKRSLSLELEIKRAAGL

ERVVLVPGNHGERFVREQMGIDPQMVVTMSNFVGYMIEEAVRLGFRQIVLIGHPGKLIKIAAGIFHTHSH

IADARMETLVAHLALLGAPLPLLTLVSECDTTEAAMEHIDAWGYQRLYNHLAERICQRVLEMLRFTQQPP

TCDAVLFSFDNQVLGSSRPLAAIARELTC

>lcl|NZ\_FO834906.1\_prot\_WP\_015958917.1\_921 [locus\_tag=BN49\_RS05865] [protein=cobalt-precorrin-7 (C(5))-methyltransferase] [protein\_id=WP\_015958917.1] [location=938123..938728] [gbkey=CDS]

MLTVVGMGPAGLQWLTPAAREAIAAAEALVGGSRHLQQFPDFAGERFALRADMPALLAWIEARTGRRVVV

LASGDPLFYGIGTRLIAHFGRERVQVIPGISAVQYLCARAGIDMNDMWLTSSHGRAVSFDALAAHRKVAM

VTDGRCGPREIAAQLMARGKGHRWMVIGENLAMENERIHWLPVSAVEDEYEMNAVVILDER

>lcl|NZ\_FO834906.1\_prot\_WP\_002915684.1\_922 [locus\_tag=BN49\_RS05870] [protein=decarboxylating cobalt-precorrin-6B (C(15))-methyltransferase] [protein\_id=WP\_002915684.1] [location=938718..939287] [gbkey=CDS]

MKDELFLRGAQVPMTKEAVRALALAKLELHRARHLIDIGAGTGSVSIEAALQNPALRVTAIERQADALRL

LAENRQRFGCDNIAIVAGVAPLAVADKADAIFMGGSGGHLTALIDWSLAQLHPGGRLVMTFILQENLHSA

LAHLRQSGIHEVDCQQLAVSTLATLGSGHYFKPHNPVFVIACQKEENHG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042486.1\_923 [locus\_tag=BN49\_RS05875] [protein=cobalt-precorrin-4 methyltransferase] [protein\_id=WP\_046042486.1] [location=939280..940053] [gbkey=CDS]

MVETFDPHCVWFVGAGPGDRELITLKGYRLLQQAQVVIYAGSLINTELLAYCPPQAECHDSAALHLEQIL

DLMEAGVKAGKTVVRLQTGDVSLYGSVREQGEELTRRGIRWQVVPGVSAFLGAAAELGVEYTVPEVSQSL

IITRLEGRTPVPAREQLEAFASHQTSMAIYLSVQRIHRVAERLVEGGYPATTPVAVIYKATWPERQTVRG

TLADIGDKVRDAGIRKTALILVGPFLGDEYHYSKLYAADFSHEYRKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042488.1\_924 [gene=cbiG] [locus\_tag=BN49\_RS05880] [protein=cobalt-precorrin 5A hydrolase] [protein\_id=WP\_046042488.1] [location=940034..941089] [gbkey=CDS]

MNTVKPESIALFCLTPGGVRLAKRLAAMLPLTCYTSEALQEEGFIPFNGGFASAAREAFSSFSALIFIGA

TGIAVRVLAPLVNDKLSDPAVVVIDERARHVISLLSGHAGGANALTRYLAGMLDADPVITTATDVNELAA

LDTLAFQLNARMTDFRAAVKTVNQMLVSGKRVGLWCDGEFTGALSRCDRRGFIPVSDLASLPALDALICV

TLRRSLPPLPLPHWKLVPQRVVAGIGCRRDTPCALLSTLLDRQLAAQRLDPLALKAIGSVSLKANEPGLR

QLAHRCRVPFETFSAEALREHEHRFPASSFVRETVGVGSVSGPVAWLLSQGNLSGETLREQGVTITLGVT

H

>lcl|NZ\_FO834906.1\_prot\_WP\_004214523.1\_925 [locus\_tag=BN49\_RS05885] [protein=precorrin-3B C(17)-methyltransferase] [protein\_id=WP\_004214523.1] [location=941089..941814] [gbkey=CDS]

MLSVIGIGPGSQAMMTMEAVEALQAAEIVVGYKTYTHLVKAFTGDKQVIKTGMCKEIERCQAAIELAQAG

HNVALISSGDAGIYGMAGLVLELVNKQQLDIEVRLIPGMTASIAAASLLGAPLMHDFCHISLSDLLTPWP

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APVDMTSLVIVGNKATYIDNGLMITPRGYAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002915627.1\_926 [locus\_tag=BN49\_RS05890] [protein=cobalt-precorrin-6A reductase] [protein\_id=WP\_002915627.1] [location=941811..942596] [gbkey=CDS]

MNHGDVLVIGGTSDARAICQQLDAADVRYTLSVATPTGERLAGDIRGQIRCGRMEWQQMAEWLRAQRTRW

VIDASHPYAEVVSQNIVRACASVGVLLSRYQRPEQLSDLRHPLLHVVGDLNEACAVARRLGERILLTTGS

KDLAAWRAGLAEKTLLARVLPVPEVVQHCSDLGFGVGEIFALCGPFSAEFNAAFYRQCRADVVVTKASGA

EGGYQEKVQPCLDAGIPCIVITRPAPLVTGDELLQSQADFTARLTRWLSAT

>lcl|NZ\_FO834906.1\_prot\_WP\_016532596.1\_927 [locus\_tag=BN49\_RS05895] [protein=sirohydrochlorin cobaltochelatase] [protein\_id=WP\_016532596.1] [location=942607..943401] [gbkey=CDS]

MKKALLVVSFGTSYHDTREKNIAACERDLAASCPDRTLFRAFTSGMIIRKLQQRDGIHIDTPLQALQKLA

EQGYQDVAIQSLHIINGDEYEKIVREVQSMRPRFQRLTLGAPLLSGHGDYVQLMQALRQQMPPLAATERV

VFMGHGASHHAFAAYACLDHMMAVQGFPARVGAVESYPEVDIVINELSRQGVTGVHLMPLMLVAGDHAIN

DMASDEDDSWKTRFNAAGIPATPWLNGLGENPAVRAMFVAHLQQALNNAMEKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532597.1\_928 [locus\_tag=BN49\_RS05900] [protein=cobalt-factor II C(20)-methyltransferase] [protein\_id=WP\_016532597.1] [location=943398..944108] [gbkey=CDS]

MSGKLYALSTGPGAADLITVRAARILGQLDVLYAPAGRKGGDSLALSIVREYLGAHTEVRCCHFPMSADS

AEKEAVWNDVTAALAQEVAAGRQVGFITLGDAMLFSTWVFLLQRIGCPDWLEIVPGVTSFAAIAARAKTP

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>lcl|NZ\_FO834906.1\_prot\_WP\_008806286.1\_929 [gene=cbiM] [locus\_tag=BN49\_RS05905] [protein=cobalt ECF transporter S component CbiM] [protein\_id=WP\_008806286.1] [location=944108..944845] [gbkey=CDS]

MNQVKSLKQLSYGGLAAAVLLIIVPQEAFAMHIMEGFLPPMWALAWWLLFLPCLWYGLVRLRRIVQEESN

QKVLLALCGAFIFVLSALKIPSVTGSCSHPTGVGLAVILFGPGVVAVLGAIVLLFQALLLAHGGLTTLGA

NGMSMAVIGPMVGYLVWKLACRAGIRRDVGVFLCAMLADLMTYFVTSVQLGVAFPDPATGAGGSILKFMG

IFCLTQIPIAIAEGLLTVMIYDQLTKRRLIAAEGH

>lcl|NZ\_FO834906.1\_prot\_WP\_016532598.1\_930 [locus\_tag=BN49\_RS05910] [protein=energy-coupling factor ABC transporter substrate-binding protein] [protein\_id=WP\_016532598.1] [location=944847..945128] [gbkey=CDS]

MKRPLILLAMVVALMILPFFINHGGEFGGSDGEAESQIQVVAPDYQPWFQPLYEPASGEIESLLFTLQGS

LGAAVIFYILGYARGRQRRDDRV

>lcl|NZ\_FO834906.1\_prot\_WP\_004143925.1\_931 [locus\_tag=BN49\_RS05915] [protein=energy-coupling factor ABC transporter transmembrane protein] [protein\_id=WP\_004143925.1] [location=945115..945792] [gbkey=CDS]

MTGFDRLSYQSRWLQVAPERKFLLWLLLMALAFTLPAWGQALTLALTAALTCWLLRVSFWRWCRWMALPF

GFLLVGVLTIVFSVSRDPQMLLASIRLGAFSIGISAPGLAVAGETFWRSLAAMAATLWLVLNLPFPQLII

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STALDIKLYQGDFHL

>lcl|NZ\_FO834906.1\_prot\_WP\_002915614.1\_932 [locus\_tag=BN49\_RS05920] [protein=energy-coupling factor ABC transporter ATP-binding protein] [protein\_id=WP\_002915614.1] [location=945801..946625] [gbkey=CDS]

MLATTDLWFRYQDEPVLKGLTLDFSRHAVTGLVGANGCGKSTLFMNLSGLLRPQQGAVLWQGEALNYSKR

GLLALRQQVATVFQDPDQQIFYTDIDSDIAFSLRNLGVAEEEIARRVDEALTLVDAQGFRQQPIQCLSHG

QKKRVAIAGALVLQARYLLLDEPTAGLDPRGRAQMIAIIRRIVGQGRRVVISSHDIDLIYEVSDAVYVLR

HGEVLAAGDPGEVFACAETMDRAGLTQPWLVKLHSELGLPLCKTEAEFFQRMHNNAIGAIKEAS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042498.1\_933 [locus\_tag=BN49\_RS05925] [protein=cobyric acid synthase] [protein\_id=WP\_046042498.1] [location=946622..948145] [gbkey=CDS]

MTLAVMLQGTASDVGKSVLVAGLCRIFHQDGLRTAPFKSQNMALNSGITPDGKEMGRAQIFQAEAAGIAP

DVRMNPILLKPTSDRQAQVVLMGQVATSMDAVSYHQYKPRLREQILAVYQSLAGEYEALVLEGAGSPAEI

NLRDRDIVNMGMAEMAQCPVILVANIDRGGVFAAIYGTLALLQPQERARVKGVIINKFRGDVALLRSGIE

QIEALTGVPVLGVMPWLDVDLEDEDGVALQAGKYHRTDRRDIDIAVVHLPHIANFTDFNALAAQPDVRVR

YVRDPQALADADLVILPGSKNTLGDLCWLRESGMAHAVEQARQRKVPLLGICGGYQMLGETIIDEVESGL

GAQPGLGVLKTVTHFAQHKTTTQVQATLGSALPDWLADAAGLRVSGYEIHMGETRREAGCPPLLQLHKAG

QAVDDGAISDDGLAFGTYLHGLFDSDAFTRALLNGLRQRKGLAPLDSALEYARYKTRQFDRLAEAMREHI

AIDKIYAIMRQHQEPLC

>lcl|NZ\_FO834906.1\_prot\_WP\_004890028.1\_934 [gene=cobU] [locus\_tag=BN49\_RS05930] [protein=bifunctional adenosylcobinamide kinase/adenosylcobinamide-phosphate guanylyltransferase] [protein\_id=WP\_004890028.1] [location=948139..948684] [gbkey=CDS]

MLTLVTGGARSGKSRHAEALIADAPQVLYIATSQIFDDEMAARIQHHRDGRPAHWRTAERWQQLDELITP

AIAPAEAILLECITTMVTNLLFALGGDSDPDGWDYAAMEQAIDDEIGVLIAACQRCPAHVVLVTNEVGMG

IVPENRLARHFRDIAGRVNQRLAAAADAVWLVVSGIGVKIK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529969.1\_935 [gene=cobT] [locus\_tag=BN49\_RS05935] [protein=nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase] [protein\_id=WP\_016529969.1] [location=948728..949783] [gbkey=CDS]

MQNLNTVLRAIPAPDADAMARAQQHIDGLLKPPGSLGRLEALAVQLAGMPGLGGQPQVAKKALLVMCADH

GVWDEGVAISPKAVTAIQAANMTRGTTGVCVLAAQAGAKVHVIDVGIDSEPLPGVVNMRVARGCGNIARG

PAMSREQGQELLLEVMRYTRALAQEGVTLFGVGELGMANTTPAAAIVSVLTGSDAQEVVGIGANLPLAKV

GNKVAVVRRAIAVNQPDPNDGLDVLSKVGGFDLLGMTGVMLGAASCGLPVVLDGFLSYAAALAACQIAPE

VKPYLIPSHYSAEKGARIALAHLGLEPYLNMGMRLGEGSGAALAMPIVEAACAMYHRMGMLAASNIVLPK

G

>lcl|NZ\_FO834906.1\_prot\_WP\_156720420.1\_936 [locus\_tag=BN49\_RS30880] [protein=hypothetical protein] [protein\_id=WP\_156720420.1] [location=949803..949940] [gbkey=CDS]

MAVPVFGGGFAGGRNKKTPLRVFQVVGKKGKSVVFPPLWLSAENQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004181152.1\_937 [gene=tssE] [locus\_tag=BN49\_RS05940] [protein=type VI secretion system baseplate subunit TssE] [protein\_id=WP\_004181152.1] [location=complement(950009..950434)] [gbkey=CDS]

MAASSLFEMLTFSFSGELPLEQVSERDQLILSVMDNMQRIINCRAGTLAHLPDYGLPDLSMIHQGMTAGI

HGLIHQIEETLLRYEPRLSQLRVELQPQPRPGHLNYLIYAQLPDTGWIRFDGIFSAEGRIVLRHLKQQER

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529968.1\_938 [gene=tssJ] [locus\_tag=BN49\_RS05945] [protein=type VI secretion system lipoprotein TssJ] [protein\_id=WP\_016529968.1] [location=complement(950438..950755)] [gbkey=CDS]

MITGVWKYRGKSTNYDTLLMQEEKTLKSDVLAKHTVWMKPAGAVSLNVPLDKETQFIAIVGQFYHPDEQS

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>lcl|NZ\_FO834906.1\_prot\_939 [locus\_tag=BN49\_RS05950] [protein=IS3 family transposase] [pseudo=true] [location=complement(950730..951962)] [gbkey=CDS]

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CL\*TCCRHEAD\*RTPAPARQKNDGK\*TP\*RSR\*IWASKKVDSARALIARGWGVSFVSRCLRVSRAQLHVI

LRRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNAL

LLERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSET

VQDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIK

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531439.1\_940 [locus\_tag=BN49\_RS05960] [protein=type VI secretion lipoprotein TssJ] [protein\_id=WP\_016531439.1] [location=complement(952051..952311)] [gbkey=CDS]

MFLTPYKRHAISVLAAVTLLSGCGLTQRVTDGTKEVASAIFYKQIKTLHLDFVSRSALNTDAQDTPLSTM

IHVWQLKTRERFDEAN

>lcl|NZ\_FO834906.1\_prot\_WP\_004181150.1\_941 [gene=tssG] [locus\_tag=BN49\_RS05965] [protein=type VI secretion system baseplate subunit TssG] [protein\_id=WP\_004181150.1] [location=complement(952292..953374)] [gbkey=CDS]

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LTSFEPGAVDNISRCLLGLIGLGIPGSENHIATPVSRFLALLSVMRLPTRTAEGITALVRLLAPQTQATV

IPHDPQQIVLPEPAGLSKRSRICLKTRALLGNTGTDVNSQLLMKLYTEDDGEARGWLPGGQLHTDLLVLL

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ESVTHVSYTL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531437.1\_942 [gene=tssF] [locus\_tag=BN49\_RS05970] [protein=type VI secretion system baseplate subunit TssF] [protein\_id=WP\_016531437.1] [location=complement(953338..955098)] [gbkey=CDS]

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PEVSLLYEQDGRSVIRLRFECSPLAGDGSQIDLSRLPLYLNADSPLACALHRALTLGVQQIWFRLPGEER

RTLDGYFSPMGFGKDDPLWPKGESAFSGYQLLLEYFTFREKFMFVALNGLENVVWPAGMSGFEIDVVLAE

SWSHDLPFSTENIRLHCVPVINLFPLEADPLHLSPLENEYLLRPMRIQDGHTEIYSVDNIISSRHTGSQA

YVPFSSFRHRGGMLRHDSPERYYHTRVKRGPSGLHDTWLILGGDAFDIDRLLEDETLSLSLTGTNGQLPR

KALQSTVLDPPVYATQHTLRVRNLCAPTQPCYPPARDRFHWRVLSHLGSNFLSMMDNAEILRGTLALYDW

TESEMNRRRLEAIVDVQHHLIQRFEKGFLLRGVDIQVTLDSNGFAGEGDITLFGELLHRFFALYADIHLF

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>lcl|NZ\_FO834906.1\_prot\_WP\_223371287.1\_943 [locus\_tag=BN49\_RS05975] [protein=hypothetical protein] [protein\_id=WP\_223371287.1] [location=complement(955255..955866)] [gbkey=CDS]

MNSLKMKGYYFLVVLLLTALCGGGYVMYQQQYRMAVHVTPESENDPEWPSKKKWFDASEWLSTPQYIKIN

DFYVINTRYVPIGDLNSDQIIFYLKKGINGSEKRFSELSVLSDLDNQEFRELMKDKLSSEYLETQFDKET

LTPTIDFFLIYFIFNNKRYEVPIRREYSGNKYHYWVLEGSVKKAGYWHERFPASYSYRKYLNK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528833.1\_944 [locus\_tag=BN49\_RS29920] [protein=hypothetical protein] [protein\_id=WP\_016528833.1] [location=complement(955863..956906)] [gbkey=CDS]

MLVGKLAYSWEKRGGNFGSLKEINERKIELMTAEQEPVENVQWVTGRDYIVVVAARTKFKDSMGNQYRFV

NCGLRQLRLFPEVNKDNYSIQRIFLMFQQGYVEKGIELINEYVEELSGRVVYVKDKAEFIKFLNSRKDKN

RVIKEMVILCHGIIDTASFDYHHENKGKEKTGEFKSRDVVDVQEAVFDYDAVVTTYACRAGISVDGKDLT

GMDAGQENSPAQKMADCWDVSVRAFEMRSDYSSIYGTKKEIRAAENYEDVIEEYEESLSGYNKKKANGDV

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>lcl|NZ\_FO834906.1\_prot\_WP\_009485635.1\_945 [locus\_tag=BN49\_RS05990] [protein=PAAR domain-containing protein] [protein\_id=WP\_009485635.1] [location=complement(957144..957404)] [gbkey=CDS]

MARRLARLGDKTTYGYVASATSSIIDGKKLALNGDRAWCNKCKGMFGIVGTARGWSEDSLFVGNGDRVAC

KCANNQVIATSDLFDE

>lcl|NZ\_FO834906.1\_prot\_WP\_162869795.1\_946 [locus\_tag=BN49\_RS05995] [protein=ImpA domain protein] [protein\_id=WP\_162869795.1] [location=complement(957477..957896)] [gbkey=CDS]

MQKNTGTTQMSELLQQLTRNCFSDRDATAVAQEQAALWQSWLLPVTEDSPVGEDPGYHDDFLLMRDEMNK

STAQGLTLTQWESELLFEVKTRQLKLLRLRAHRHADKAALARKMGNLLGTLVVMDPARAAVLCDTQHKD

>lcl|NZ\_FO834906.1\_prot\_WP\_046042502.1\_947 [locus\_tag=BN49\_RS06000] [protein=type VI secretion protein VasK] [protein\_id=WP\_046042502.1] [location=complement(957862..961227)] [gbkey=CDS]

MKSANNKLTIIADVLLLLLFAAVLGFIIWRFGDLFGLTGDKNKFYIWLAGIMSFIFLRASWYFSRLYRVR

RERRQSEEQGEYPEKEIRYEPGQRTSLYSELFFHLRDRYGLFWQRQVRLLLVTGEPEQVEAIAPGLTEQR

WQEGDHTVLIYGGKASAEPDTTLLASLKKLRRFRPLDGIIWPLTEKQSTQTAQLDKGWRELGNGGKLLGF

QAPLYLWQVCDDGGYQAGRTLQSVGCLLPERSTPEQLATQLEAQTPQLTEQGMSQLLTNNRHDFLLRLAH

TLTERGIAHWQTVLKPLLAGGAFPSLHLRGLMFSPPLAAVPEAAPHAWLSSLVWAGVTGDNAKGRTVGFP

WLRTALMACFCVLAIWWTGMMTSFFANRALIQETGTHTARAINTRLPLAEQLVALHTLQGELERLQYRIR

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VATARREEIDWVLSDRQQDASADISPEALRTRLMERYFTDFAGSWLTFLNSIRWKKEDSLSGVLDQLTLM

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TNDWFSFYTLLIDENDIFNLPVRIAKEFIILTDCNEREYTRMEADFSRVLAEMNIMLPSGSIRLVPSLLF

EQLDAWLKVTEEKIYIVLVLQLNGKENYSDGIVSFLFAADDVVKKYQLDEKARIFRPMVVVADRFDKDLD

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530473.1\_949 [locus\_tag=BN49\_RS06010] [protein=hypothetical protein] [protein\_id=WP\_016530473.1] [location=complement(962669..963040)] [gbkey=CDS]

MLKSLLTGLFFIYFLAGNAYAEDYNDIFWGMLKKENQEIVFVRCDSPPLKMKIVRTADANQENIEKAYQT

FNQSKGQSMYFAFIGNVKDTGNGNYVFNMYDVMETKTGRCNLTDALNNWNVSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_009485630.1\_950 [locus\_tag=BN49\_RS06015] [protein=hypothetical protein] [protein\_id=WP\_009485630.1] [location=complement(963149..964222)] [gbkey=CDS]

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TGYWYEGSLTYYYEESLYGPLALPMQLPLYELDHSVYLREGDPVTIDGLYLPDLLDAGARLMYLRENIPD

AWQGRVRTQYVNDVGQQEYYWEEGAWTKTNWIRIRRVKNRFINVPLEGFFPRGTPEELYNWPQRQQQYIT

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VWVSEAG

>lcl|NZ\_FO834906.1\_prot\_WP\_032104126.1\_951 [locus\_tag=BN49\_RS06020] [protein=hypothetical protein] [protein\_id=WP\_032104126.1] [location=complement(964262..965713)] [gbkey=CDS]

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SIRQPIETTWKLLVSIRSQANTMLEKALAPLNETLEKLAARLRQEGDNYYKAHTGANPHRPTRLKDAEEA

ELLVHNKPDWVDVGVTEKYPGLKQASAEQKSLMRLEKDKEGWPALSEDNIKSFHQMRYVELPQNEKLYRV

LDPASSDNSFCWMREAEFMALKSKSQWRRRFAVWKSWNENGEYVVYTVPPGTTMKVWEGPAASQSRSVTD

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GQDFVFNLKSDYPSREQVMQYDEDDLTFISRLLSEVGIWFRFSTDARLKIGVIEFYDDQSGYERGLTLPL

RHPSGMSDSGTEAVWGLNTAYSVVSRSVTTRDYNYREAMAEMTTGQFDVTGGDNTTYGEAYHYADNFLKT

GDKATPESGAFYARIRHERYLNGRAILKGQSTSSLLMPGLEIKVEGNDAPEVFRKGILITGITASAARDR

SYELTFTAIPYSERYGYRPPLIRRPVMAGTLPARVTSTTANDVYAHIDKDGRYRVNLDFDRDTWKPGFES

LWVRQSRPYAGDTYGLHLPLLAGTEVSIAFEDGNPDRPYIAGVKHDSAHTDHVTIQNYKRNVLRTPANNK

IRLDDERGKEHIKVSTEYGGKSQLNLGHLVDAGKQQRGEGFELRTDMWGAIRAKKGVFISADAQEKAQGQ

VLDMQAAITQLENALSIAKSLSQAAEVAKAHGADLDGHTSLNGALSELVKAGIVLSAPEGVGIVSPQGVR

LGSGESSIGLMAGTNIDAGAMEKVTVSAGDAVSVFARKGGIKLYANQGKVEVEAQNERMRLTSRHGMKIS

STEDVVEIEAEKELVLKCGKAYIRLSGGGVEVGGPKNILLKSANVQKMSKAQLPVEMPVLPGKGNYDLSL

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VHLDMAVLAGRLRRFVGGLATVRRRAGIKVPLLLWSWLPGTGREDDLPWFICAGGKVQVVTPAGESSPTA

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YDAVPADNDAAKAHHLSVLKDDANILDSYFREGEPLRLSLGLYPGERLRQPVWRVIRDYRPPEKKRDVAD

ALPVQSVRLDSMALFDVGQARLKDGSTKVLINALVNIRARPGWLIVVTGYTDTTGNKKANQQLSLRRAEA

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PQGVSAI

>lcl|NZ\_FO834906.1\_prot\_WP\_004181140.1\_954 [gene=tssL] [locus\_tag=BN49\_RS06035] [protein=type VI secretion system protein TssL, short form] [protein\_id=WP\_004181140.1] [location=complement(970193..970858)] [gbkey=CDS]

MTQERKIDIDVLLRDTFLTVVELRQGTSARHGQELYRHCLQQVEGVRERLTAAGFSQQDIEHITYAQCAL

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EEMAVECHALSLRFAHDNNQDYITCPLARLTRNGQGNWSQDESYIPPLLALSAHIGLVERLDTLLLQLQA

KCRRLMALRRESNQRMADFAVADVSLFWLLNALNSAEPVLSDFLRYPSIHPELVWRELARLAGALLTFSL

EHNVSAIPAYVHDAPASVFPPLFTLLSELLEASLPSRVIALELESLPGNRWKAELHDPRLREEADFYLSV

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IGKVLIDRGEVKKEDMSMQAIREWGEKHSEAEVRELLEQNPSFVFFKPQSFAPVKGASAVPLIGRASVAS

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MSVVISDAWRQRFGGTARLYGEKALRCFADAHVCVVGIGGVGSWAAEALARTGIGAITLIDMDDVCVTNT

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RER

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MNKVVLYCRPGFEKECAAEITDKAARLEVFGFARVKEDSGYVIFEGYQQDDGEKLVRDLPFSSLIFARQM

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MKAARQQAIVDLLITHSSLTTETLSKQLNVSRETIRRDLSELQAQGKVLRNHGRAKVIHQRSQDSGDPFH

MRLKSHYAHKADIAREALAWIDEGMVIALDASSTCWYLARQLPDRPLHVFTNSQPICQELAKRDQITLTC

SGGTLQRKYGCYVNPALISQLKSLEIDLFIFSCEGIDPQGALWDSNAFNADFKSILLKRAAQSLLLIDKS

KFNRSGEARIGHLDDVTHIVSDAPQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002915538.1\_966 [gene=fucU] [locus\_tag=BN49\_RS06105] [protein=L-fucose mutarotase] [protein\_id=WP\_002915538.1] [location=complement(981790..982212)] [gbkey=CDS]

MLKTISPLISPELLKVLAEMGHGDEIIFSDAHFPAHSMGPQVIRADGLRVSDLLQAIIPLFELDSYAPPV

VMMAAVEGDALDPTVEQRYRQALSAQAPCPDIVRIDRFAFYDRAQKAFAIVITGECAKYGNILLKKGVTP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531483.1\_967 [gene=fucK] [locus\_tag=BN49\_RS06110] [protein=L-fuculokinase] [protein\_id=WP\_016531483.1] [location=complement(982214..983632)] [gbkey=CDS]

MKQDVILVLDCGATNVRAMAVDRQGKIIARAAMANASDIAAEKSDWHQWSLEAIMQRFADCCRQIHDQLA

SCTVRGITVTTFGVDGALVDEQGALLYPIISWKCPRTAAVMENISQYMPARQLQQIAGVGAFAFNTLYKL

VWLKENHPQLLAQAHAWLFISSLINHRLTGEFTTDLTMAGTSQMLDLRQRDFSAPILQATGLPRRLFPRL

VEAGQPIGALLPEAAALLGLPVGIPVISAGHDTQFALFGAGAGQDEPVLSSGTWEILMVRSAQVDTSLLC

DYSGSTCELDSQPGRYNPGMQWLASGVLEWVRKLLWSADTPWQTLIDEAQAIPPGAQGVRMQCDLLASQH

AGWQGVTLNTTRGHFYRAALEGLSDQLAQHLQTLEKIGGFRAKELLLVGGGSRNALWNQIKANRLGIPIK

VLDDAETTVAGAAMFGWYGVGEFSSPEQARAQVAYRYRYFWPQTEPELIEEA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531482.1\_968 [gene=fucI] [locus\_tag=BN49\_RS06115] [protein=L-fucose isomerase] [protein\_id=WP\_016531482.1] [location=complement(983740..985515)] [gbkey=CDS]

MKKISLPKIGIRPVIDGRRMGVRESLEAQTMNMAKATAALISEKLRHACGARVECVIADTCIAGMAESAA

CEEKFSSQNVGVTITVTPCWCYGSETIDMDPLRPKAIWGFNGTERPGAVYLAAALAAHSQKGIPAFSIYG

HDVQDADDTSIPADVEEKLLRFARAGLAVASMKGKSYLSLGGVSMGIAGSIVDHNFFESWLGMKVQAVDM

TELRRRIDQKIYDETELEMALAWADKHFRYGEDQNAEQYKRNETQSRAVLKESLLMAMCIRDMMQGNPKL

AEKGLVEESLGYNAIAAGFQGQRHWTDQYPNGDTAEALLNSSFDWNGVREPFVVATENDSLNGVAMLMGH

QLTGTAQVFADVRTYWSPDAVERVTGQPLTGRAEHGIIHLINSGSAALDGSCQQRDAQGNPTMKPHWEIE

QNEADACLAATEWCPAIHEYFRGGGFSSRFLTEGGVPFTMTRVNIIKGLGPVLQIAEGWSVALPKAMHDQ

LDARTNSTWPTTWFAPRLTGKGPFSDVYSVMANWGANHGVLTIGHVGADFITLAAMLRIPVCMHNVEEAK

IYRPSAWAAHGMDIEGQDYRACQNYGPLYKR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042523.1\_969 [gene=fucP] [locus\_tag=BN49\_RS06120] [protein=L-fucose:H+ symporter permease] [protein\_id=WP\_046042523.1] [location=complement(985548..986858)] [gbkey=CDS]

MGNTTIPTQSYRAMESGQSKSYIIPFALLCSLFFLWAVANNLNDILLPQFQQAFTLTNFQAGLIQSAFYF

GYFIIPIPAGMLMKKFSYKAGILTGLFLYACGAALFWPAAEVMNYTLFLIGLFIIAAGLGCLETAANPFV

TVLGPESGGHFRLNLAQTFNSFGAIIAVVFGQSLILSNVPHQPQEVLDKMTPEQLSAWKHCLVLSVQTPY

MIIVAIVLLVALLIVCTRFPSLQSDDHSDSAQSTFFASLTRLMRIRHWRWAVLAQFCYVGAQTACWSYLI

RYAIEEIPGMTAGFAANYLTATMVCFFIGRFTGTWLIRRFAPHNVLAIYAFIAMLLCLLSAFSGGHVGLL

ALTLCSAFMSIQYPTIFSLGIKHLGQDTKYGSSFIVMTIIGGGIVTPVMGFVSDAAGNIPTAELVPALCF

AIIFIFASFRSQAATN

>lcl|NZ\_FO834906.1\_prot\_WP\_002915470.1\_970 [gene=fucA] [locus\_tag=BN49\_RS06130] [protein=L-fuculose-phosphate aldolase] [protein\_id=WP\_002915470.1] [location=987425..988072] [gbkey=CDS]

MERNRLARQIIDTCLEMTRLGLNQGTAGNVSVRYQGGMLITPTGIPYEKLTEDKIVFIDADGQHEQGKLP

SSEWRFHQAAYQTRPDAQAVVHNHAVHCTAVSILNRPIPAIHYMIAAAGGNSIPCAPYATFGTRELSEHV

AVALKHRKATLLQHHGLIACEASLEKALWLAHEVEVLAQLYLSTLAITDPVPVLDDEAIAIVLEKFKTYG

LRIEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530415.1\_971 [gene=fucO] [locus\_tag=BN49\_RS06135] [protein=lactaldehyde reductase] [protein\_id=WP\_016530415.1] [location=988100..989248] [gbkey=CDS]

MANRMILNETAWFGRGAINALTDEAVRRGYRKVLIVTDSTLARCGVAAKVTDKLDAAGLAWDIFSDVIPN

PTIAVVQQGLQAFQRSGADYLIAIGGGSPQDTCKAIGIIQRNPEFANVRSLEGLSPTRQPSVPIFAVPTT

AGTAAEVTINYVITDEEQRRKFVCVDPHDIPQVAFIDADMMDAMPPALKAATGVDALTHAIEGYLTRGAW

ALTDALHLKAIEIIAGALRGSVAGDAGAGEAMALGQYVAGMGFSNVGLGLVHGMAHPLGAFYNTPHGVAN

AILLPHVMRFNAEATGEKYRDIARAMGVRVEALSLTAAREAAVEAVCQLNRDVGIPGHLREVGVRKEDIP

ALAQAALADVCTGGNPREASLADIVGLYQAAW

>lcl|NZ\_FO834906.1\_prot\_WP\_004142871.1\_972 [gene=xni] [locus\_tag=BN49\_RS06140] [protein=flap endonuclease Xni] [protein\_id=WP\_004142871.1] [location=complement(989307..990062)] [gbkey=CDS]

MAVHLLIVDALNLIRRIHAVQGSPCVDTCLHALEQLIVHSQPTHAVAVFDDEDRAHGWRHQRLPEYKAGR

APMPETLVAEMPALRAAFEQRGIRCWASPGSEADDLAATLAVKVAQAGHQATIVSTDKGYCQLLSPTIRI

RDYFQKRWLDAPFIASEFGVTPEQLADYWGLAGISSSKVPGVAGIGPKSAAQLLNEFQDLEGLYARLAEV

PEKWRKKLAAHQEMAFTCREVARLQTDLQLDGNLQQLRLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004174618.1\_973 [locus\_tag=BN49\_RS06145] [protein=sigma-54-dependent Fis family transcriptional regulator] [protein\_id=WP\_004174618.1] [location=complement(990159..992102)] [gbkey=CDS]

MLNPESPSTAPALIDPASKAFQSLLDKLAPTEATVLIVGETGTGKEVVARYLHHHSARRQQPFLAVNCGA

LTESLAEAELFGHEKGAFTGAQQGQPGWFEAAEGGTLLLDEIGELSLPLQVKLLRVLQEREITRVGSRKA

IKVNVRVIAATHVDLAQAIRERRFREDLYYRLNIAVVPLPPLRQRRQDIPLLAHHFLSLYARRLGRPTLR

LAPESLARLMDYSWPGNIRELENTLHNAVLLSKEEEISPAQLRLATLNDAPGPASDHELDDFIRHQLALP

GEPLWQRVTSALIRHAMAHCDDNQSQAAALLGISRHTLRTQLANLGLIKSRRRPPAPPRAFANAAGADRE

LRIGYQRFGSLGILKARQSLETAFASLGVNVLWSEFPAGPQLLHALACNEIDFGTTGEAPPVFAQASNSE

LMYVAWEPPAPRSVAMVVPQGSDIRQLSDLRGKRIALNKGSNVHWLLLQILEDAGLGLNDVRVVYTPPKY

PLTASDYLAVDAWMMWDPLLSDAEHTGELRVVASGEGRVNNHQFYLSRRDYLAQHGDIMRRLLTELTHTG

QFIDSHRGEAARLLSAELGIDARSLSMALARRSHRPRPMDLSVIRAQQTIADRFYALGLIAKPVPVREAV

WYGEPAPDVIRPLMAVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004219275.1\_974 [locus\_tag=BN49\_RS30885] [protein=hypothetical protein] [protein\_id=WP\_004219275.1] [location=992180..992296] [gbkey=CDS]

MQMRQRMRGGCAICNSAARRSRFQCIDFKRLIFYSPLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915347.1\_975 [gene=ssuD] [locus\_tag=BN49\_RS06155] [protein=FMNH2-dependent alkanesulfonate monooxygenase] [protein\_id=WP\_002915347.1] [location=992374..993546] [gbkey=CDS]

MTQQAPDKINVFWFLPTHGDGRYLGTTEGGRPVDLPYLQQVALAADSLGYYGVLIPTGKSCEDSWLVASA

LAPLTRRLRYLVAVRPGLQPPTLAARMAATLDRLSEGRLLINVVTGGDPVENKGDGIFLSHSERYQVTRE

FLDVYTRLLRGEKVDYHGEHIHVEGAEVLFPPVQENGPPLYFGGSSDAAIDVAAEQIDSYLTWGEPPELV

AEKLAVVRERAAARGRTLQYGIRLHVIVRETEEEAWAAADRLIAHLDDDTIAQAQKIFARMDSAGQARMS

ALHQGSRDNLRIAPNLWAGVGLVRGGAGTALVGNPQQVAERIREYQALGISNFIFSGYPHLEEAHRFAEL

VMPLLPLENGASSKARSVNTGPFGETIGGDKRPVRQVSAS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042538.1\_976 [locus\_tag=BN49\_RS06160] [protein=FAD/NAD(P)-binding protein] [protein\_id=WP\_046042538.1] [location=993593..994990] [gbkey=CDS]

MSAEPHIVIIGGGFSGAAVAIELLRLAPNEVRVTLLEPRQSPGAGVAYSTAEPTHRINVPAARMQLAGDE

EGAFDHWYRHQPAFTVDVQALRPDGSVYPQRGQFGRYVAQRFADAAASSGGRLRHLRDRALAFHQGMVTT

DGGLQLKADLLVLAISHPPPSLPAQAEAWRHHPALIANPWQPGALDAIAPHARVAVMGTGLTMADTVATL

DRLGHRGSIVAFSRHGLLSRGNLSGAGTTWPGDYQQGSLRQRLRQIRLDVAYAAQQGLSWQVVLDAVRQQ

GQRIWQALSVADRQRFLRHLRHYWDVHRYRVAPQVAEVLEARQRTGSLQVQAARLLSISGEGETLRLTLA

RRGGGVQTLSVDHLILTTGPAHRALTDSQPFLQDLARRGLIRADALGMGLEVDSRSRAVAEPHVEALPVL

VAGPAARGRFGELMGLPQVADHAADVAAQALLTLGIPQDSRCPAY

>lcl|NZ\_FO834906.1\_prot\_WP\_002915313.1\_977 [locus\_tag=BN49\_RS06165] [protein=LLM class flavin-dependent oxidoreductase] [protein\_id=WP\_002915313.1] [location=995064..996470] [gbkey=CDS]

MSSQREIRLNAFDMNCVGHQSPGLWAHPRDRSWQYKDLEYWVDLARLLERGKFDGLFIADVLGIYDVLNG

SGDAAIRQATQVPVNDPLALITPMALVTEHLGFGLTASLSFEHPYPFARRLSTLDHLTKGRVGWNIVTSY

LESGARNIGQQTQTDHDTRYDYADEYLQVIYKLLEGSWEDGAVLRDRERKIFSDPRKIHPINHQGQFFSV

PGIHLCEPSPQRTPVLYQAGASSRGKQFAAGHAECVFVAAPSKVLLKKTVADIRRRAAEAGRDPHSILIF

NLQTVIVGDTDREAQAKWQEYKQYVSYEGALALLSGWTGIDFGQYQPDQVLKYLHTNAIQSAVEAFSTAD

PNRQWTVQALADWAGIGGFGPLVVGSAQTVADELQSWVEETDVDGFNLAYAVTHETFRDVVELLVPELQK

RGVFKQEYREGTLREKLFGGGPRLAAPHPGASYRRDARTAASVEEKVT

>lcl|NZ\_FO834906.1\_prot\_WP\_020317275.1\_978 [locus\_tag=BN49\_RS06170] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_020317275.1] [location=996467..997489] [gbkey=CDS]

MIAIDDLHKSYRTADGRLSAVLKGLSLQVPERSITAVVGPSGAGKSTLARCISLLEQPDSGSIRINGQDL

SALSGEALRRERRAIGTVFQSSALLSRRTAWENVALPLAWLGVVERDIKARVGELLESVGLSHKADAWPA

QLSGGQRQRIGIARALALRPSVLLADEATSGLDPQATASVLALLKRLRDEYQLAIVLITHEMDAVRTAAD

AVAEIRDGTIVQYGRIEDLLARPDSLLGQQLLPLTPAAATHSDLLLRLSYRWDVPVATDWISRLSQQWGL

QIDLLGGHVEVINGRLAGRLQAGVRFQGERLSPARLQGLLAQLGITAEILDSAPLLREAV

>lcl|NZ\_FO834906.1\_prot\_WP\_015958893.1\_979 [locus\_tag=BN49\_RS06175] [protein=ABC transporter permease] [protein\_id=WP\_015958893.1] [location=997486..998184] [gbkey=CDS]

MKPTVISQDTPWGEIPSLLLPAYGETWLMVAIVMLFVVTLGGLVGVVLFNASPRGLFPHALLYRLLNWVV

NMGRSLPFLVLMAAIIPFTYWLTGTTIGIPAAVVPMIAAGVPFFGRLVENALRELPAEVTAVGVVCGGSR

WQIIASAQLSEAMPALAAAVTLNLVSMIEYSAIAGTIGAGGIGYLAVVYGYQRFDNHIMIATIVALIATI

QLIQFLGDRLVNRLRHTQGNLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002915265.1\_980 [locus\_tag=BN49\_RS06180] [protein=MetQ/NlpA family ABC transporter substrate-binding protein] [protein\_id=WP\_002915265.1] [location=998181..999059] [gbkey=CDS]

MTTEQFELRKARRWPWLAALAVIILLAIAFWWWRGHTQSQQVVFGSTLKIHYEPAMAGEQRIIEYINQHI

APDYGLKLEAVGVQDPVQADRAVAEGQYAGTIYQHQWWLKQVVDANGFALSTTVPVFQWAFGIYSDRYSS

VQALPNGATIVVPDDGANQGQALWLLQRIGLISLDPAVEPRTAKLKNIVGNPHQFVFKELDLLTMPRALN

SVDAAIGYVSQFDAGKVPREKGILFPPAPRTFASQLVIGTPYLSQENIVKLKQAFSDPRIQTWLKTTDDP

LVKDVLVPVSAE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532411.1\_981 [locus\_tag=BN49\_RS06185] [protein=MFS transporter] [protein\_id=WP\_016532411.1] [location=999253..1000674] [gbkey=CDS]

MSTLPVDNPGIASVPVSSVGDVARLINSGKEQAKYARMIVFLALGGVFLDAYDLTTLSYGIDDVVREFQL

SPLLTGLVTSSIMVGTIVGNIIGGWLTDKYGRYSVFMADMFFFVISAIAAGLAPNVWVLIGARFLMGIGV

GIDLPVAMSYLAEFSRFAGKGNKAARLAAWCPMWYAASTVCFLIIFGLYFLLPQEHLDWLWRASLLFGAV

PALLIIAVRRRFMNESPLWAANQGDLTSAVRILRDSWGIHAHEVPAAKPAPAPKVSFRVLFEKPYRERTI

VAGVMNICISFEYTAIAFFLPSILAQFLGAGVFETISASLGLNALFAFTGGLLGMHLAWKYPSRHVAIAG

FALQFVALIVLALVGQPHATAGIVLAIAMLGLWLFAEGFGPGAQLMIYPALSYPTAIRATGVGFSRALSG

IGSALALFILPLLQASLGTQMFWVVSLAAIIPIFFLLAVRHEPTREDIDALHE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532410.1\_982 [locus\_tag=BN49\_RS06190] [protein=acyl-CoA dehydrogenase family protein] [protein\_id=WP\_016532410.1] [location=1000685..1001908] [gbkey=CDS]

MTLLSTGTDYDALAAAFRPIFTRIAQGAAEREQQRILPDEPIRWLKEAGFGTLRIPREKGGWGASLPQLS

ALLIELAQADSNLPQALRAHFAFVEDQLNQPDSAGRDRWFRRFLDGELVGSGWTEIGAVKLGEVNTRVTP

TEGGWRLDGEKFYSTGALYADWIDVFARRSDTASDVIALVSTQQTGVVREDDWDGFGQRLTGSGTTRFTG

ARVETEHVYDFAQRFRYQTAFYQHVLLATLAGIGLAVERDAAQGVKHRSRMYSHGNAAVPRDDAQVLQVV

GQISSWAWATRAAVLQAAESLQQAYVAHVSDDEALIARRNQLAEVEAAQAQVIASDWIPRAATELFNALG

ASDTRTRLALDRHWRNARTVASHNPVIYKARNIGNWLVKGEAPTFIWQIGNGEKTAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915261.1\_983 [locus\_tag=BN49\_RS06195] [protein=aliphatic sulfonate ABC transporter substrate-binding protein] [protein\_id=WP\_002915261.1] [location=complement(1001954..1002895)] [gbkey=CDS]

MSNRFRPAWLLVLAALSTSALAKAPETVNIGYQKANIFALLKYRGTLDESLKKQGIAVRWVEFPAGPQML

EGLNVGSIDLAATGDAPPAFAQAAQADLVYLAHSPANPKTEAIVVPEQSAIHSVADLKGKRVGLNKGSDV

NYLLVAALEKAGLSYKDITPVYLPPADARAAFQRGAIDAWVIWDPFLAEVETNAKARQIRNAEGLVPHYT

FYLASRKFADTYPETAKQVVDELGKLSAWANSHQDEAAGLLSTSTGLDKAIWLKTLARLPYGAERMTPAV

YNEQQALADTFTRIGLLPVKVDVRSATWSLDKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002915259.1\_984 [locus\_tag=BN49\_RS06200] [protein=L-serine ammonia-lyase] [protein\_id=WP\_002915259.1] [location=complement(1003034..1004401)] [gbkey=CDS]

MISVFDIFKIGIGPSSSHTVGPMKAGKQFTDDLIARGLLAEVSKVVVDVYGSLSLTGKGHHTDIAIIMGL

AGNLPDTVDIDAIPGFIQDVNTHGRLMLANGQHEVDFPVDQCMNFHADNLSLHENGMRITALAGDKVLYS

QTYYSIGGGFIVDEEHFGQTTEAPVAVPYPYKNAADLQRHCRETGLSLSGLMMQNELALHSKEALEQHFA

AVWEVMSAGIERGITTEGVLPGKLRVPRRAAALRRMLVSQDTTNSDPMAVVDWINMFALAVNEENAAGGR

VVTAPTNGACGIVPAVLAYYDKFIRKVNSNSLARYMLVASAIGSLYKMNASISGAEVGCQGEVGVACSMA

AAGLAELLGGSPGQVCIAAEIAMEHNLGLTCDPVAGQVQVPCIERNAIAAVKAVNAARMALRRTSEPRVC

LDKVIETMYETGKDMNAKYRETSRGGLAMKIVACD

>lcl|NZ\_FO834906.1\_prot\_WP\_016531149.1\_985 [locus\_tag=BN49\_RS06205] [protein=HAAAP family serine/threonine permease] [protein\_id=WP\_016531149.1] [location=complement(1004467..1005756)] [gbkey=CDS]

METTQTSTIVSGETRSGWRKTDTMWMLGLYGTAIGAGVLFLPINAGVGGMIPLIIMAILAFPMTFFAHRG

MTRFVLSGKNPGEDITEVVEEHFGVGAGKLITLLYFFAIYPILLVYSVAITNTVETFMAHQLHMTPPPRA

ILSLILIVGMMTIVRFGEQMIVKAMSVLVFPFVIALMVLALYLIPQWNGAALETLSLSGASVTGNGLLMT

LWLAIPVMVFSFNHSPIISSFAVAKREEYGEGAEKKCSSILARAHIMMVLTVMFFVFSCVLSLSPADLAA

AKEQNISILSYLANHFNAPIIAWMAPIIAMIAITKSFLGHYLGAREGFNGMVIKSLRSKGKSIEINKLNK

LTALFMLLTTWIVATLNPSILGMIETLGGPIIAMILFLMPMYAIQKVPAMRKYSGHISNVFVVIMGLIAI

SAIFYSLFS

>lcl|NZ\_FO834906.1\_prot\_WP\_002915258.1\_986 [gene=ppnN] [locus\_tag=BN49\_RS06210] [protein=nucleotide 5'-monophosphate nucleosidase PpnN] [protein\_id=WP\_002915258.1] [location=complement(1006266..1007633)] [gbkey=CDS]

MITHVSPLGSMDMLSQLEVDMLKRTASSDLYQLFRNCSLAVLNSGSLTDNSKELLSRFENFEINVLRRER

GVKLELINPPEDAFVDGRIIRSLQANLFAVLRDILFVYGQIHNTVRFPNLDLESSVHITNLVFSILRNAR

ALHVGEAPNMIVCWGGHSINENEYLYARRVGTQLGLRELNICTGCGPGAMEAPMKGAAVGHAQQRYKDSR

FIGMTEPSIIAAEPPNPLVNELIIMPDIEKRLEAFVRIAHGIIIFPGGVGTAEELLYLLGILMHPDNKAQ

VLPLILTGPKESADYFRVLDEFITHTLGESARRHYRIIIDDPAEVARQMKKAMPLVKESRRETDDAYSFN

WSIRISPDLQMPFDPTHENMANLKLSPDQPVEVLAADLRRAFSGIVAGNVKEVGIQAIEQYGPYKLHGDP

EMMRRMDDLLQGFVAQHRMKLPGGTAYIPCYEIIA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174633.1\_987 [gene=queF] [locus\_tag=BN49\_RS06215] [protein=NADPH-dependent 7-cyano-7-deazaguanine reductase QueF] [protein\_id=WP\_004174633.1] [location=complement(1007745..1008590)] [gbkey=CDS]

MSSYDNHQALAGLTLGKSTDYRDTYDASLLQGVPRSLNRDPLGLHADNLPFHGADIWTLYELSWLNGKGL

PQVAVGHVELPDTSLNLVESKSFKLYLNSFNQTRFASWQDVAETLTRDLSACAQGKVKVSLYRLDELEGQ

PIARLHGTCIDDQDIEIDNYQFSADYLQGAASGKIVEETLVSHLLKSNCLITHQPDWGSVQIQYRGAKID

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Q

>lcl|NZ\_FO834906.1\_prot\_WP\_002915253.1\_988 [gene=syd] [locus\_tag=BN49\_RS06220] [protein=SecY-interacting protein] [protein\_id=WP\_002915253.1] [location=1008659..1009204] [gbkey=CDS]

MDHQTAEALRAFTQRYCAVWQQQRHSLPRSEELYGVPSPCVVDTQGEAVFWQPQPFSLAQNISAVERALD

IVVQQPLHSYYTTQFAGDMSGRFAGETLTLLQTWSEEDFQRVQENLIGHLVVQKRLKLSPTLFIATLESE

LDVISVCNLSGEVVKETLGTAKRITLSPSLAGFLNHLEPVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002915249.1\_989 [locus\_tag=BN49\_RS06225] [protein=YqcC family protein] [protein\_id=WP\_002915249.1] [location=1009836..1010165] [gbkey=CDS]

MTLHDSVRDRLRAIEALLRETEHWQETAPDSSAFASDKPFCLDTLEPLEWLQWVLIPRMHQLLESGQPLP

QNFAVAPYYEMALDQAHPVRESMLAELLLLDALFAGEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915236.1\_990 [gene=truC] [locus\_tag=BN49\_RS06230] [protein=tRNA pseudouridine(65) synthase TruC] [protein\_id=WP\_002915236.1] [location=1010165..1010959] [gbkey=CDS]

MLEIIYQDDWLVAVNKPSGWLVHRSWLDRDEKVVVMQTVRDQIGQHVFTAHRLDRPTSGVLLMGLSSEAG

RLLAQQFEQHQIRKRYHAIVRGWLMEEALLDYPLVEELDRIADKFAREDKGPQPAVTHYRGLATVEMPVA

TGRYPTSRYGLVELEPKTGRKHQLRRHLAHLRHPILGDSKHGDLRQNRSAAEHFGCHRLMLHASELSLTH

PFTGEPLTLRAGFDDVWMRALSQFGWRGLLPLNERVEFADDSGQDEENKVNPGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915235.1\_991 [locus\_tag=BN49\_RS06235] [protein=flavodoxin] [protein\_id=WP\_002915235.1] [location=1010964..1011407] [gbkey=CDS]

MAEVGIFVGTMYGNSLLVAEEAEAILSGLGHKATVYEDPQVNDWESYTGKYVLVVTSTTGQGDLPDSIVP

LYEGIKDMYQPHLRYGIIALGDSTYANFCGGGLKFDQLLQEQGAKRIGEMLKIDASEDPEPESVSNPWVE

QWATLLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002915225.1\_992 [locus\_tag=BN49\_RS06240] [protein=MFS transporter] [protein\_id=WP\_002915225.1] [location=1011879..1013231] [gbkey=CDS]

MSSLSQAATAAEKRTNARYWIVVMLFIVTSFNYGDRATLSIAGSEMARDIGLDPVGMGYVFSAFSWAYVI

GQIPGGWLLDRFGSKRVYFWSIFIWSMFTLLQGFVDIFSGFGIIVALFTLRFLVGLAESPSFPGNSRIVA

AWFPAQERGTAVSIFNSAQYFATVIFAPIMGWLTHEVGWSHVFFFMGGLGIVISFVWLKVIHDPNNHPGV

NQKELDYIAEGGALINMDQKSSAQKVPFSVKMGQIKQLIGSRMMIGIYIGQYCINALTYFFITWFPVYLV

QARGMSILKAGFVASIPAVCGFVGGVLGGVISDWLMRRTGSLNIARKTPIVLGMLLSMTMLMCNYVNVEW

MVIGFMAMAFFGKGIGALGWAVMADTAPKEISGLSGGLFNMFGNISGIVTPIAIGYIVGTTGSFNGALIY

VGIHALVAVLSYLVLVGDIKRIELKPVAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531146.1\_993 [locus\_tag=BN49\_RS06245] [protein=glucarate dehydratase family protein] [protein\_id=WP\_016531146.1] [location=1013234..1014574] [gbkey=CDS]

MTTQSSPIITEMKVIPVAGHDSMLLNIGGAHNAWFTRNIVVLTDNAGHTGVGEAPGGEVIYQTLLAAIPQ

VVGQEVARLNRVVQQVHKGNQATDFDTFGKGAWTFELKVNAVAALEAALLDLLGQVLNVPVCELLGPGKQ

RDAVTVLGYLFYIGDRQKTDLGYLDHTPGDHEWYRLRHQQALSSEAVVRLAEAAQDRYGFKDFKLKGGVL

PGEQEIDTARALKKRFPDARITVDPNGAWLLDEAIALCKGLQDVLTYAEDPCGAEQGFSGREVMAEFRRA

TGLPVATNMIATNWREMGHAVMLNAVDIPLADPHFWTLSGAVRVAQLCDDWGLTWGCHSNNHFDISLAMF

THVGAAAPGNPTAIDTHWIWQEGDARLTKNPLQIINGSIAVPDAPGLGVELDWEQVRRAHEAYKALPGGA

RNDAGPMQYLIPGWTFDRKRPVFGRH

>lcl|NZ\_FO834906.1\_prot\_WP\_002915223.1\_994 [gene=gudD] [locus\_tag=BN49\_RS06250] [protein=glucarate dehydratase] [protein\_id=WP\_002915223.1] [location=1014592..1015932] [gbkey=CDS]

MTTFSSTPVVTTMQVIPVAGHDSMLMNLSGAHAPYFTRNIVIIKDNAGHTGVGEIPGGEKIRQTLEDAIP

LVVGKTLGEYKNVLGAVRNQFADRDAGGRGLQTFDLRTTIHVVTGIEAALLDLLGQHLGVNVASLLGDGQ

QRSEVEMLGYLFFVGNRHATPLAYQSQPDEQCEWYRLRHEEAMTPDAVVRLAEAAYEKYGFNDFKLKGGV

LAGFEEAEAISALAKRFPNARVTLDPNGAWLLEEAIQIGKQLKGVLAYAEDPCGAEQGFSGREVMAEFRR

ATGLPTATNMIATDWRQMGHTLSLQSVDIPLADPHFWTMQGSVRVAQMCHEFGLTWGSHSNNHFDVSLAM

FTHVAAAAPGKITAIDTHWIWQEGNQRLTKQPFEIKGGMVQVPSTPGLGVELDMDRVMQANELYKKHGLG

ARDDAMAMQYLIPGWTFDNKRPCMVR

>lcl|NZ\_FO834906.1\_prot\_WP\_004210599.1\_995 [locus\_tag=BN49\_RS06255] [protein=glycerate kinase] [protein\_id=WP\_004210599.1] [location=1016005..1017144] [gbkey=CDS]

MKIVIAPDSWKESLSALEVASAIEQGFREIYPDAEYVKLPVADGGEGTVEAMVAATGGLLVPLTVTGPLG

EPVEAFYGLSGDRQCAFIEMAAASGLESVPPAQRNPLLTTSWGTGELIRHALDAGVRQIIIGIGGSATND

GGAGMAQALGAKLLTAEGQQIASGGGALETLALIDLSELDSRLADCRIDVACDVTNPLTGPQGASAVFGP

QKGATAQMIDRLDSGLRHYARIIARDLDIDVLSLEGGGAAGGMGAALYAFCGAQLRPGIEIVTDALQLAE

RVADADLVITGEGRIDSQTIHGKVPVGVARVAKRFNVPVIGIAGSLTADVGVVHQHGLDAVFSVLYTICT

LDEALANAAANLRMTARNVAAVLQMGDRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151066.1\_996 [gene=barA] [locus\_tag=BN49\_RS06260] [protein=two-component sensor histidine kinase BarA] [protein\_id=WP\_004151066.1] [location=complement(1017302..1020052)] [gbkey=CDS]

MTNYSLRARMMILILAPTVLIGLLLSIFFVAHRYNDLQRQLEDAGASIIEPLAVSSEYGMNLQNRESIGQ

LISVLHRRHSEIVRAISVYDSHNRLFVTSNYQLNPSELQIPKGEAFPRHLSVIRDGDMMILRTPIVSESY

SPDESPESDAKMPGNMLGYVALELDLKSVRLQQYKEIFISSVMMLFCIGIALIFGWRLMRDVTGPIRNMV

NTVDRIRRGQLDSRVEGFMLGELDMLKNGINSMAMSLAAYHEEMQHNVDQATSDLRETLEQMEIQNVELD

LAKKRAQEAARIKSEFLANMSHELRTPLNGVIGFTRLTLKTDLNATQRDHLTTIERSANNLLAIINDVLD

FSKLEAGKLILESIPFLLRTSLDEVVTLLAHSAHDKGLELTLNIKNNVPDNVIGDPLRLQQIVTNLVGNA

IKFTEHGNIDVLVEQRAISNSRVQIEIQIHDTGIGIPERDQSRLFQAFRQADASISRRHGGTGLGLVITQ

RLVKEMGGDISFHSQPNRGSTFWFHISLDLNPNAIPDTLNTDGLVGKRLAYVEANATAAQCTLEMLAATP

LEVIYSPTFSSLAEAQYDILLVGIPVSMRDLSPHREKLAKACAMSDNVLLALPCHAQVSAEALKRDGVAA

CLLKPLTTTRLLPALVATSHALASAPLMQIDSHKLPMTVMAVDDNPANLKLIGALLDDLVQQVILCDSGQ

QAVDKAKQLQMDLILMDIQMPDMDGIRACELIHHLSHHQQTPVIAVTAHALEGQREKLLSAGMNDYLAKP

IEEEKLHALLLRYQPGLHSVVPASLPPAEPIVDHNQTLDWQLALRQAAMKPDLAREMLQMLIAFMPEVRN

KVEEQLVGEQPEGLVDLIHKLHGSCSYSGVPRLKKLCHTLESQLRAGTAAEDLEPELLELLDEMDNVARE

ACRMGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002915220.1\_997 [gene=rlmD] [locus\_tag=BN49\_RS06265] [protein=23S rRNA (uracil(1939)-C(5))-methyltransferase RlmD] [protein\_id=WP\_002915220.1] [location=1020166..1021470] [gbkey=CDS]

MAQFYSAKRRVTTRQIITVTVNDLDPFGQGVARHQGKALFVSGVLPHEQAEVALVEDKKQYARAEVKRRL

TDSPQRQAPRCPHFGVCGGCQQQHASVPLQQQSKRAALGRLMKREVDDVIAGAPWGYRRRARLSLNYQPK

TQQLQMGFRQANAKAIVDVVQCPVLVPQLEALLPAVRECLSALSALRHLGHVELVQADNGPLMVLRHTAA

LPATDREKLERFSQTHGLSLYLAPQSEILEHIHGEAPWYTSDGLRLVFSPRDFIQVNDGVNQQMVRTALE

WLDLRPEDRVLDLFCGMGNFTLPLATRAAHVVGVEGVPALVEKGRENAARNGLSNVTFFHENLEEDVTRQ

AWAKHGFDKVLLDPARAGAPGVMPHIIKLAPRRVVYVSCNPATLARDSETLLQAGYQIQRLAMLDMFPHT

GHLESMVLFERRLT

>lcl|NZ\_FO834906.1\_prot\_WP\_002915217.1\_998 [gene=relA] [locus\_tag=BN49\_RS06270] [protein=GTP diphosphokinase] [protein\_id=WP\_002915217.1] [location=1021592..1023829] [gbkey=CDS]

MVAVRSAHLNKAGEFDPKKWIASLGISSQQSCERLAETWDYCREKTQGHPQADLLLWRGVEMVEILSTLS

MDIDTLRAALLFPLADGEVVSEEVMQESVGKSVVTLIHGVRDMAAIRQLKATHTDSVSSEQVDNIRRMLL

AMVDDFRCVVIKLAERIAHLREVKDAPEDERVLAAKECTNIYAPLANRLGIGQLKWELEDYCFRYLHPAE

YKRIAKLLHERRIDREHYIEEFVGHLRSEMKAEGVKAEVYGRPKHIYSIWRKMQKKHLAFDELFDVRAVR

IVAERLQDCYAALGIVHTHYRHLPDEFDDYVANPKPNGYQSIHTVVLGPSGKTVEIQIRTRQMHEDAELG

VAAHWKYKEGAGAGTSGGRGYEDRIAWLRKLIAWQEEMADSGEMLDEVRSQVFDDRVYVFTPKGDVVDLP

AGSTPLDFAYHIHSDVGHRCIGAKIGGRIVPFTYQLQMGDQIEIITQKQPNPSRDWLNPNLGYVTTSRGR

SKIHAWFRKQDRDKNILAGRQILDDELEHLGISLKDAEKHLLPRYNFNELDELLAAIGGGDIRLNQMVNF

LQAQFNKPSAAEQDAAALKQLQQKTYTPQNRTKDNGRVVVEGVGNLMHHIARCCQPIPGDEIVGFITQGR

GISVHRADCDQLAELQSHAPERIVDAVWGESYSAGYSLVVRVEANDRSGLLRDITTILANEKVNVLGVAS

RSDTRQQLATIDMTIEIYNLQVLGRVLGKLNQVPDVIDARRLHGG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529010.1\_999 [gene=mazG] [locus\_tag=BN49\_RS06275] [protein=nucleoside triphosphate pyrophosphohydrolase] [protein\_id=WP\_016529010.1] [location=1023941..1024732] [gbkey=CDS]

MTQIDRLLGIMRRLRDPENGCPWDKEQTFATIAPYTLEETYEVLDAIQREDFDDLRGELGDLLFQVVFYA

QMAQEEGRFNFDDICAAISDKLERRHPHIFGEASAGNSTEVLARWEQIKSAERAEKAQHSALDDIPHSLP

ALMRAHKIQRRCSAVDFDWTSLGPVLDKVHEEIDEVMHEAQQAVVDEAKLEEEVGDLLFATVNLSRHLGV

KAEVALQKANLKFERRFREVERIVAARGLEMTGVDLDTMEEVWQEVKRQETDL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529009.1\_1000 [gene=pyrG] [locus\_tag=BN49\_RS06280] [protein=CTP synthase (glutamine hydrolyzing)] [protein\_id=WP\_016529009.1] [location=1025013..1026650] [gbkey=CDS]

MTTNYIFVTGGVVSSLGKGIAAASLAAILEARGLNVTIMKLDPYINVDPGTMSPIQHGEVFVTEDGAETD

LDLGHYERFIRTKMTRRNNFTTGRIYSDVLRKERRGDYLGATVQVIPHITNAIKERVLAGGEGHDVVLVE

IGGTVGDIESLPFLEAIRQMAVEIGREHTLFMHLTLVPYMAAAGEVKTKPTQHSVKELLSIGIQPDILIC

RSDRAVPANERAKIALFCNVPEKAVISLKDVDSIYKIPGLLKSQGLDDYICKRFSLTCPEANLAEWEQVI

YEEANPAGEVTIGMVGKYIELPDAYKSVIEALKHGGLKNRVTVNIKLIDSQDVETRGVEILKDLDAILIP

GGFGYRGVEGKIATARYARENNIPYLGICLGMQVALIEFARNVAGMENANSTEFVPDCTYPVVALITEWR

DEDGNVEVRSEKSDLGGTMRLGAQQCQLSDDSLVRQLYGEPTITERHRHRYEVNNMLLKPIEAAGLRVAG

RSGDDQLVEIIEVPNHPWFVACQFHPEFTSTPRDGHPLFAGFVKAASEYQKRQAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002915213.1\_1001 [gene=eno] [locus\_tag=BN49\_RS06285] [protein=phosphopyruvate hydratase] [protein\_id=WP\_002915213.1] [location=1026732..1028030] [gbkey=CDS]

MSKIVKVIGREIIDSRGNPTVEAEVHLEGGFVGMAAAPSGASTGSREALELRDGDKSRFLGKGVTKAVAA

VNGPIAQAILGKDAKDQAGIDKIMIDLDGTENKSNFGANAILAVSLANAKAAAASKGLPLYAHIAELNGT

PGKYSMPVPMMNIINGGEHADNNVDIQEFMIQPVGAPTLKEAVRMGSEVFHHLAKVLKSKGMNTAVGDEG

GYAPNLGSNAEALAVIAEAVKAAGYELGKDITLAMDCAASEFYKDGKYVLAGEGNKAFTSEEFTHFLEEL

TKQYPIVSIEDGLDESDWEGFAYQTKVLGDKIQLVGDDLFVTNTKILKEGIEKGIANSILIKFNQIGSLT

ETLAAIKMAKDAGYTAVISHRSGETEDATIADLAVGTAAGQIKTGSMSRSDRVAKYNQLIRIEEALGEQA

PFNGRKEIKGQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174640.1\_1002 [locus\_tag=BN49\_RS06290] [protein=SDR family oxidoreductase] [protein\_id=WP\_004174640.1] [location=complement(1028094..1029203)] [gbkey=CDS]

MTTLLITGVTGFLGGAALEKILHQETRLDLLLLVRADSPEAGLERVKENMRKFNIAEEKLAMLRQQHILL

GDLASPEHFLNDPRLEQVTHVLNCAAVASFGSNPLIWKVNVEGTLRLAQRMAQVTGLQRFLHVGTAMSCS

PEPDSLVAESAEFRERAEHLVEYTHSKSTIEQLMQQQCPTLPLVIARPSIVVGHTHHGCRPSSSIFWVFS

MGLMLQKFMCSMEDRIDVIPVDYCADALLMLLNQPLAHGEVVHISAGEENSVKFAEIDRAMAQALEQAPV

GDKYAQVSYETLVKMRRELKGIFGPCNERLMLKAMRLYGAFATLNVRFSNDKLLSMGMPKPPRFTDYIDR

CVETTRGLSIPQQMAVDFK

>lcl|NZ\_FO834906.1\_prot\_WP\_002915210.1\_1003 [gene=queE] [locus\_tag=BN49\_RS06300] [protein=7-carboxy-7-deazaguanine synthase QueE] [protein\_id=WP\_002915210.1] [location=1029678..1030349] [gbkey=CDS]

MQYPINEMFQTLQGEGYFTGVPAIFIRLQGCPVGCAWCDTKHTWDKLADREVSLFSILAKTKESDKWGPA

SSEDLLAIIGRQGWTARHVVITGGEPCIHDLTPLTSLLEQNGFSCQIETSGTHEVRCSPNTWVTVSPKVN

MRGGYDVLSQALQRADEIKHPVGRVRDIEALDELLETLSDDKPRIIALQPISQKEDATRLCIDTCIARNW

RLSMQTHKYLNIA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174641.1\_1004 [gene=queD] [locus\_tag=BN49\_RS06305] [protein=6-carboxytetrahydropterin synthase QueD] [protein\_id=WP\_004174641.1] [location=complement(1030390..1030755)] [gbkey=CDS]

MMSTTLFKDFTFEAAHHLPHVPEGHKCGRLHGHSFMVRLEITGEVDPHTGWIMDFAELKAAFKPTYDRLD

HYYLNDIPGLENPTSEVLAKWIWDEMKPRVPLLSAVMVKETCTAGCVYRGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004174642.1\_1005 [gene=cysJ] [locus\_tag=BN49\_RS06315] [protein=NADPH-dependent assimilatory sulfite reductase flavoprotein subunit] [protein\_id=WP\_004174642.1] [location=1031072..1032871] [gbkey=CDS]

MTTQAPPSNLLPLNPEQLARLQAATTDFTPTQLAWVSGYFWGVLNQQSGTAVAAPAPAAEVPTITLISAS

QTGNARRVAEALRDDLLAAKLNVKLVNAGDYKFKQIAAEKLLVVVTSTQGEGEPPEEAVALHKFLFSKKA

PKLDGTAFAVFGLGDTSYEFFCQSGKDFDNKLAELGAERLLDRVDADVEYQAAAAEWRARVVEALKARAP

VAAPAQLATSGAVNDIHTSPYTKEAPLTATLSVNQKITGRNSEKDVRHIEIDLGDSGLRYQPGDALGVWY

QNDPQLVKELVELLWLKGDEPVTVEGKTLPLSEALQWHFELTVNTATIVENYATLTRSESLLPLVGDKAQ

LQQYAAATPIVDMVRFSPAQLDAEALIGLLRPLTPRLYSIASSQAEVESEVHVTVGVVRYEIEGRARAGG

ASSFLADRVEEDGEVRVFIEHNDNFRLPANPETPVIMIGPGTGIAPFRAFMQQRAADGAQGKNWLFFGNP

HFTEDFLYQVEWQSYVKEGLLTRIDLAWSRDQQQKIYVQDKLREQGAELWRWINDGAHIYVCGDANRMAK

DVENTLLEVIAEYGAMDAEAADEFLSELRVERRYQRDVY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529008.1\_1006 [gene=cysI] [locus\_tag=BN49\_RS06320] [protein=assimilatory sulfite reductase (NADPH) hemoprotein subunit] [protein\_id=WP\_016529008.1] [location=1032871..1034583] [gbkey=CDS]

MSEKHPGPLVVEGKLSDAERMKLESNYLRGTIAEDLNDGLTGGFKGDNFLLIRFHGMYQQDDRDIRAERA

AQKLEPRHAMLLRCRLPGGVITTTQWKAIDKFAAENTIYGSIRLTNRQTFQFHGILKKNVKPVHQMLHSV

GLDALATANDMNRNVLCTSNPYESQLHAEAYEWAKKISEHLLPRTRAYAEIWLDQKKVATTDEEPILGQT

YLPRKFKTTVVIPPQNDIDLHANDMNFVAIAENGKLVGFNLLVGGGLSIEHGNKKTYARTASEFGYLPLE

HTLAVAEAVVTTQRDWGNRTDRKNAKTKYTLERVGVETFKAEVERRAGIKFEPIRPYEFTGRGDRIGWVK

GIDDKWHLTLFIENGRILDYPGRPLKTGLLEIAKVHQGEFRITANQNLIVASVPEDQKARIEKLARDHGL

MNAVTPQRENSMACVSFPTCPLAMAEAERFLPSFIDKVEGVMSKHGVSDEHIVTRVTGCPNGCGRAMLAE

VGLVGKAPGRYNLHIGGNRNGTRIPRMYRENITESEILDSLDEPVGRWAKEREAGEGFGDFTVRAGIIRP

VLDPARDFWE

>lcl|NZ\_FO834906.1\_prot\_WP\_002915177.1\_1007 [gene=cysH] [locus\_tag=BN49\_RS06325] [protein=phosphoadenosine phosphosulfate reductase] [protein\_id=WP\_002915177.1] [location=1034682..1035416] [gbkey=CDS]

MSVLDLNALNALPKVERILALAETNAQLEKLDAEGRVAWALENLPGNYVLSSSFGIQAAVSLHLVNQIRP

DIPVILTDTGYLFPETYQFIDELTDKLKLNLKVYRAAESAAWQEARYGKLWEQGVEGIEKYNEINKVEPM

NRALKELNAQTWFAGLRREQSGSRATLPVLAVQRGVFKVLPIIDWDNRTVYQYLQKHGLKYHPLWDQGYL

SVGDTHTTRKWEPGMAEEETRFFGLKRECGLHEG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529007.1\_1008 [locus\_tag=BN49\_RS06330] [protein=CRISPR-associated helicase/endonuclease Cas3] [protein\_id=WP\_016529007.1] [location=1035623..1038286] [gbkey=CDS]

MSIYNYWGKTRQGEPGGGDDYHLLCWHSLDVAAMGYWMVKRDIYGLAGYFRRLGINDIENAAQFFAWLLC

WHDIGKFSRSFQQLYTHDNLCVQKDSRNTYEKISHASLGYWLWNSHFSDCPELFPNSSLSIRKLKRVITL

WMPLTTGHHGRPPVGMRALDNFHPSDIKAAHDFLLAIKSLFPDMEIPSFWDDDAGVELFSHLSWFISAAV

VLADWTGSSTRFFPRVSQRMQLDVYWRQANAQAEQAVNVFPPAAAVAPFTGIETLFPFIQHPTPLQKAVL

ELDISQPGPQLFILEDVTGAGKTEAALILTHRLMSAGKAQGLFFGLPTMATANAMFDRLAQSWLALYQSD

ARPSLVLAHSARGLMEGFNQRIWPGAVSGSEEPDDEQSFSQGCAAWFADSNKKALLAEVGVGTLDQALMA

VMPFKHNNLRLLGLDNKVLLADEIHAYDAYMSRILESLIEQQARSGNCVILLSATLSQQQRDKLVASFSR

GSGCALAAPLLGDDDYPWLTQVAGREVISRYVATRKEVERSVNIGWLDNEEACLTRIEQSASEGRCIAWI

RNSIDDAVRIYRQLLARGAIPAEKISLFHSRFAFYDRQRIETETLSHFGKDDSTQRAGRVLIATQVIEQS

LDIDMDDMISDLAPIDLLIQRAGRLQRHIRDRRGRLKIGGEDERAAPQLLILAPEWDEAPQEEWLTSALR

NSAYVYPDHGRLWLTQRVLRQQGAIRMPQSARLLIESVYGEDIGIPDGLAKAEQAQLAKYYCDRAFAHQM

LLNFKPGYSPDSSDFLADKLSTRLAEESITLWLAKNVDGQLLPYACGEHQWEMSMLRVRESWWRKHKAEF

TLLAEKPLQQWCVQQHQNPDFAVVIIVTDSPDCGYSASEGLIGTMEV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529006.1\_1009 [gene=casA] [locus\_tag=BN49\_RS06335] [protein=type I-E CRISPR-associated protein Cse1/CasA] [protein\_id=WP\_016529006.1] [location=1038298..1039854] [gbkey=CDS]

MNTFSLLTTAWLPVRYRDGTTGKLAPVGLTDEDVVDIAATRADLQGAAWQFLIGLLQCAVAPKNRNGWED

TWEEGLSAETLVAALAPQEAAFQFGPDTPSFMQDFDSLGGDKVSIASLLPEVPGAQTTKFNKDHFIKRGV

TNSFCPHCAALALFSLQLNAPSGGKGYRTGLRGGGPLTTLIELQEYEGERLTPLWRKLWLNVLPQDAADM

PLPAAYDESVFPWLAPTRTSEQASAITTPEQVDKLQAYWGMPRRIRLDFAATQPGTCDICASESDGLLSQ

MAVKNYGINYDGWRHPLTPYRLALKGDGGFFSVKPQPGGLIWRDWLGLSQDNQTESNSEYPAQVVKVFNA

RGLRNIKAGLWGFGADFDNMKIRCWYEHHFPLLTDESTIPDLRKAAQTAARLLSLLRSALKEAWFDDPKG

ARGDFSFIDIDFWNQTQPLFLNLIHELENGQPAQERLDKWQRELWLFVRRCFDDRVFTNPYENNDLARCM

AARKKYFATSAEKQSAKAAKAKKQEAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004142782.1\_1010 [gene=casB] [locus\_tag=BN49\_RS06340] [protein=type I-E CRISPR-associated protein Cse2/CasB] [protein\_id=WP\_004142782.1] [location=1039851..1040393] [gbkey=CDS]

MNVVSDEHKATLRQWHEELQEKRGLRASLRRSATLNDVCLSEGFHSLMVQTHSLWNTQGKAWRFTALALV

AALAAQVKTIDDRQTFAAQLGQKTGDTPVMSRLRFARLSAVKTPDELLRQLRRAISLLHGSVNLLSLAED

IFRWCREQDDLLNHRRRQQRPIEFIRIRWALDYYQAGDAE

>lcl|NZ\_FO834906.1\_prot\_WP\_009308513.1\_1011 [gene=cas7e] [locus\_tag=BN49\_RS06345] [protein=type I-E CRISPR-associated protein Cas7/Cse4/CasC] [protein\_id=WP\_009308513.1] [location=1040412..1041467] [gbkey=CDS]

MTTFIQLHLLTAYPAANLNRDDTGAPKTVMLGGATRLRISSQSLKRAWRTSELFEHALAGHIGIRSGRIA

REAAEILVKSGIEPRKAVDYVKAIGECFGKVKTKADQNDPLKCSETEQLAHISPAEFDAVKALAHRLAEE

KRAATKEEAALLRHDRMAVDIAMFGRMLADQPTYNVEAACQVAHAFGVSETIVEDDFFTAVDDLRAASED

AGAGHLGETGFGSALFYTYICIDKDLLVNNLNGNEELANKTLRAFTEAALKVSPTGKQNSFASRAYASWA

LAEKGTDQPRSLAAAFYQPINGGDQLDVAVQRITALRENMNTVYGQQTAFQHFDVMNKQGSMNDVLDFIC

A

>lcl|NZ\_FO834906.1\_prot\_WP\_016529005.1\_1012 [gene=cas5e] [locus\_tag=BN49\_RS06350] [protein=type I-E CRISPR-associated protein Cas5/CasD] [protein\_id=WP\_016529005.1] [location=1041478..1042224] [gbkey=CDS]

MSQYLVFQLHGPMASWGVDVPGEVRHSHELPSRSALLGLLLAALGIRREEEQRLNAFNQHYSFLLCASSE

PRWARDYHTVQMPKEVRKARYFSRREELQDPELLSALISRRDYYTDAWWMIAVAVTPDAPYSLEQLHEAL

RYPVFPLYLGRKSHPLALPLMPLLLEGHAAEVLRQAYRQYQERFNLLRLSLRQLQDQCWWEGEHAGLVAN

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>lcl|NZ\_FO834906.1\_prot\_1013 [gene=cas6e] [locus\_tag=BN49\_RS06355] [protein=type I-E CRISPR-associated protein Cas6/Cse3/CasE] [pseudo=true] [location=1042206..1042856] [gbkey=CDS]

MYLSRITLYTAQLSPLRLLHLVERGEYVMHQWLWQLFPGGQQRQFLYRREALQGAFRFFVLSPQLPAESE

IFEIQSRSFNPELRAGQRLCFSLRANPTICKAGKRHDLLMDAKR\*VKEQVEPRDIWAHQQQAALAWLTRQ

GEQSGFSLAETVVDAYRQQQIRREKSRQTIQFSSVDYTGMLVVNDPALFLQRLASGYGKSRAFGCGMMMI

KPGDGA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529002.1\_1014 [gene=cas1e] [locus\_tag=BN49\_RS06360] [protein=type I-E CRISPR-associated endonuclease Cas1e] [protein\_id=WP\_016529002.1] [location=1042853..1043773] [gbkey=CDS]

MTFVPLNPIPLKDRTSMIFLQYGQIDVLDGAFVLIDKTGIRTHIPVGSVACIMLEPGTRVSHAAVRLAST

VGTLLVWVGEAGVRVYSSGQPGGARADKLLYQAKLALDDDLRLKVVRKMYELRFREAPPARRSVEQLRGI

EGSRVRQTYALLAKRYGVKWHGRNYDPKDWARGDVVNQCISAATSCLYGISEAAILAAGYAPAIGFIHSG

KPLSFVYDIADIIKFDSVVPKAFEIAASHPAEPDKEVRLACRDIFRSTKLTGKLIPLIEEVLSVGEIEPP

QPPPDMLPPAIPEPESMGDKGHRGHG

>lcl|NZ\_FO834906.1\_prot\_WP\_009308509.1\_1015 [gene=cas2] [locus\_tag=BN49\_RS06365] [protein=type I-E CRISPR-associated endoribonuclease Cas2e] [protein\_id=WP\_009308509.1] [location=1043773..1044066] [gbkey=CDS]

MSMLMVVTENVPPRLRGRLAIWLLEIRAGVYVGDTSKRIREMIWQQVIQLSDGGNVVMAWATNSESGFEF

QTWGENRRIPVDLDGLRLVSFLPVENQ

>lcl|NZ\_FO834906.1\_prot\_WP\_042940406.1\_1016 [locus\_tag=BN49\_RS06370] [protein=hypothetical protein] [protein\_id=WP\_042940406.1] [location=complement(1045472..1047493)] [gbkey=CDS]

MLTRKLPLAAFLAATLVAASSHACGPFFPNYLLADRQANLLYLPEGSFALESSRLVLADPRLPQWRDTSA

DKPAAPTAQDLLLKEIRASGSLAAPEKMAADLPTASRLYVLGAVAFAERDSRARDYFRQLLALPVEQQGE

WGLKARYSLARDLMRDYPLTDSRSSHGSEQELREAFDLYQQIIDAVREGQQDPELLSLASLGQQGRIKHW

QSDPIAAAHLYARQAAQGSPSGSLSLRYTVDVLNHPENEQFLQPGLDDPVIQQLLIASFFTRSSNLLYEP

EPRPFDPTEVKNYHNELIAKLAQKVDRDMAGSDRLIALAYRNGQYPLVTLMLKNAKENGLTAWVRAKMAL

RAGDVNAAAAWYAKAAASFPPNETWGFQSYSDDIVGEEFVTPVCRIHAEQAILALNRDDYLQAMRLMYQA

KENYWPDVAHIAERVLTVNELLAFVDKYVPAPSPSAPTTPKNAGRDSADARLRNLLARRLMRAGQYQKAL

AYFALAEDRDAARAFIDAFPKKGHKTAQAQGWWQAALILRHQGMELTGYEMAPDFALYGGGYSWPYYNQG

PEDNSAVTSWISDGERQRVQRSLPKQDSHFLHYRWQAVTLAEKAADLLPYKSQAYAAVLCNATGWVWGRD

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529000.1\_1017 [locus\_tag=BN49\_RS06375] [protein=DUF3142 domain-containing protein] [protein\_id=WP\_016529000.1] [location=complement(1047480..1048667)] [gbkey=CDS]

MINLRCSGVFFLLLAASAGALADSQVYIWQRVWNDQHKTALQQSQALFATLRVLGIQFHPQEGVRLARVN

TSLLQQDGRPVWLVVRLDGSLTQLDTTTMLPQIKRLVTHWRKAGVNLTAIEIDYDAPTSRLSDYQRLLMA

MRQGLPSDITLSITALPTWLTSPGLRPLLKAVDSSVLQLHSVQSPGTGLFDPTLARRWSRQYALIAPHPF

YLALPAYGSALIAAPGQPASVESESPLWIAAEKQELSVSPQQIDTFIRELEQQPPYHFSGIVWFRLPLDN

DTRAWSLSTLAAVIRHQPLTSCWQWLALPDKASASAESTLYELAIKNTGNIDAPLPAKITLTTEDCLAAD

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>lcl|NZ\_FO834906.1\_prot\_WP\_009308506.1\_1018 [locus\_tag=BN49\_RS06380] [protein=aminopeptidase] [protein\_id=WP\_009308506.1] [location=complement(1048703..1049758)] [gbkey=CDS]

MFSALCRRLLPLALGTGFVFAAAPAFSALGDTASSQARHIATVFPGRMTGTPPEMLSADYLRQQFALMGY

QSDVRSFNTRYIYTDSNQRKNWHNATGSTVIAAHEGKVRQQIIIMAHLDTYAPQSDKDVENNLGGLTLQG

IDDNAMGLGVLLELAEHLKNVPTRYGIRFIATSGEEEGRLGAQNLLQRMSEAEKKNTLLVINLDNLVVGD

KLYFNSGRSTPASVRKLTRDRALAIARSKGIAAYTNPGLNPAYPKGTSCCNDASVFDNAGIPVLSVEATN

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MPLFAELKQRPVLVIGGGEIAERKIKFLLRAQAQVQVVAETLSPALADLAARQALSWRATEFSDSLVDDV

FLVIAATEDEALNQRVFAAANARYRLVNVVDNQALCSFVFPSIVDRSPLLVAISSSGKAPVLSRILREKI

EALLPTNLGRLAESASYWRNHLKTRLTTTEARRRFWERVFTGRFASLMVAGNSAEAEKALQDELDKPERE

TGEIILVGAGPGDAGLLTLRGLQVIQQADVVFHDHLVTQPVLELVRRDAELICVGKRAGEHSVPQHETNQ

LLVEAAKAGKTVVRLKGGDPFIFGRGAEELQAAAEAGIPFQVVPGVTAAAGATAYAGIPLTHRDYAQSAV

FVTGHYKPDSAPFDWSLLAKSQQTLAIYMGTMKAAEISAQLIAHGRDSDTPVAVISRGTRDDQQTITGTL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002915160.1\_1020 [gene=cysD] [locus\_tag=BN49\_RS06390] [protein=sulfate adenylyltransferase subunit CysD] [protein\_id=WP\_002915160.1] [location=1051421..1052329] [gbkey=CDS]

MDQKRLTHLRQLEAESIHIIREVAAEFSNPVMMYSIGKDSSVMLHLARKAFYPGTLPFPLLHVDTGWKFR

EMYEFRDRTAKAYGCELLVHKNPEGVAMGINPFVHGSAKHTDIMKTEGLKQALNKYGFDAAFGGARRDEE

KSRAKERIYSFRDRFHRWDPKNQRPELWHNYNGQINKGESIRVFPLSNWTELDIWQYIYLENIEIVPLYL

AAERPVLERDGMLMMIDDDRIDLQPGEVIEKRMVRFRTLGCWPLTGAVESEAQTLPEIIEEMLVSTTSER

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>lcl|NZ\_FO834906.1\_prot\_WP\_004181094.1\_1021 [gene=cysN] [locus\_tag=BN49\_RS06395] [protein=sulfate adenylyltransferase subunit CysN] [protein\_id=WP\_004181094.1] [location=1052339..1053766] [gbkey=CDS]

MNTTIAQQIANEGGVEAYLHAQQHKSLLRFLTCGSVDDGKSTLIGRLLHDTRQIYEDQLSSLHNDSKRHG

TQGEKLDLALLVDGLQAEREQGITIDVAYRYFSTEKRKFIIADTPGHEQYTRNMATGASTCDLAILLIDA

RKGVLDQTRRHSFISTLLGIKHLVVAVNKMDLVEFSEARFNEIREDYLTFAEQLPGNLDIRFVPLSALEG

DNVASQSANMPWYSGPTLLEVLETVEIQRVVESQPLRFPVQYVNRPNLDFRGFSGTVASGTVQVGQRLKV

LPSGVESSVARIVTFDGDLQEAAAGEAITLVLKDEIDISRGDLLVDAQASLPAVQSASIDVVWMAEQPLT

PGQSYDIKIAGKKTRARVDAIRYQVDINNLTQREVESLPLNGIGLVELTFDEPLVLDPYQQNPVTGGLIF

IDRLTNVTVGAGMVNEPHLQASTSASQYSAFELELNQLIRKHFPHWDARDLLGGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002915158.1\_1022 [gene=cysC] [locus\_tag=BN49\_RS06400] [protein=adenylyl-sulfate kinase] [protein\_id=WP\_002915158.1] [location=1053766..1054371] [gbkey=CDS]

MAQHDENVVWHAHPVTQQQREQHHGHRGVVLWFTGLSGSGKSTVAGALEEALHERGVSTYLLDGDNVRHG

LCSDLGFSDEDRKENIRRVGEVARLMVDAGLVVLTAFISPHRAERQMVRERLGEGRFIEVFVDTPLAICE

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>lcl|NZ\_FO834906.1\_prot\_WP\_002915157.1\_1023 [locus\_tag=BN49\_RS06405] [protein=DUF3561 family protein] [protein\_id=WP\_002915157.1] [location=1054422..1054748] [gbkey=CDS]

MRNTQNLSIIRSEPPPAIGDETTWSLSGAAVGFISWLLALGIPFLLYGSNTLFFLLYTWPFFLALMPVAV

VVGIALHSLLNGKLLYSVSATILTVGLMFALLFLWLLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915156.1\_1024 [gene=ftsB] [locus\_tag=BN49\_RS06410] [protein=cell division protein FtsB] [protein\_id=WP\_002915156.1] [location=1054889..1055206] [gbkey=CDS]

MGKLTLLLLALLVWLQYSLWFGKNGLHDYTRVNDDVTAQQATNAKLKARNDQLFAEIDDLNGGQEAIEER

ARNELSMTRPGETFYRLVPDASKRNQASGQQQNNR

>lcl|NZ\_FO834906.1\_prot\_WP\_004174645.1\_1025 [gene=ispD] [locus\_tag=BN49\_RS06415] [protein=2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase] [protein\_id=WP\_004174645.1] [location=1055226..1055936] [gbkey=CDS]

MAATFPGVCAVVPAAGFGRRMQTECPKQYLSIGNKTILEHAVAALLADARVQRVVIAVSPGDRRFSQLPL

AQHPQITVVDGGAERADSVLAGLQALPEAQWVLVHDAARPCLHQDDLSRLLSLCETSRVGGILAAPVRDT

MKRAEPGKTAIAHTVDRNDLWHALTPQLFPRELLVDCLTRALNEGATITDEASALEYCGFHPQLVAGRAD

NIKVTRPEDLALAEFYLTRSRHQEKA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181093.1\_1026 [gene=ispF] [locus\_tag=BN49\_RS06420] [protein=2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase] [protein\_id=WP\_004181093.1] [location=1055936..1056415] [gbkey=CDS]

MRIGHGFDVHAFGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKLFPDTDPAFKG

ADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIAEDLGCHMDDVNVKATTTEKLGFT

GRGEGIACEAVALLRKADK

>lcl|NZ\_FO834906.1\_prot\_WP\_004185423.1\_1027 [gene=truD] [locus\_tag=BN49\_RS06425] [protein=tRNA pseudouridine(13) synthase TruD] [protein\_id=WP\_004185423.1] [location=1056412..1057461] [gbkey=CDS]

MIAFDQLTWLHGKPQSSGLLKANPEDFLVVEDLGFAPDGEGEHVLVRILKNGCNTRFVADALAKFLKIHA

REVSFAGQKDKHAVTEQWLCARVPGKEMPDLSKFQLEGCQVLEYARHKRKLRLGALKGNQFTVILREISD

RQDVETRLQAIAERGVPNYFGAQRFGIGGSNLQGALRWAESGAPVRDRNKRSFWLSAARSALFNQQVSIR

LKKTEFNQVVDGDALQLAGRGSWFVVTPEELEVSQARVHNRELMITATLPGSGDWGSQRDALAFEQAAIA

EETALQALLVREKVEAARRAMLLYPQQLSWNWWDDVTVELRFWLPAGSFATSVVRELINTTGDYANIAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004174648.1\_1028 [gene=surE] [locus\_tag=BN49\_RS06430] [protein=5'/3'-nucleotidase SurE] [protein\_id=WP\_004174648.1] [location=1057442..1058203] [gbkey=CDS]

MRILLSNDDGIHAPGIQTLAKALREFAEVQVVAPDRNRSGASNSLTLESSLRTFTFENGDIAVQMGTPTD

CVYLGVNALMRPRPDIVVSGINAGPNLGDDVIYSGTVAAAMEGRHLGFPALAVSLNGYQHYDTAAAVTCT

ILRALSREPLRTGRILNINVPDLPLDQIKGIRVTRCGNRHPADQVIPQQDPRGNTLYWIGPPGDKRDAGP

GTDFAAVDEGYVSVTPLHVDLTAHQAHEVVTDWLERVGVDRQW

>lcl|NZ\_FO834906.1\_prot\_WP\_002915108.1\_1029 [locus\_tag=BN49\_RS06435] [protein=protein-L-isoaspartate(D-aspartate) O-methyltransferase] [protein\_id=WP\_002915108.1] [location=1058197..1058823] [gbkey=CDS]

MVSKRVESLLNQLRTQGIVDERVLEAIALVPREKFVDEAFEHKAWENTALPIGQGQTISQPYMVARMTEL

LTLTPESRVLEIGTGSGYQTAILAHLVHHVCSVERIKSLQWQARRRLKQLDLHNVSTRHGDGWQGWQARA

PFDAIIVTAAPPEIPTALLAQLDDDGVLVLPVGEEHQFLKRIRRRGNEFIIDTVEAVRFVPLVKGELA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149542.1\_1030 [gene=nlpD] [locus\_tag=BN49\_RS06440] [protein=murein hydrolase activator NlpD] [protein\_id=WP\_004149542.1] [location=1058949..1060085] [gbkey=CDS]

MSAGSTKFTVSRIAALSLVSLWLAGCTNTNNPPAPVSSAGGAASSSTNSGMLITPPPSGVKSAPQAQPIQ

PMQTQTIQPQPAPVAQEPVQTVNGRIVYNRKYGDIPKGSYTGGSTYTVKRGDTLFYIAWVTGNDFRDLAQ

RNNIPAPYALNVGQVLQVGNASGQPITGENAVSQASARASGGATTSTTSAQKSTAVVASQPTITYSESSG

EQSATKMLPNNKPATTTTTVVAPVTAPTTVSTTQPTASSTSTSSPISAWRWPTDGKVIENFSGAEGGNKG

IDIAGSKGQAIVATADGRVVYAGNALRGYGNLIIIKHNDDYLSAYAHNDTMLVREQQEVKAGQKIATMGS

TGTSSTRLHFEIRYKGKSVNPLQYLPQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915106.1\_1031 [gene=rpoS] [locus\_tag=BN49\_RS06445] [protein=RNA polymerase sigma factor RpoS] [protein\_id=WP\_002915106.1] [location=1060243..1061235] [gbkey=CDS]

MSQNTLKVHDLNEDAEFDENGIEVFDEKALVEEEPSDSDLAEEELLSQGATQRVLDATQLYLGEIGYSPL

LTAEEEVYFARRALRGDVASRRRMIESNLRLVVKIARRYSNRGLALLDLIEEGNLGLIRAVEKFDPERGF

RFSTYATWWIRQTIERAIMNQTRTIRLPIHIVKELNVYLRTARELSHKLDHEPSAEEIAEQLDKPVDDVS

RMLRLNERITSVDTPLGGDSEKALLDILADEKENGPEDTTQDDDMKQSIVKWLFELNAKQREVLARRFGL

LGYEAATLEDVGREIGLTRERVRQIQVEGLRRLREILQGQGLNIEALFRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002915104.1\_1032 [locus\_tag=BN49\_RS06450] [protein=hypothetical protein] [protein\_id=WP\_002915104.1] [location=complement(1061288..1061665)] [gbkey=CDS]

MNPYLQEVLDAHVLIERWLSHGEGSAEALMKRFAADFTMIPLSGEKMDYPTVSRFFHHAGGSRPGLDIVV

DQMEIISEWHDGAAVLYRESQTLADSSQNVRWSTAIFQQAEGKIVWRHLQETRLG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530224.1\_1033 [locus\_tag=BN49\_RS06455] [protein=MFS transporter] [protein\_id=WP\_016530224.1] [location=complement(1061662..1062864)] [gbkey=CDS]

MTYRHRVATVFLFGFFLDLINMFIASIAFPAISRALAVSVSQLAWVSNAYILGLTVVVPFSAWLSERWGA

KRLFLLSLGLFSLGALAAGLANSLSELILWRTLQGMGGGLLIPLGQALTWPLFQPHERAKLSAAVMLVGL

LAPACSPAIGGLLVEAFSWRWVFFASLPVALLTFVLAVRWLNDTPGPVRPTRFLPLSLLADPLLRFAMLI

YLCVPGMFIGVNVVGMFYLQRVTGMAPGAIGALMVPWSLASFAAITFTGRYFNRFGPRPLVVIGCLLQAM

GIMLLLKIDADSPLALLILAFTLMGGGGSLCSSTAQSSAFLHTPAEEMPDASALWNLNRQLSFFAGSALL

ALLLRVFPPAYAWQGIFISAAVITLLPLLFCLRLNNRAIIHRLHTTLEKS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530223.1\_1034 [locus\_tag=BN49\_RS06460] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530223.1] [location=1062973..1063860] [gbkey=CDS]

MLNLQRVTMFIAVVDAGSFTQAAAALGQTKAVVSFNVRQLENELGVTLLLRSTRRLRLTDAGVLFYQRGV

ALLNVAENLQDEVRASHSGLSGELRITTTPEYGAQVIIPALAAFARRHPALRVRHVSSSHHADLISERFD

VAIRLGTLADSRYRATRIASFAILPVASPAWLASHPVQTLSDLAQAEWIIHERLPTPLRWQLRTDHQTEV

DFAIASAPRFSADSATALMSFALAGCGVALLPAWLVAKKVAQRELVPLLPEYHFPQQGVYALYPDSQHLP

TRVRAFIDFLREKVG

>lcl|NZ\_FO834906.1\_prot\_WP\_002915102.1\_1035 [locus\_tag=BN49\_RS06465] [protein=MarR family transcriptional regulator] [protein\_id=WP\_002915102.1] [location=complement(1063869..1064276)] [gbkey=CDS]

MELRNEAFHLLRQLFQQHTARWQQALPDLTKPQYAVMRSVAEHPGIEQVALIEAAVSTKATLAEMLSRME

ARGLVRREHDPADKRRRFVYLTDEGEALLNRSIPQGNEVDDEFLGRLSDDEREQFSRLVHKMMAP

>lcl|NZ\_FO834906.1\_prot\_WP\_016530222.1\_1036 [locus\_tag=BN49\_RS06470] [protein=UbiX family flavin prenyltransferase] [protein\_id=WP\_016530222.1] [location=1064450..1065043] [gbkey=CDS]

MKLIIGMTGATGAPLGVALLQALRDMPEVETHLVMSKWAKTTIELETPWTAREVAALADFSHSPADQAAT

ISSGSFRTDDMIVIPCSMKTLAGIRAGYAEGLVGRAADVVLKEGRKLVLVPREMPLSTIHLENMLALSRM

GVAMVPPMPAYYNHPETVDDITNHIVTRVLDQFGLDYHKARRWNGLRTAEQFAQEIE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151060.1\_1037 [locus\_tag=BN49\_RS06475] [protein=UbiD family decarboxylase] [protein\_id=WP\_004151060.1] [location=1065043..1066470] [gbkey=CDS]

MAFDDLRSFLQALDDQGQLLKISEEVNAEPDLAAAANATGRIGDGAPALWFDNIRGFNDARVTMNTIGSW

QNHAISLGLPPNTPVKKQIDEFIRRWDNFPVTPERRANPAWAENTVDGDDINLFDILPLFRLNDGDGGFY

LDKACVVSRDPLDKDNFGKQNVGIYRMEVKGKRKLGLQPVPMHDIALHLHKAEERGEDLPIAITLGNDPI

ITLMGATPLKYDQSEYEMAGALRESPYPIATAPLTGFDVPWGSEVILEGVIEGRKREIEGPFGEFTGHYS

GGRNMTVVRIDKVSYRSKPIFESLYLGMPWTEIDYLMGPATCVPLYQQLKAEFPEVQAVNAMYTHGLLAI

ISTKKRYGGFARAVGLRAMTTPHGLGYVKMVIMVDEDVDPFNLPQVMWALSSKVNPAGDLVQLPNMSVLE

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>lcl|NZ\_FO834906.1\_prot\_WP\_002915098.1\_1038 [locus\_tag=BN49\_RS06480] [protein=hypothetical protein] [protein\_id=WP\_002915098.1] [location=1066481..1066717] [gbkey=CDS]

MICPRCADEKIEVMATSPVKGVWTVYQCQHCLYTWRDTEPLRRTSREHYPEAFRMTQKDIDEAPQVPHVP

PLLPEDKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915097.1\_1039 [locus\_tag=BN49\_RS06485] [protein=type I toxin-antitoxin system Hok family toxin] [protein\_id=WP\_002915097.1] [location=1067056..1067208] [gbkey=CDS]

MLTKYALVAIIVLCITVLGFTLLVHSSLCELSIKERNIEFKAVLAYESKK

>lcl|NZ\_FO834906.1\_prot\_WP\_046042556.1\_1040 [gene=mutS] [locus\_tag=BN49\_RS06490] [protein=DNA mismatch repair protein MutS] [protein\_id=WP\_046042556.1] [location=complement(1067327..1069888)] [gbkey=CDS]

MSTIDNLDAHTPMMQQYLKLKAQHPDILLFYRMGDFYELFYDDAKRASQLLDISLTKRGASAGEPIPMAG

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KGFGYATLDISSGRFRLSEPADRETMAAELQRTNPAELLYAEDFAESSLIEGRRGLRRRPLWEFEIDTAR

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DGGVIAPGYSEELDEWRALADGATDYLDKLEIRERERLGLDTLKVGYNAVHGYYIQISRGQSHLAPIHYV

RRQTLKNAERYIIPELKEYEDKVLTSKGKALALEKQLYDELFDLLLPHLADLQTSASALAELDVLVNLAE

RAETLNYCCPTFSDKPGIRISEGRHPVVEQVLKEPFIANPLQLAPQRRMLIITGPNMGGKSTYMRQTALI

ALLAYIGSYVPAQKVEIGPIDRIFTRVGAADDLASGRSTFMVEMTETANILHNATEHSLVLMDEIGRGTS

TYDGLSLAWACAENLANKIKALTLFATHYFELTQLPEKMEGVANVHLDALELGDTIAFMHSVQDGAASKS

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QALEWIYRLKRLV

>lcl|NZ\_FO834906.1\_prot\_WP\_004181075.1\_1041 [locus\_tag=BN49\_RS06495] [protein=DUF1493 family protein] [protein\_id=WP\_004181075.1] [location=complement(1070157..1070489)] [gbkey=CDS]

MKSIQDQVLDLFKDEISTRLDKNWKEIPLELDYDLFDAPGDDLHDALNKFEQKFNVDLSSVKWSCYFPWE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004188736.1\_1042 [locus\_tag=BN49\_RS28700] [protein=hypothetical protein] [protein\_id=WP\_004188736.1] [location=complement(1070489..1070938)] [gbkey=CDS]

MDTTEELNGTYFYHGQSNLSAGELFDVIFLEQFCDELGIGIESGAAILAGQPWLKTRTKPGEAIKGTSVV

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KDRIQWTSF

>lcl|NZ\_FO834906.1\_prot\_WP\_002915094.1\_1043 [locus\_tag=BN49\_RS06500] [protein=Hcp family type VI secretion system effector] [protein\_id=WP\_002915094.1] [location=complement(1070950..1071432)] [gbkey=CDS]

MAIPGNMWIYDDGGALIKGGCDVADREFSIEFKGFHHNLSIPTDNATGKPTGTRQHSPMIIVKEFDYSSP

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WKHCDGNIIFTDAWNERQTA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530219.1\_1044 [locus\_tag=BN49\_RS06505] [protein=heme ABC transporter ATP-binding protein] [protein\_id=WP\_016530219.1] [location=complement(1071711..1072490)] [gbkey=CDS]

MVNEYCAQGLSLHLGKRQIFDNVSVALRGGEMTALIGPNGAGKSTLLRLLTGYLTPDSGTRHLAGKPLEA

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QRVQLARCLAQLWRDGAPQGWLFLDEPTSALDLYYQQHLLRLLKRLTAGGQLHVCVVLHDLNLAALWADR

ILLLHQGHLVAQGTPQEVIQQPVIHRWYGADVRLVQHPDNAVPQVYLAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004185411.1\_1045 [locus\_tag=BN49\_RS06510] [protein=iron ABC transporter permease] [protein\_id=WP\_004185411.1] [location=complement(1072483..1073478)] [gbkey=CDS]

MRPALARRLLLMTLLLVSLTLFATTLGAMRLPLVNLLPSGDDMLRHIWLTIRLPRVLLALLVGAALALSG

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SLSRLLLVGIAINALCGALVGVLSWLSNDAQLRQLSLWGMGSLGQAEWPTLLVAATLIIPAALAVWWMAS

RLNLLQLGDEEAHYLGVNVQALQRWLLLCSAVLVAAAVAISGVIGFIGLVVPHLMRLWLGPDHRGLIPGS

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530218.1\_1046 [locus\_tag=BN49\_RS06515] [protein=hemin ABC transporter substrate-binding protein] [protein\_id=WP\_016530218.1] [location=complement(1073478..1074296)] [gbkey=CDS]

MMRWLLLLIAFPLLSHAAVERLVTLGGDVTEIVYALHAEESLVARDSTSSWPPAAQKLPDVGYLRQLNAE

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QIAAIPTQPVAKRVLFILSHGGMNTLVAGQHTAADGAIRAAGLQNAMQGFDHYRAMSQEGVAASQADLVV

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>lcl|NZ\_FO834906.1\_prot\_WP\_042941207.1\_1047 [locus\_tag=BN49\_RS06520] [protein=hemin-degrading factor] [protein\_id=WP\_042941207.1] [location=complement(1074293..1075324)] [gbkey=CDS]

MPNAHPDLWQRYQATKAASTAKYARDIAAEMGISEAELTAARLGHDAVRLSDDARALIAALERVGETKCI

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TTQTDMTAWETLIAEYRVAAPAPLTLRPLEPVKYADTADGAALENDWRAMTDVHQFFGLLRKYQLSRQQA

FRLVSDDLACRVDRHALPSLLETVRQEGNEIMIFVGNRGCVQIFTGALEKLAPMRGWLNIFNTTFTLHLR

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>lcl|NZ\_FO834906.1\_prot\_WP\_004174666.1\_1048 [locus\_tag=BN49\_RS06525] [protein=TonB-dependent receptor] [protein\_id=WP\_004174666.1] [location=complement(1075396..1077759)] [gbkey=CDS]

MYKSTPSAAWCKKRLLVTSLFAAIYQTSAIAADTSAVSGEAVDDTSEQMTVTAPAPVQKAGSEHSISARE

LENKGANDFGSIMRYEPLISATGASGGSGNGKSGFDRGGYTGYNIRGMESNRVGIDVDGIAQPNATGRGY

VGRAGLNTFGIGRDYIDPYMYGSVDIQSGATSTETANSAIGGNVSFRPKSADDYLRPGKTSAFGYRSGYD

SADRSWHNGVTVAGGDEFLRGILVYSRRDGQETENNSGTVDAYPANWHSDAFLASGIWQPNDEHKLTSTF

DYYHKTNHTHYDTWDSSGNSTIGTANQTSQTRRWGLSLKDDWTPMNDYLDSVSTKIYYQHTEAHDWTYMP

DSVTRRMQTVNSNYDTDTWGLQTALAKTLGRHDLSAGFNASTSKTQRPFSQSPIPSVYSEIMQPEADSRS

YTLGGFVQDKINFDLDSHNFAVIPGVRVVHQSTKPENLSDLAANSSVLSESSVANLYGKNSDTQVLPSLT

FQYDLTPRLMTYLQYQRGAQFPNASQLYGSWNLGSSYAGSQQYALIGNTDLKTETSDNLEWGLKGEVTEG

ITLRTALFYNSYKNFIAYTRYTRANNPGQFTNVPSNIYTIYQAENRDKAYIYGGEISTKFNFGTWFEQVD

GLSATLALGYSEGKSKSSYSGDKYVDLDSVAPMKAIVGVAWDDPAKRYGTALTATFVKGKQATATNRESY

SNSGSAITDASSDYMRVPGYGMLDWTAYWQVAKNVRLNGGVYNLTDRKYWDYLSSRNIETGTNQDANDKA

LAVMPGRTWQLGVNVDF

>lcl|NZ\_FO834906.1\_prot\_WP\_002915045.1\_1049 [locus\_tag=BN49\_RS06530] [protein=SelT/SelW/SelH family protein] [protein\_id=WP\_002915045.1] [location=1077975..1078268] [gbkey=CDS]

MNSKAAITITYCSQCNWMLRASWMAQELLHTFSTDIASVTLVPGTGGIFTIDVDGQQIWERKQDGGFPDA

AELKRRVRDVCFPEKPLGHVDKGDQKG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042561.1\_1050 [locus\_tag=BN49\_RS06535] [protein=thiamine pyrophosphate-requiring protein] [protein\_id=WP\_046042561.1] [location=complement(1078308..1080017)] [gbkey=CDS]

MASITLSAAELLLHRLQALDVAYIFINSGTDYPPVIEAWAKARATGQKVPELVICPHENAAIGMAHGYYL

GTGKVQAVMVHTNVGLANAACGVINLANSNIPVLIFGGRTPISEHSHFGCRNTPIGYGQEMRDQAALIRE

SVKWDFELRLADQIGEHVDRAWAIASSLPKGPVYLSLPREPLCETFAVDEAALQAGPSQQPVRYAPVRED

IARAAEAIACARHPVIFAQRGARTAEGFARLDSLVREWAIPLVEYWGTEVTLSADNPLLAGADPSVWLAD

ADVILVVDSQAPWMIAEGDCRQDCTVIQMGPDPLFSRYPVRGYRADINLAGETDEVFSLLEEALRPLQAA

RQQHVAERAAYTQNRIQQQKNQRDALLHASQTGAITKPWLSYCLGHLANQHRGRIVSELTTLPQFAGLTH

AESYYQEALAGGLGEALPIALGLQLARREELIIAAVGDGSYLFANPAVCHHIAEVMKLPVLVVVGNNGGW

GAVAGGTKALYPDGYTARAETIPATAFTTSPDFAAIAASSRAAALSVSRAEDLPGVLEEAVSLIHTCRQS

VLVDVQLAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915041.1\_1051 [locus\_tag=BN49\_RS06540] [protein=AEC family transporter] [protein\_id=WP\_002915041.1] [location=complement(1080053..1080994)] [gbkey=CDS]

MTQNNILLISGAILPVIITVIIGYISGKRKDFNWQQAGDINKIVMLYALPLSIFSNMVMTPRHIVMTMGP

VAVAIILALILSFVIPLLVARYLFRRDLALSTLQALAIGSPAVPFIGTSVLAFLFGTVSASLITVSSITQ

NVFQLPLVMILMSVATGDKSQHISFGARVVNAIKQPVVWSPVIALIIVLADIHIPQTISMSLGLLGKASG

GLALFAAGIVLYTRSIVITTATIITVIARNILVPGACYLILLKMGFSMEQIKEVVLTMAIPVGSIAIIIA

MQYKTGEQEMASTMALSIIASIITMGGFIFLTF

>lcl|NZ\_FO834906.1\_prot\_WP\_004181063.1\_1052 [locus\_tag=BN49\_RS06545] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004181063.1] [location=1081179..1082066] [gbkey=CDS]

MPMKFKQIQAFITVAREGNMTLAAEKMGITQSGLSRLLLSLEADLSASLFERHKHGMALSEYGSAFLPYA

LTMLNTEQKAREEIELIRGAGKGILRIGCVSSLLTSHFIDKLAAFHQHHPQIHLRIVDRIDSELYKLLLM

HDIDIALCGPLPHDEKIVVRGKINWQDRICIVARQHHPLHQAADVTLEAMLDYPWIMPPPSSTPMNILAD

IFRARQLPCPQPVIECASSSAIKAFLCESDLLTSMPAPVYRHEEALGLLRPFELEGSVFIRDFYAYSHFG

VLSGAALQLIQHLKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004900121.1\_1053 [locus\_tag=BN49\_RS06550] [protein=nitrous oxide-stimulated promoter family protein] [protein\_id=WP\_004900121.1] [location=1082133..1082474] [gbkey=CDS]

MGKRIEREKMTIQRMIALYQRRCPEAQADNAHYQALNAYADKRLDKCVFGENKPACKQCPVHCYQPAKRE

EMKQIMRWAGPRMLWRHPILTIRHLLDDRRPVPPLPEKYRPKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004181059.1\_1054 [locus\_tag=BN49\_RS06555] [protein=metal ABC transporter permease] [protein\_id=WP\_004181059.1] [location=complement(1082541..1083395)] [gbkey=CDS]

MLNLFLAPFQFPFMVNAIAISIVVAIPCALLSVFLVLKGWALMGDAMSHAVFPGVVLAYIIGIPFAIGAF

IAGLLCAVTTGFLDDNSRLKRDTIMGIVFSGMFGAGLVLYVAIQSDVHLDHILFGDMLGISLSDIGQTTA

IALVIALIIGLKWRDFLLHAFDPTQAKASGLRGGLLHYGLLCMIALTIVATLQSVGIILSISLLIAPGAI

ALLLVRRFIHALLLAVAVAIGCSAGGVWLAFYLDSAPAPTIVVLFTALFVVAFVASTIRDSQKQKTSAII

PGGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004145794.1\_1055 [gene=sitC] [locus\_tag=BN49\_RS06560] [protein=iron/manganese ABC transporter permease subunit SitC] [protein\_id=WP\_004145794.1] [location=complement(1083389..1084237)] [gbkey=CDS]

MSWLLEPFGYHYMLNAMWVSALVGGVCAFLSCYLMLKGWSLIGDALSHSIVPGVAGAYMLGLPFALGAFL

SGGLAAGSMLFLQQRSRLKEDAIIGLIFSSFFGIGLFMVSLNPTSVNIQTIILGNILAIAPEDIIQLAAI

GFISMAILLLKWKDLMVTFFDEHHARSIGLNTRGLKLLFFTLLAACTVAALQTVGAFLVICLVVTPGATA

WLLTDRFPRLLAIAVAIGSLTSFFGAWLSYYLDGATGGIIVVAQTLLFLITFIFAPKHGLLASRRRAREA

AC

>lcl|NZ\_FO834906.1\_prot\_WP\_016532613.1\_1056 [locus\_tag=BN49\_RS06565] [protein=manganese/iron ABC transporter ATP-binding protein] [protein\_id=WP\_016532613.1] [location=complement(1084234..1085055)] [gbkey=CDS]

MNAAQAGLYVDQLTVTWRNGHTALRDASFSVPRGSIAALVGVNGSGKSTLFKALMGFVRVGHGEIAILGQ

PVNRALRQNLVAYVPQSEEVDWSFPVLVEDVVMMGRYGHMGWLRRAKPRDREIVDAALARVGMSEYRHRQ

IGELSGGQKKRVFLARAIAQQGQVILLDEPFTGVDVQTEARIISLLRELRDEGCTMLVSTHNLGSVSEFC

DYTVMVKGTVLASGPTETTFTAENLERAFSGVLRHVALTGAEAQVITDDERPFISRRAAGGPR

>lcl|NZ\_FO834906.1\_prot\_WP\_002915032.1\_1057 [locus\_tag=BN49\_RS06570] [protein=metal ABC transporter substrate-binding protein] [protein\_id=WP\_002915032.1] [location=complement(1085052..1085969)] [gbkey=CDS]

MLHLTPLKSLLLASALALLAATPASAQEKFRVITTFTVIADMAQNVAGDAAVVSSITKPGAEIHDYQPTP

GDIKRAQGAQLILSNGLNLERWFARFYQHLQGVPEVVVSEGIQPMGISAGPYSGKPNPHAWMSADNALIY

VDNIRDALVKYDPPHADTYRRNAEAYKEKIRQTMAPLQARLAQLPADKRWLVTSEGAFSYLARDYGLREL

YLWPINADQQGTPQQVRKVIDTMKKERIPTIFSESTISDKPARQVAREAGAHYGGVLYVDSLSAADGPVP

TWLDLLRVTTETIVNGIQDGMRKQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002915031.1\_1058 [locus\_tag=BN49\_RS06575] [protein=LacI family transcriptional regulator] [protein\_id=WP\_002915031.1] [location=complement(1086148..1087110)] [gbkey=CDS]

MPTIDDVSRLANVSRATVSRVLTGTRGVREESREAVLRAVEELNYRPSFAAQNLASQTSSHVGLVISAQD

ESHGARLLPLLSQALKGLNKSLLVQYVSDPVEQAAVIDDLQRQCVAVVVLGAVAADAPRNVIAFDRFGVA

GSNSQGYDFAFATESACRYVIGKGHRNIALLVDSDSDDASRQMLEGYRNVLQNYSIPFNRQLVLTANDDV

EQALLTLINSFSKYSVIIVKRDRYAAEAMRLLREFTIAVPQEVSLLSLEDSPLASLLYPPLTCISWPLEA

LLDNCIQRIRSLIDDRPTFTAEGRSLAGRLIPRQSVADIS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151053.1\_1059 [locus\_tag=BN49\_RS06580] [protein=ROK family protein] [protein\_id=WP\_004151053.1] [location=complement(1087167..1088081)] [gbkey=CDS]

MLHLGIDIGGTKMEAVLLDPAGECVQRLRRPTHKESYDAFMRQLLTLIADIRAVSPQPFTLGIGLPGAID

PQSGRIKNCNCLVLNGHDLRRDIMQQLGQPVWMANDADCFTLSEAVDGAGAGATTVFGVIIGTGCGGGIA

VHQQLLSGPNAIAGEWGHNPLPGYTPERDGPPQPCYCGKTNCIESFLSGTGFARRYGEQARAEAIVAAAQ

NGDPRALAHWRHFIDAFARSLASVINILDPQVIVLGGGLSNVSQIYRDLPAAIVPWIFSDTCRTQIKPAR

FGDASGVRGAAWLPRLPGAAQGPR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914983.1\_1060 [locus\_tag=BN49\_RS06585] [protein=PTS lactose/cellobiose transporter subunit IIA] [protein\_id=WP\_002914983.1] [location=complement(1088132..1088446)] [gbkey=CDS]

MELEEQVMGIIINAGQSRSLCYEALHAAKAGDFATADAKMQEAAHYSREAHLVQTQLIEADEGEGKTKMT

LVMVHAQDHLMTSILAKELIAELIAIYRAQPLHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914981.1\_1061 [locus\_tag=BN49\_RS06590] [protein=PTS cellobiose transporter subunit IIC] [protein\_id=WP\_002914981.1] [location=complement(1088470..1089792)] [gbkey=CDS]

MSSLYAKLIDVIERQITPMAGAIGQQKYVTSIRDGFITALPFMIVGSFLLVFIFPPFSPDTTWGFARAWL

QFSLDHRDALMLPFNFSMGVMTLFIAVGIAASLAKHHHLDSLTAGMLSLMSFLLVAAPLKDGQISTAYFS

GQGIFTAILVAIYSTELYAFLKRHNITIRLPPEVPAGVARSFEILIPVLAIILTLHPLNLFIEAQLGMII

PEAIMSLVKPLVAASDTLPAILLSVLVCQVLWFAGIHGALIVTGIMNPFWMANLSVNQAAMAAGTAIPHI

YVQGFWDHYLLIGGVGSTLPLALMLLRSKAVHLRTIGRMGVVPGVFNINEPILFGAPIIMNPLFFLPFVL

VPMVNATLAYFALKLDLVSRVVSMTPWTTPAPIGASWAANWSFSPVILCLICMATAMVMYLPFLKAYEKQ

LLAQERENAVGQADNAAQTA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914979.1\_1062 [locus\_tag=BN49\_RS06595] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_002914979.1] [location=complement(1089802..1090116)] [gbkey=CDS]

MKKIMLCCSAGMSTSLLMKKMIAEAEQRGLPVEINAYGVAEFAEQVGHYQVVLLGPQVKYMQQDLQKQAD

KYGIRVEPINMMDYGMQKGAAVLDFALSLIENKN

>lcl|NZ\_FO834906.1\_prot\_WP\_023317224.1\_1063 [locus\_tag=BN49\_RS06600] [protein=PTS transporter subunit EIIC] [protein\_id=WP\_023317224.1] [location=1090294..1091565] [gbkey=CDS]

MNIQLMNVAVDIIEQRLAPLANVLTRNNHITAMRDSFALAMPFVIVGSLLVPILFPPVSIDGASRFGQVY

LLLRPILLPTFQLTIGLVALIVAFGASASLAKQYRLPERLCGLTGCLAFLLFIGFRETAVSNVYLGGMGI

FTALISSTYSIEIIRFFYKKGWCIRLPDEVPLMTRNGFQLLIPLLVVMLSISVMNAILLQTTGRIVPELI

SEAVRPLVLASDTLMAVLISLFICNLLWFIGIHGALIITGIMNPFWMTYLFENQQALAAGSPTLPHVYLQ

GFWDFYLLIGGIGSTLPLVLMAMRSRSRQLKSVAKIGLLPSLFNINEPILFGFPVIMNPVFLLPFLFVPL

INACIAWYLTQLGILDRAVAMLPWSMPSPLGAAWSANGSWKNLCMSLFAMFNAWMLYRPFFKVYERQLAE

TER

>lcl|NZ\_FO834906.1\_prot\_WP\_002914972.1\_1064 [locus\_tag=BN49\_RS06605] [protein=carbohydrate porin] [protein\_id=WP\_002914972.1] [location=1091828..1093165] [gbkey=CDS]

MIKLKHSIPLALLSLAGASSPACADPKYDFALHGYIRSGILANSDGNRADSVGLMPDGKWRLGNEEDTKI

ELIPTVTLTADSGVVAKVQANLTHQSKCTSDWNCQDDDGHDVQFREGFAELSNLDFAPEMTFWAGKRYSS

SNTSSHQFDWEYIQYNGTGGGFDNMDLGFARFDAGVYAFSPTDETKAYPVDKGDQGYPDDYSLNLWLKKI

AGTGFDLELIGHHMNRNENHPTSAEKGYGVTGIYNFDGFYGLTGGYSRLALQYGKGLAAGDSLGKNGWGW

ANLENTQSWRVVLDSVASMGDLEISTFAFWQKDKNYRWWTEDENGWGRSMWVAGIRPYHQITRNFAMQYE

LGYEYLDDKNYKGVNGKGKGGLTKVTVAPTLTFDSGFWARPQLRFFVTYAKWDKGVSDALDGNYNWDTNT

ITAGGYSRSGSTDTVNFGVQAEVWF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529177.1\_1065 [locus\_tag=BN49\_RS06610] [protein=hypothetical protein] [protein\_id=WP\_016529177.1] [location=1093178..1095370] [gbkey=CDS]

MKPMKNLLLMGLLSALGAGGALAAERSHFTHFITRDGATLKDGDKVFRFAGIHAPELHRIEDDARGPCRA

DPRGWGQYFKWPTAQEQQNWIQAMVQTGAKAQRVYVLSVQQEFDKACGRETHILAPETADGMPRLNEKAM

RVYDNMIAEADKQGLRLILPFIDHWWWWGGREQLAAFYHEKAEDFYRTDSKTFKAYLDVIRQVITRTNTV

TGRAYYDEKAIMAWETGNELEDTNADFLHQTAAWIKKWAPHQLVVDGTYKKINPFALTDPNVDIVSNHYY

TNADNNHPGQVTQDLRAVGGQKVYLVGEFGLLPADQLNAIMQSIVHSEVNGAQAAGGLIWGFRGHRHDGG

FYWHKESTGHYSYHLPGFAKEGEANQEQAVVDLVRTAAAQMAGQQTMTPLPKPEAPLLRETTSPFAINWM

GAAVGRSYDVERAASPTGPWTVVGRDISDGVNEWNPETMVLFRDDYRQLQLGHTYYYRVTAKNESGRSAH

SNVISVQHSEENQPPIVTLEPALTTTQDQGVELTASWQDDGLPSREVKVGWQHAGDGQVHFCHADRAQTR

AWFTAPGTYALTFTADDGLLKSSKTVTVTVGEATGKAPADFCRYHGEVYGVAEGRLTVMKSDKDALTVGE

DGFLGPFANEGDKVSWQVQAPWSGQFLLNVTFNGKWGGKQNSFVVNGGAPQTVAFPQTDEQGQQLRIPVT

LKAGSNQIDFGRFAGDWGYMFIKSIEVVAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002914970.1\_1066 [locus\_tag=BN49\_RS06615] [protein=glycoside hydrolase family 1 protein] [protein\_id=WP\_002914970.1] [location=1095421..1096821] [gbkey=CDS]

MQQYQFPQGFLWGAAASGPQTEGVTNKRHRSIWDSWFAEQPERFYQQVGPQTVCDTYHQYPQDVALMKQT

GFNSFRTSIQWSRLIADLETGAPDPDAVRFYHAYLDEMIANGIEPMINLYHFDMPEALQKQYGGFESAHV

AELFARFARTAFSLFGHKVKYWITFNEPIVPVEGGYLYDFHYPCKKDGRLAAQVAFNIMLAHAKAVTAYR

ELALAGEIGVVLNLTPSYTLTDSDADKKAAGYADLFFNRSFLDPLVKHEFPKALCEILAAHDCLPTTSKD

DAALILSADIDFLGVNYYVPRRVKARESEYDLDYFTPEYYFENAVNPQGRFNPYRDNNEILPQAIYDIAA

NIRDNYGNIKWYLAEIGIAMDRQSEGEPGADGVIDDTFRIQLMEEHLVQLHRAIADGANCFGVHQWTFID

NWSWINAFKRRYGFWRLDLETGERQIKRNALWFAELATSNGFTSDK

>lcl|NZ\_FO834906.1\_prot\_WP\_004185384.1\_1067 [gene=flhA] [locus\_tag=BN49\_RS06620] [protein=formate hydrogenlyase transcriptional activator FlhA] [protein\_id=WP\_004185384.1] [location=complement(1096875..1098947)] [gbkey=CDS]

MSYTPMSDLGQQGLFDITRLLLQQPDLAALSETLTRLVQQSALADEAAIILWNAGNHRAARYACDEAGHP

VSYEDETVLAHGPVRRLLSRPDALHCDHETFADTWPQLIRSGLYRPFGYYSLLPLAADGRIFGGCEFLRR

DNRPWSEKEFQRLHTFAQIVAVVTEQIQNRVSNNVDYDLLCHERDNFRILVAITNAVLSRLDIDELVSEV

AKEIHRYFRIDAISVVLRSDRKGKLNIYSTHYLDASHPVHDQSEVDEAGTLTERVFKSKEMLLLNLHEHD

TLAPYEKMLFEMWGNKIQTLCLLPLMSGNTLLGVLKLAQCDEQVFTTTNLKLLRQIAERVSIAIDNALAY

REIQRLKERLVDENLALTEQLNNVESEFGEIIGRSEAMNNVLKQVEMVAQSDSTVLILGETGTGKELIAR

AIHNLSGRNGRRMVKMNCAAMPAGLLESDLFGHERGAFTGASAQRIGRFELADKSSLFLDEVGDMPLELQ

PKLLRVLQEQEFERLGSNKLIQTDVRLIAATNRDLKQMVIDREFRSDLYYRLNVFPIHLPPLRERPDDIP

LLVKAFTFKIARRMGRNIDSIPAETLRTLTRMEWPGNVRELENVIERAVLLTRGNVLQLSLPERDIVEAP

RTPAVLPEEGEDEYQLIVRVLKESNGVVAGPKGAAQRLGLKRTTLLSRMKRLGINKDELV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529178.1\_1068 [gene=hypE] [locus\_tag=BN49\_RS06625] [protein=hydrogenase expression/formation protein HypE] [protein\_id=WP\_016529178.1] [location=complement(1099184..1100194)] [gbkey=CDS]

MKSVQLAHGSGGQAMQQLIGDLFMQAFANSWLAEQEDQARLDLAALAAQGDRLAFSTDSYVIDPLFFPGG

NIGKLAVCGTANDVAVSGAIPRYLSCGFILEEGLEMATLEAVVASMADTARAAGIAIVTGDTKVVPRGAA

DKLFINTAGIGAIPADIRWGTQQISAGDVLLVSGTLGDHGATILNLREQMGLDGALSSDCAVLTPLIQTL

RPLSGVKALRDATRGGVNAVAHEFAAASGCGIELQEATLPVNDTVRGVCELLGLDALNFANEGKLVLAVA

RDEAENVLAHLRSHALGRDAAIIGEVVARPGVRSVGLYGVKRTLDLPHTEPLPRIC

>lcl|NZ\_FO834906.1\_prot\_WP\_004145781.1\_1069 [gene=hypD] [locus\_tag=BN49\_RS06630] [protein=hydrogenase formation protein HypD] [protein\_id=WP\_004145781.1] [location=complement(1100191..1101312)] [gbkey=CDS]

MRYVDEYRAPEQVMQLVAHLQQRARLLPHTAARPLRIMEVCGGHTHAIFKFGLDQLLPENIEFIHGPGCP

VCVLPMGRIDACIEIASRPGVIFCTFGDAMRVPGKNGSLLQAKARGADVRIVYSPMDALRLAQQNPQREV

VFFGLGFETTMPATALTLRQARERNVDNFYFFCQHITLLPTLRSLLDQPENGIDAFLAPGHVSMVIGTEA

YGFIASDYHRPLVVAGFEPLDLLQGAVMLVEQTIAQRSDVENQYRRVVPDAGNPLAQAAMADVFRLDGDS

EWRGLGVISDSGVQLTPAYQRFDAEAHFRPAPQRVCDDPRARCGEVLTGRCKPHQCPLFASTCNPQSAFG

ALMVSSEGACAAWYQYRSQENEV

>lcl|NZ\_FO834906.1\_prot\_WP\_002914934.1\_1070 [locus\_tag=BN49\_RS06635] [protein=HypC/HybG/HupF family hydrogenase formation chaperone] [protein\_id=WP\_002914934.1] [location=complement(1101312..1101584)] [gbkey=CDS]

MCIGIPGQICAIDGVLAKVEVCGIQRDVDLTLVGAVDEQGQPRLGQWVLVHVGFAMSVINEAEARDTLEA

LQNMFDVEPDVGALLYGEER

>lcl|NZ\_FO834906.1\_prot\_WP\_004181043.1\_1071 [gene=hypB] [locus\_tag=BN49\_RS06640] [protein=hydrogenase nickel incorporation protein HypB] [protein\_id=WP\_004181043.1] [location=complement(1101575..1102447)] [gbkey=CDS]

MCTTCGCGEGNLYIEGDERNPHSAFRSAPFAPAPRQTMTITGVKTDHFAPTRTPEGDLHYGHGEAGTHAP

GQSQRRMLEVEIDVLDKNNRLAARNRARFAAKQQLVLNLVSSPGSGKTTLLTETLTRLKGRADCAVIEGD

QQTVNDAARIRATGTPAIQVNTGKGCHLDAQMIADAAPRLPLADRGILFIENVGNLVCPASFDLGERHKV

AVLSVTEGEDKPLKYPHMFAAASLMLLNKVDLLPYLNFDVERCLACAREVNPHIEIILVSATSGEGMEQW

LTWLETQRCA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914928.1\_1072 [gene=hypA] [locus\_tag=BN49\_RS06645] [protein=hydrogenase maturation nickel metallochaperone HypA] [protein\_id=WP\_002914928.1] [location=complement(1102451..1102795)] [gbkey=CDS]

MHEITLSQRALEIIEQQAQQAGARRVTGVWLKVGAFSCVEASALTFCFELVCRGTLAEGCELHIAEQQAE

CWCDRCQQYVHLVSQHVRRCPHCNNDQLQIVADDGLQIQRLELE

>lcl|NZ\_FO834906.1\_prot\_WP\_002914925.1\_1073 [gene=hycA] [locus\_tag=BN49\_RS06650] [protein=formate hydrogenlyase regulator HycA] [protein\_id=WP\_002914925.1] [location=1103005..1103454] [gbkey=CDS]

MTIWEISEKADYIADRHRQQQEQWHIYCNSLVQGITLSKARLHHAMSCAPDKELCFVLFGHFQVFVALAE

GFNSHTIEYYVENKNGGDKYLIAQATLAMDGTVDGRISNRSRDQVLEHYLAIIATVYDRLYDAMEQDQPV

DLSHLALTH

>lcl|NZ\_FO834906.1\_prot\_WP\_004151047.1\_1074 [locus\_tag=BN49\_RS06655] [protein=4Fe-4S dicluster domain-containing protein] [protein\_id=WP\_004151047.1] [location=1103537..1104145] [gbkey=CDS]

MNRFVIADSTVCIGCRTCEAACSETHRQHGLQAMPRLQVMRNEKESAPQMCHHCEDAPCATVCPVNAIQR

VDGAVQLNESLCVSCKLCGIACPFGAIEFSGSRPLDIPANANTRLAPPAPPAPARVSSLLDWVPGVRAIA

VKCDLCHFDDQGPACVRTCPTNALMLVDSRDIAQASKRKRQLTFNTDLGDLSLFQAQQGERE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530823.1\_1075 [gene=hycC] [locus\_tag=BN49\_RS06660] [protein=formate hydrogenlyase subunit 3] [protein\_id=WP\_016530823.1] [location=1104142..1105968] [gbkey=CDS]

MSVIGLVNQAVAWYAASAVLAFLFAMRKPLSGAIAGIGGAVASAMLVVAGGAALLMPERIHGGMLQFLHL

TIRVGGVNALWLLAIGLSALPVSLFNISWHRHPQVKANGPLVNLLLATATCAVVVTNIGSLVVMAEIMAL

CAAFLTGCAASGKLWFALGRLGTLLMAWTCWLVWSTYGTLELAQINLQAVDMMQNPLLWLPGLVGFALLA

GAIPLHGWAPQAHAGASAPAAALFSTVVMKVGLYGMLTVSLAGGVPPLWWGVMLMALGMITAFIGGLYAL

MEHNIQRLLAYHTLENIGIILLGLGAFVTGVATRNSTLMVLGFIGGMYHLINHSLFKTTLFLGAGAVWFR

TGHRDIEKLGGIGKKMPLISLAMLVGLMAMAALPPLNGFAGEWVIYQSFFKMSTGDLFIGRLLGPLLAVG

LAITGALAVMCMAKVYGVTFLGAPRTKEAENATCAPWLMTLSVVLAAVFCLVGGIAAPWLLPLVSGAFPV

QAQVSSVVSQPMIALLLIACPLLPFLLMIFFKGDRLAARSRGAAWVCGYDHEQSMVVTAHGFAMPVKEAF

APLLKLRHWLNPVRLVPGWQSASAPALLRGIALVELAVLVVIVISRGA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149485.1\_1076 [locus\_tag=BN49\_RS06665] [protein=respiratory chain complex I subunit 1 family protein] [protein\_id=WP\_004149485.1] [location=1105971..1106894] [gbkey=CDS]

MSLLIALLQALVLFAVAPLLSGIVRVARARLHNRRGPGVLQEYRDILKLLGRQSVGPDASGWVFRLTPYV

MVGVMLTIATALPVVTVDSPLPVLGDLITLIYLFAIARFFFAISGLDTGSPFTALGSSREAMLGVLVEPI

LLLGLWVAAQVAGSTHISAITDTLYHWPAARSIPLILALCACAFATFIEMGKLPFDLAEAEQELQEGPLS

EYSGSGFGILKWGISLKQLVVLQMFVGVFFPWGQMTSFSVGGLLLALVVAIVKLVVGVLIIALFENSMAR

LRFCATSRVTWAGFGFAFLAFVSLLVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151044.1\_1077 [gene=hycE] [locus\_tag=BN49\_RS06670] [protein=formate hydrogenlyase subunit HycE] [protein\_id=WP\_004151044.1] [location=1106911..1108620] [gbkey=CDS]

MSEEKIGQHYLAALHQAFPGVVLDEAWQTKDQLTITVKVNYLPEVVEFLYYQQGGWLSVLFGNDERKLNG

HYAVYYVLSMEQGTKCWITVRVEVDANKPEYPSVTPRVPAAVWGEREVRDMYGLVPVGLPDERRLVLPDD

WPDELYPLRKDSMDYRQRPAPTTDAETYEFINELGSKKNNVVPIGPLHVTSDEPGHFRLFVDGENIIDAD

YRLFYVHRGMEKLAETRMGYNEVTFLSDRVCGICGFAHSTAYTTSVENAMGIVVPERAQMIRAILLEVER

LHSHLLNLGLACHFTGFDSGFMQFFRVRETSMKMAEILTGARKTYGLNLIGGIRRDLLKEDMIQTRQLAQ

QMRRDVQELVDMLLSTPNMEQRTVGIGRLDPEIARDFSNVGPMVRASGHARDTRADHPFVGYGLLPMEVH

SEQGCDVISRLKVRINEVYTALNMIDFGLDNLPGGPLMVEGFTYIPHRFALGFSEAPRGDDIHWSMTGDN

QKLYRWRCRAATYANWPTLRYMLRGNTVSDAPLIIGSLDPCYSCTDRMTVVDVRKKKSKVVPYKELERYS

IERKNSPLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002914893.1\_1078 [locus\_tag=BN49\_RS06675] [protein=formate hydrogenlyase complex iron-sulfur subunit] [protein\_id=WP\_002914893.1] [location=1108630..1109172] [gbkey=CDS]

MFTFIKKVIKTGTATHAYPLEPMPVDKNFRGKPEHTPQQCIGCAACVNACPSNALTVEIDLATNQLAWQF

NLGRCIFCGRCEEVCPTAAIKLSPEYELAVWKKEDFLQQSRFAICHCRECQRPFAVQKEIDYAIALLKHN

GDTRAELHRESFETCPECKRQKCLVPSDRIELTRHMREAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002914891.1\_1079 [locus\_tag=BN49\_RS06680] [protein=NADH-quinone oxidoreductase subunit B family protein] [protein\_id=WP\_002914891.1] [location=1109172..1109939] [gbkey=CDS]

MSTLLGPRDENGIPVPMTVDESIASMKASLLKKIKRSAYVYRVDCGGCNGCEIEIFATLSPLFDAERFGI

KVVPSPRHADILLFTGAVTRAMRSPALRAWQSAPDPKICISYGACGNSGGIFHDLYCVWGGTDKIVPVDV

YIPGCPPTPAATLYGFAMALGLLEQKIHARLPGELDEQPTELLHADMVQPLRVRIDREARRLAGYRYGRQ

IADDYMRLLGQGDSQVLRWLEAEKDPRLTEIVTHLNQVVEGARIR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914887.1\_1080 [locus\_tag=BN49\_RS06685] [protein=formate hydrogenlyase maturation HycH family protein] [protein\_id=WP\_002914887.1] [location=1109936..1110346] [gbkey=CDS]

MSETVVFSQLSRKFIDENDATPDQAQQVVYYSLAIGHHLGVIDCLEAALSCPWDAYLAWIATLEAGSAAR

RKMEGVPKYGEIVIDSSHVAMLANAFDKAQSAQTPQQQAWSKTLLSMLHDIHQESAIYLMVRRLRD

>lcl|NZ\_FO834906.1\_prot\_WP\_004174683.1\_1081 [gene=hycI] [locus\_tag=BN49\_RS06690] [protein=hydrogenase maturation peptidase HycI] [protein\_id=WP\_004174683.1] [location=1110339..1110809] [gbkey=CDS]

MTDVLLCVGNSMMGDDGAGPLLAEMCAANPAGQWVVIDGGSAPENDIVAIRELRPERLLIVDATDMGLNP

GDIRIIDPDDIAEMFMMTTHNMPLNYLVDQLKEDVGEVIFLGIQPDIVGFYYPMTQPVKEAVARVYQQLA

GWQGKGGFTQLEAADD

>lcl|NZ\_FO834906.1\_prot\_WP\_002914883.1\_1082 [locus\_tag=BN49\_RS06695] [protein=type I toxin-antitoxin system SymE family toxin] [protein\_id=WP\_002914883.1] [location=complement(1110806..1111114)] [gbkey=CDS]

MSAQHPTAARGIARAIRQLTVGYVRKRHEDRKTRETRRYTRHAALSLNGDWLEQAGFPVGTQVRVSVSPG

KLVIENLELAAPGTGLPSGQSCAGGEPGSPQG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530820.1\_1083 [locus\_tag=BN49\_RS06700] [protein=6-phospho-beta-glucosidase] [protein\_id=WP\_016530820.1] [location=complement(1111296..1112720)] [gbkey=CDS]

MASFPQGFLWGGALAANQSEGAYLEGGKGLTTVDTLPHGAHRLPVKLGLEKRFTLREDEFYPSHQAIDFY

HRYKEDIALMAEMGFSVFRTSIAWSRLFPCGDEQQPNPQGIAFYRSLFEECKKHGIEPLVTLCHFDVPMH

LVMEYGSWRNRKMVDFFSHYARTCFEAFDGLVKYWLTFNEINIMLHSPYSGAGLVFEEDENQEQVKYQAA

HHELVASALATKIAHEINPQNQVGCMLAGGNFYPYSCKPEDVWMALEKDRENLFFIDVQARGAYPVWAAR

VFREKGVTIAKQPGDDEILKNTVDFVSFSYYASRCASAEMNASNTNAANIVKSLKNPHIPASEWGWGIDP

LGLRITMNMMYDRYQKPLFLVENGLGARDEIDANGDINDDYRISYLREHIRAMRDAIGDGIPVMGYTSWG

CIDLVSASTGEMSKRYGFVYVDRDDAGNGTLARKRKKSFFWYQKVIASNGADLD

>lcl|NZ\_FO834906.1\_prot\_1084 [gene=ascF] [locus\_tag=BN49\_RS06705] [protein=PTS cellobiose/arbutin/salicin transporter subunit IIBC] [pseudo=true] [location=complement(1112747..1114189)] [gbkey=CDS]

MSKNYAALAQQIVAAIGGVDNVAAVTHCMTRLRFVVKDDEQVDSSTLKGLAGVLGVVRSDNQCQVIIGNT

VSQAYREVVNLLPGDLRPAEPQGKAPLTLKRIGAGILDALIGTMSPLIPAIIGGSMVKLLAMILEMSGAL

PKGSPTLTLLALIGDGAFFFLPLMVAASAAVKFKTNMSLAIAIAGVLVHPGFIELMAKAAQGEHVEFAFI

PVTAVKYTYTVIPALVMT\*CLSYIERWVDRITPAVTKNFLKPMLIVLIAAPLAILLIGPLGIWIGSAISA

LVYTIHSYLGWLSVAIMGGLWPLLVMTGMHRVFTPTIIQTIAETGKEGMVMPSEIGANLSLGGSSLAVAW

KTKNPELRQTALAAAASAILAGISEPALYGVAVRLKRPLIASLISGFICGAVAGIAGLASHSMAAPGLFT

SVQFFDPANPMTIVWVFGVMALSVVLSFALTLILGFEDIPVEQAAADARARQARAQASHA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174685.1\_1085 [locus\_tag=BN49\_RS06715] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_004174685.1] [location=1114457..1115470] [gbkey=CDS]

MATMLEVAKRAGVSKATVSRVLSGNGYVSQETKDRVFKAVAESGYRPNLLARNLATKTTQTLGLVVTNTL

YHGVYFSELLYHVARMTEDKGRQLILADGKHSAQEEREAIQYLLDLRCDAIIIYPRFLTVDEMDEIVENH

SQPIMVLNRRLRRHASHCVWSDQKASAMRVVERLIALGHRDIAFITGSLDSPTGVERLAGYKDALAGHGI

ALNEALIAEGRWTPETGAAGVESLRQRGVTYSALVASNDDMAIGAMKQLHQLGVKVPEQVSVVGFDDIAL

APYMVPSLASVRVPVTEMIKESINRLIFMLDGGEFNFQQSFPGALIERESLVAGPCA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914875.1\_1086 [gene=hydN] [locus\_tag=BN49\_RS06720] [protein=electron transport protein HydN] [protein\_id=WP\_002914875.1] [location=1115607..1116134] [gbkey=CDS]

MNRFIIADASKCIGCRTCEVACVVSHQEHQDCASLTPHTFQPRIHVIKGVNVSTATACRQCEDAPCANVC

PNGAISRDKGFVHVMQERCIGCKTCVVACPYGAMEVVVRPVIRHSGAGLNVVAEKAEANKCDLCFHRESG

PACMEVCPTHALVCVDRNKLEQMNIEKRRRTALAW

>lcl|NZ\_FO834906.1\_prot\_WP\_046042571.1\_1087 [gene=hypF] [locus\_tag=BN49\_RS06725] [protein=carbamoyltransferase HypF] [protein\_id=WP\_046042571.1] [location=1116143..1118383] [gbkey=CDS]

MNGVQIRIRGKVQGVGFRPFVWQLARAQARCGDVCNDGDGVLVRLVGGDDGFTAALADHCPPLARIDSTA

CIPYRWAATPQDFTIRESGAGRMRTQIVPDAATCPACLAEMNDPRARRYRYPFINCTHCGPRLTIIRAMP

YDRPFTAMAPFPLCSPCEAEFRDPADRRFHAQPVACPDCGPRLEWRAEGEALDGEAALQAAIARLAAGDI

VAIKGIGGFHLACDAGNPAAVATLRARKHRPAKPLAVMLPTATGLPAAAAALMGSPAAPIVLIAKAQVSG

LCDEIAPGLAEVGVMLPSNPLQHLLLQGLARPIVMTSGNLSGRPPALSNAQALNELADIADGFLLHNRDI

VQRMDDSLVRSSGEMLRRARGYVPDALPLPPGLGDIPPLLALGADMKNTFCLARGSEAVLSQHFGDLGEE

GVEQQWRSAMQLMQSIYAFVPQRVVVDAHPGYRSTQWAASLPLPLPLETVLHHHAHAAACLAEHRWPLDG

GDVIALTLDGIGMGENGALWGGECLRVNYRECEHLGGLPAVALPGGDLAARQPWRNLLAHCLAFVPDWQD

YPQAATLRQRNWPLLAQAIERGINAPRASSCGRLFDAVACALDCAPESLSYEGEAACRLEALAASCPGVS

HPVTLPWRDDALDLATFWRQWLSWQATPAQKAWAFHDALACGLAAMARDCATVRGIDTMVCSGGVLHNRL

LAARLTFYLADFTLLFAQQLPAGDGAIAYGQAVIAAARGQAQGIQP

>lcl|NZ\_FO834906.1\_prot\_WP\_016532303.1\_1088 [locus\_tag=BN49\_RS06730] [protein=HoxN/HupN/NixA family nickel/cobalt transporter] [protein\_id=WP\_016532303.1] [location=1118380..1119393] [gbkey=CDS]

MIMTVLRQQPRAAGLVLGLIAANFLAWCWALQAFGDSGALMAASLLAWGYGLRHAVDTDHIAAIDNVTRK

MMQQGRRPFAVGAWFSLGHSSIVVLASAAIAATATAFSTQMSWLHDTGSVIGTAVSALFLLAMAFINLVI

LRSVWRSFRAWKRGEPVSDEIVSGGGVMSWLFGKTFRLISRSWQMYLVGFLFGLGFDTATEIGVLGISAA

GASSGISVWSIMVFPALFASGMALVDTLDNVLMVGAYGWAFSKPQRKLYYNMTITGTSVVVALFIGGLEA

LGLLMDKFALSGGIWRWVGALNDNLGDAGFVVVGLFVACWALSVLNYRWRGYDNLAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004211583.1\_1089 [gene=norW] [locus\_tag=BN49\_RS06735] [protein=NADH:flavorubredoxin reductase NorW] [protein\_id=WP\_004211583.1] [location=complement(1119490..1120623)] [gbkey=CDS]

MSDGIVIIGSGFAARQLVKNIRKQDAQIPLTLIAADSMDEYNKPDLSHVISRGQKADDLTLQSAGEFAEQ

YTLRLFPHTWVSDIDAENRLVKSQDNQWRYDKLVLATGATPFIPSVPGRELMLTLNSQREYGAAQSRLHD

AKRVLIVGGGLIGCELAMDFCRAGKAVTVVDNSASVLAALMPPEASSRLQHRLTEMGVHLMLKTQLEGLE

QTADGIRVSLDRQRAITVDAVVAAAGLRPETSLARHAGLQINRGIVVNSQLQTSDPAIYALGDCAEINGV

VLPFLQPILLSAMCLSKNLLAQAGELKLPPMLVKVKTPDLPLHLAGDTRRDDLTWNIVAAKEGLVAKGVD

AENQLRAFVVSEDKMKEAFALLKQLVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004145759.1\_1090 [gene=norV] [locus\_tag=BN49\_RS06740] [protein=anaerobic nitric oxide reductase flavorubredoxin] [protein\_id=WP\_004145759.1] [location=complement(1120620..1122068)] [gbkey=CDS]

MSIVVKNNILWVGQRDWEVRDFHGTEYKTLRGSSYNSYLIREEKNVLIDTVDHKFSREFVQNLRREIDLA

DLDYIVINHAEEDHAGALTELMMQIPDTPIYCTANAIDSINGHHHHPEWNFHVVKTGDTLDIGNGKQLIF

VETPMLHWPDSMMTYLTGDAVLFSNDAFGQHYCDEHLFNDEVDQTELYEQCQRYYANILTPFSRLVTPKI

TEILGFNLPVEMIATSHGVVWRDNPTQIVEKYLEWAADYQEDRITIFYDTMSNNTRMMADAIAQGITEVD

PRVAVKIFNVARSDKNDILTNVFRSKGVLVGTSTMNNVMMPKIAGLVEEMTGLRFRNKRASAFGSHGWSG

GAVDRLSTRLQDAGFEMSLSLKAKWRPDIDALELCRQHGRDIARQWALSPLPVAEAATTPEPQDCACAAA

AAADLGPMMQCSVCQWVYDPAKGEPNQDVQPGTPWSEVPDNFLCPECSLGKDVFDVLATEAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004890240.1\_1091 [gene=norR] [locus\_tag=BN49\_RS06750] [protein=nitric oxide reductase transcriptional regulator NorR] [protein\_id=WP\_004890240.1] [location=1122256..1123806] [gbkey=CDS]

MSFSVDELARIAIDLQSDIGHTDRFSRLITTLRQILGCDASALLRYEAHQFVPLAIDGLAQDVLGRRFAL

EGHPRLEAIARAGDVVRFPADSDLPDPYDGLIPGHESLKVHACVGLPLFAGQTLIGALTLDGMDADRFDS

FSDEELRLIAALVAGALNNALLIARLEAQNVLPAQAVNYPLPERQEIIGLSGPMLQLKKEIDIVAASDLN

VLISGETGTGKELVAKAVHQGSPRAANPLVYLNCAALPESVAESELFGHVKGAFTGAISNRSGKFEMADN

GTLFLDEIGELSLALQAKLLRVLQYGDIQRVGDDRSLRVDVRVLAATNRDLRQEVVEGRFRADLYHRLSV

FPLSVPPLRERESDVVLLAGYFCEQCRLRMGLARVILAEAARNRLQQWSWPGNVRELEHAIHRAVVLARA

TQAGDEVVLEPQHFQFAVAAPMLPTETAAAAPATGNINLREATDSFQREAISRALEANQGNWAATARALE

LDVANLHRLAKRLGLKGSPPGKSSAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004174691.1\_1092 [gene=gutQ] [locus\_tag=BN49\_RS06755] [protein=arabinose-5-phosphate isomerase GutQ] [protein\_id=WP\_004174691.1] [location=complement(1123769..1124734)] [gbkey=CDS]

MSNFLLEAGRQTLMLELQEASRLPERLGDDFIRAAETIIHCEGKLIVSGIGKSGHIGKKLAATFASTGTP

AFFVHPAEALHGDLGMLDSRDVMLFISYSGSAKELDLIVPRLEEKGIPLLAMTGKSTSPLALAAKAVLDI

AVEREACPMHLAPTSSTVNTLMLGDALAMAVMQARGFNEEDFARSHPAGALGARLLNKVHHLMRRDEEVP

RVNTEANVMDAMLELSRTGLGLVAVCDEANRVQGVFTDGDLRRWLVAGGTLNDGVTRAMTRNGVTLQADS

RAVEAKERLMKHKISAAPVVDENGQLVGAINLQNFYQAGIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004181024.1\_1093 [locus\_tag=BN49\_RS06760] [protein=DNA-binding transcriptional repressor] [protein\_id=WP\_004181024.1] [location=complement(1124727..1125500)] [gbkey=CDS]

MKPRQRQAAILEFLQSQGKCSVEELAQHFDTTGTTIRKDLVTLENAGTVIRTYGGVVLNKDEADPPIDHK

TLINTHKKAQIAEAAVRYIHDGDSIILDAGSTVLQMVPLLSHFNNITVMTNSLHIVNALSEFDNEQTILM

PGGTFRKKSASFHGQLAENAFEQFSFDKLFMGTDGIDLNAGVTTFNEVYTVSKAMCNAAREVILMADSSK

FGRKSPNIVCGLERVDKLITDADIDPEFQRALEAKGIAVIITGEHHE

>lcl|NZ\_FO834906.1\_prot\_WP\_004145754.1\_1094 [gene=gutM] [locus\_tag=BN49\_RS06765] [protein=transcriptional regulator GutM] [protein\_id=WP\_004145754.1] [location=complement(1125567..1125926)] [gbkey=CDS]

MVTALIIVAAIAWLTQLAFGGWQIRRFNRAFDSLCQQGRVGVGRSAGRFQPRAIVAIAVDDNDRISDTLL

MKGFTIFASPQKIPALAGKHIAELQPDVIFPHDPRCQNALSLALNPKHG

>lcl|NZ\_FO834906.1\_prot\_WP\_002914815.1\_1095 [gene=srlD] [locus\_tag=BN49\_RS06770] [protein=sorbitol-6-phosphate dehydrogenase] [protein\_id=WP\_002914815.1] [location=complement(1126083..1126862)] [gbkey=CDS]

MNQVAVVIGGGQTLGEFLCRGLAAEGYRVAVVDIQSEKASRVAQEINAEYGEGMAYGFGADATSEASVTA

LAHGVDEIFSRVDLLVYSAGIAKAAFISDFALGDFDRSLQVNLVGYFLCAREFSRLMIRDGIKGRIIQIN

SKSGKVGSKHNSGYSAAKFGGVGLTQSLALDLAEYGITVHSLMLGNLLKSPMFQSLLPQYATKLGIDESE

VEQYYIDKVPLKRGCEYQDVLNVLMFYASPQASYCTGQSINVTGGQVMF

>lcl|NZ\_FO834906.1\_prot\_WP\_004174693.1\_1096 [gene=srlB] [locus\_tag=BN49\_RS06775] [protein=PTS glucitol/sorbitol transporter subunit IIA] [protein\_id=WP\_004174693.1] [location=complement(1126875..1127237)] [gbkey=CDS]

MTVIYQTTITHIGACATMALEEQMLITFREGAPADIEEYCFIHNHGELAGTLQPGAELQLGEQRYPVTAV

GEVAEQNLRELGHITLRFDGHREAEFPGTVHVAGPVPDAIAPGCVLKFVA

>lcl|NZ\_FO834906.1\_prot\_WP\_015958868.1\_1097 [locus\_tag=BN49\_RS06780] [protein=PTS glucitol/sorbitol transporter subunit IIB] [protein\_id=WP\_015958868.1] [location=complement(1127251..1128231)] [gbkey=CDS]

MTRIRIEKGTGGWGGPLELDAVKGKKIVYITAGTRPAIVDRIASLTGWQPVDGFKEGEPAESDIGVAIID

CGGTLRCGLYPKRRIPTVNIHATGKSGPLAQYITEDIYVSGVKEDNIQCIAPDSAGVSEPPAENKSAGRD

YDTSKKITEQSDGLLAKVGMGMGSVVAVLFQAGRDTIDTVLKTILPFMAFVSALIGIIMASGIGDWIAHG

LAPLASHPLGLVTLALICSFPLLSPFLGPGAVIAQVIGVLIGVQIGLGNIPPHLALPALFAINAQAACDF

IPVGLSLAEARQDTVRVGVPSVLVSRFLTGAPTVLIAWFVSGFIYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002914812.1\_1098 [locus\_tag=BN49\_RS06785] [protein=PTS glucitol/sorbitol transporter subunit IIC] [protein\_id=WP\_002914812.1] [location=complement(1128228..1128791)] [gbkey=CDS]

MIDVVTHGAEWFIGLFQKGGEVFTGMVTGILPLLISLLVIMNALINFIGQQRIEKLAQRCAGNPISRYLL

LPCIGTFVFCNPMTLSLGRFMPEKYKPSYYAAASYSCHSMNGLFPHINPGELFVYLGIANGLTTLGLPLG

PLAVSYLLVGLVTNFFRGWVTDLTTSIFERKMAIQLSQKVHLSGATS

>lcl|NZ\_FO834906.1\_prot\_WP\_004174694.1\_1099 [gene=mltB] [locus\_tag=BN49\_RS06790] [protein=lytic murein transglycosylase B] [protein\_id=WP\_004174694.1] [location=1129068..1130147] [gbkey=CDS]

MLKRRYLALLPLCVLLAACSSKPKTPAETEMASGTGGFLLEPQHNVMQMGGDFANNPAAAQFIDKMVAKH

GFDRQQLQEILSQAKRLDYVLRLMDRQAPTGLPPTGPTGAWLRYKKQFITPDNVQNGVVFWNQYQDALNR

AYQVYGVPPEIIVGIIGVETRWGRVMGKTRILDALATLSFSYPRRAEYFSSELETFLLMARSESDDPLDL

KGSFAGAMGYGQFMPSSYKQYAVDFNGDGHINLWDPVDAIGSVANYFKQHGWVSGDLVAVQALGQAPGLE

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AVAQARGGY

>lcl|NZ\_FO834906.1\_prot\_WP\_021440606.1\_1100 [locus\_tag=BN49\_RS06795] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_021440606.1] [location=1130484..1131194] [gbkey=CDS]

MVSNLVGGDAAMIELEQLVAGYDGVAITPPLSGMICPGSLTAIVGLNGCGKSTLLKTLAGFLPPVSGRLR

WQGKRPVIGWLAQRHALESQFPLNVQDVVSQGAWPGVSLLRGLGGGTRRRIGTVLERVGLAGLAKTPIEA

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LLLTPQRACWGATRAVLPAFSHVRSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149458.1\_1101 [locus\_tag=BN49\_RS06800] [protein=metal ABC transporter permease] [protein\_id=WP\_004149458.1] [location=1131191..1132054] [gbkey=CDS]

MIWHTFFQPFIEFGFMRRALVVCLALSLSTTMLGVFLLLRRMSLMGDALSHAILPGVAVGYLLSGMSLLA

MTLGGFIAGIVVALVAGWVSRRTPLKEDASFAGFYLGSLALGVTLVSLRGSSVDLLHLLFGSILAVDRDA

ALFVSGVASLTLLCIALCYRGLVSEAFDSAWLQVNHRRLPALLHGLFLALLVLNLVAGFQVLGTLMAVGV

MMLPAVAARCWARTLPGILLLAAGMGALCAWLGLSLSWAISLPAGPAIVLTASALFFVSLFFGTRSRLLV

GWRTLMG

>lcl|NZ\_FO834906.1\_prot\_WP\_016531227.1\_1102 [locus\_tag=BN49\_RS06805] [protein=metal ABC transporter substrate-binding protein] [protein\_id=WP\_016531227.1] [location=1132062..1132940] [gbkey=CDS]

MKRSAIVVALALGLMAQGAMAKTLNVVSSFSVLGDIAQQVGGEHVHVDTLVGPDGDPHTFEPSPKDSALL

SKADVVVVNGLGLEGWLDRLIKASGFKGELVVASKGVKTHTLDEEGKTVTDPHAWNSAANGALYAQNILD

GLVKADPEDKAALTSSGKRYIDQLTSLDGWAKAQFSAIPQAKRKVLTSHDAFGYFGRAYNVTFLAPQGLS

SESEASAAQVAALIKQIKADGVHTWFMENQLDPRLVKQIASATGAQPGGELYPEALSKPGGVADSYVKMM

RHNVELIANSMK

>lcl|NZ\_FO834906.1\_prot\_WP\_046042581.1\_1103 [gene=pncC] [locus\_tag=BN49\_RS06810] [protein=nicotinamide-nucleotide amidase] [protein\_id=WP\_046042581.1] [location=1133080..1133577] [gbkey=CDS]

MTDSELMQLSEKIGRALKARGATVTAAESCTGGWIAKAITDIAGSSAWFERGFVIYSNEAKSQMIGVSEA

TLRDNGAVSEPVVVEMAIGALRAARADYAISVSGVAGPDGGSVEKPVGTVWFGVASVSGQGVTRRECFAG

DREAVRRQATAYALNLLWQQFLQNT

>lcl|NZ\_FO834906.1\_prot\_WP\_002914769.1\_1104 [gene=recA] [locus\_tag=BN49\_RS06815] [protein=recombinase RecA] [protein\_id=WP\_002914769.1] [location=1133668..1134726] [gbkey=CDS]

MAIDENKQKALAAALGQIEKQFGKGSIMRLGEDRTMDVETISTGSLSLDIALGAGGLPMGRIVEIYGPES

SGKTTLTLQVIAAAQREGKTCAFIDAEHALDPVYARKLGVDIDNLLCSQPDTGEQALEICDALARSGAVD

VIVVDSVAALTPKAEIEGEIGDSHMGLAARMMSQAMRKLAGNLKQSNTLLIFINQIRMKIGVMFGNPETT

TGGNALKFYASVRLDIRRIGAVKEGDNVVGSETRVKVVKNKIAAPFKQAEFQILYGEGINFYGELVDLGV

KEKLIEKAGAWYSYNGDKIGQGKANAITWLKENPAAAKEIEKKVRELLLNNQDAKPDFVVDGNDAEETEQ

DF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529460.1\_1105 [gene=recX] [locus\_tag=BN49\_RS06820] [protein=recombination regulator RecX] [protein\_id=WP\_016529460.1] [location=1134794..1135294] [gbkey=CDS]

MTDPSSRRSGYARLLDRAIRILAMRDHSEQELRRKLVAPVMSKNGPEALDVTPDELEQVVAWCIENRYLD

DNRFVGQFIASRSRKGYGPARIRQELSQKGIARQVVDQAMRECDIDWVSFAREQAQRKYGEPLPSAFTEK

VKVQRFLLYRGYLMEDIQEIWRNFAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002914765.1\_1106 [gene=alaS] [locus\_tag=BN49\_RS06825] [protein=alanine--tRNA ligase] [protein\_id=WP\_002914765.1] [location=1135545..1138172] [gbkey=CDS]

MSKSTAEIRQAFLDFFHSKGHQVVASSSLVPHNDPTLLFTNAGMNQFKDVFLGLDKRNYSRATTAQRCVR

AGGKHNDLENVGYTARHHTFFEMLGNFSFGDYFKQDAIKYAWELLTGENWFALPKEKLWVTVYETDDEAF

DIWANEVGVPRERIIRIGDNKGAPFASDNFWQMGDTGPCGPCTEIFFDHGDHIWGGPPGSPEEDGDRYIE

IWNIVFMQFNRQADGTMEPLPKPSVDTGMGLERIAAVLQHVNSNYDIDLFRDLIASVAKVTGATDLTNKS

LRVIADHIRSCAFLVADGVIPSNENRGYVLRRIIRRAIRHGNMLGAKDTFFWKLVAPLIDVMGSAGDELK

QQQAQVEQVLKTEEEQFARTLERGLALLDEELSKLKGDTLDGETAFRLYDTYGFPVDLTADVCRERNIKV

DEAGFEAAMEEQRRRARESSGFGADYNAMIRVDGASEFKGYDHLELNGKVTALFIDGKAVDSVSAGQEAV

VILDQTPFYAESGGQVGDKGELKGAGFSFAVSDTQKYGQAIGHIGKVASGTLKVGDAVQADVDEARRQRI

RLNHSATHLMHAALRQVLGTHVAQKGSLVNDKALRFDFSHFEAMKPEEIRAVEDLVNAQIRRNLAIETNI

MDIDAARASGAMALFGEKYDDRVRVLRMGDFSTELCGGTHAARTGDIGLFRITSESGTAAGVRRIEAVTG

EGAMAILHAQSDQLNDIAQLLKGDSHNLGEKVRAALERTRQLEKELQQLKEQAAAQESANLSSKAEEING

VKLLVSELTGVEPKMLRTMVDDLKNQLGSTIVVLATVADGKVSLIAGVSKDVTDRVKAGELVGMVAQQVG

GKGGGRPDMAQAGGTDASALPAALASVKGWVSAKL

>lcl|NZ\_FO834906.1\_prot\_WP\_000906486.1\_1107 [gene=csrA] [locus\_tag=BN49\_RS06830] [protein=carbon storage regulator CsrA] [protein\_id=WP\_000906486.1] [location=1138536..1138721] [gbkey=CDS]

MLILTRRVGETLMIGDEVTVTVLGVKGNQVRIGVNAPKEVSVHREEIYQRIQAEKSQQSSY

>lcl|NZ\_FO834906.1\_prot\_WP\_002914359.1\_1108 [locus\_tag=BN49\_RS06865] [protein=BON domain-containing protein] [protein\_id=WP\_002914359.1] [location=1140242..1140556] [gbkey=CDS]

MKWFKAIPAFCATLLVTTALAGCAGSATKESTGGYIDDTVVTTKVKTALFNDKDIKSSEISVQTFKGRVQ

LSGFVSSAESAKRAVEVTRRVQGVRMVENDLRIK

>lcl|NZ\_FO834906.1\_prot\_WP\_004174701.1\_1109 [gene=yqaB] [locus\_tag=BN49\_RS06870] [protein=fructose-1-phosphate/6-phosphogluconate phosphatase] [protein\_id=WP\_004174701.1] [location=1140682..1141248] [gbkey=CDS]

MYEGYAGLIFDMDGTILDTEPTHRQAWNEVLGRYGMRFDEQAMVALNGSPTWRIAQAIIELNQADLDPHR

LAQEKTQAVKAMLLDSVRPLPLIEVVKAWHGRRPMSVGTGSESAVAEALLAHLGLRHYFSAVVAADHVVN

HKPAPDTFLLCAERMGVAPEKCVVFEDADFGLQAAKRAGMDAVDVRLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002914355.1\_1110 [locus\_tag=BN49\_RS06875] [protein=DedA family protein] [protein\_id=WP\_002914355.1] [location=1141245..1141673] [gbkey=CDS]

MSDALSLTSLFASSFLSATLLPGNSEVVLVAMLLAGVSHPWWLVLIATIGNSLGGVTNVILGRLFPLRKT

SRWQERAAGWLKRYGAVTLLLSWAPVVGDLLCLLAGWMRISWGPVLFFLCLGKALRYIAIAAATLQGMTW

WH

>lcl|NZ\_FO834906.1\_prot\_WP\_002914353.1\_1111 [gene=gshA] [locus\_tag=BN49\_RS06880] [protein=glutamate--cysteine ligase] [protein\_id=WP\_002914353.1] [location=1141740..1143296] [gbkey=CDS]

MIPDVSQALAWLEKHPQALQGIQRGLERETLRVNADGTLATTGHPPALGSALTHKWITTDFAEALLEFIT

PVDGDIEHMLTFMRDVHRYTARQLGDERMWPLSMPCYIAPGQDIELAQYGTSNVGRLKTLYREGLKNRYG

ALMQTISGVHYNFSLPMAFWQAKCGVEDAESGKEAISAGYFRSIRNYYRFGWVIPYLFGASPAICSSFLQ

GKPTTLPFEETGNGMYYLPYATSLRLSDLGYTNKSQSNLGITFNDLHEYVAGLKRAIKTPSEEYAKIGLQ

KDGKYLQINSNILQIENELYAPIRPKRVTRRGETPSDALLRGGIEYIEVRSLDINPFSPIGVDAQQVRFL

DLFMVWCALADAPEMSSDELLCTRTNWNRVILEGRKPGLTLGIGCESAQFPLAQVGKDLFRDLRRVAQTL

DSIHGGQAYQQVCDELLACFDDPELTFSARILRSMIEEGIGGTGRALADRYRTQLREEPLEILSEDDFIA

ERDASVARQKKVEAEDSEPFEALLARHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914351.1\_1112 [gene=luxS] [locus\_tag=BN49\_RS06885] [protein=S-ribosylhomocysteine lyase] [protein\_id=WP\_002914351.1] [location=1143453..1143968] [gbkey=CDS]

MPLLDSFTVDHTRMEAPAVRVAKKMNTPHGDEITVFDLRFCVPNQEVMPERGIHTLEHLFAGFMRDHLNG

NGVEIIDISPMGCRTGFYMSLIGTPDEQRVADAWKAAMADVLKVKDQNQIPELNVYQCGTYTMHSLEEAQ

DIARHIIERDVRINSNDELALPKEKLQELHI

>lcl|NZ\_FO834906.1\_prot\_WP\_046042588.1\_1113 [locus\_tag=BN49\_RS06890] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_046042588.1] [location=1144021..1144788] [gbkey=CDS]

MTTTLSFSFQHRPLVPFAHDYAHGDQEDWHQHDCAQLLHILSGVVRVATPVGYWVVPPGRGVWLPAGTPH

ALRMTGNVAARTLFIDPLARADLPAGCQIVQITPLLRELIVSSLALAERYAPASRDERIYELILDEIRGM

AVLPFGLPEPQSETLRRLCQQVREAPGEAWSSGQAAKACSMSERTLNRHFQQQTSLTWSEWVRRAKLMEA

LVRLAQGHSVLRVALELGYGSHSAFSAMFRRVMGVAPSDYFRPPA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531941.1\_1114 [gene=leuA] [locus\_tag=BN49\_RS06895] [protein=2-isopropylmalate synthase] [protein\_id=WP\_016531941.1] [location=complement(1144767..1146443)] [gbkey=CDS]

MLSHPAEKYRPYPPIALPDRRWPDRQISHAPRWLSTDLRDGNQALAEPMDSARKLQFWDLLLECGFKEIE

VAFPSASQTDFNFVRQLIDEQRIPEDVTIQVLTQARDPLILRTFEALRGARRATVHLYNATAPLFRELVF

GMDKAEVIALATRATRLIRQQSEQQPETRWQYEYSPETFCFTEPEFALEICEAVADVWQPCAERPMIVNL

PATVEVNTPNVYADQIEYFCRHFSRRGEVCISVHPHNDRGTGVASAELAVMAGADRVEGCLFGNGERTGN

VCLVTLAMNLYSQGIDPELRFEQMNRVVEVVENCNQIPVHPRHPWAGSLAYTAFSGSHQDAIKKGFDARQ

PGDPWQMPYLPIAPQDIGCSYEAVIRVNSQSGKSGSAWLIEQNHGLKLPRGLQQDFSQHVQQATDSDGKE

MTHHALWQLFRTRYGLQAQPALTLLDYQSASQQDGQLSLQATLRHHGETRRLQGQGNGLLSAAASGLSAL

FRQPFMIKDYHEHTLGARSDSRSVAYIRCVFPQGESYWGVGIDNDVARASLQALCNALSAADQAGGRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002914342.1\_1115 [gene=emrB] [locus\_tag=BN49\_RS06900] [protein=multidrug efflux MFS transporter permease subunit EmrB] [protein\_id=WP\_002914342.1] [location=complement(1146580..1148118)] [gbkey=CDS]

MQQQKPLEGAQLVIMTIALSLATFMQVLDSTIANVAIPTIAGNLGSSLSQGTWVITSFGVANAISIPITG

WLAKRVGEVKLFLWSTTAFAIASWACGVSNSLTMLIFFRVIQGIVAGPLIPLSQSLLLSNYPPAKRSIAL

ALWSMTVIVAPICGPILGGYISDNYHWGWIFFINVPIGVAVVLMTLQTLRNRETKTEQRRIDGVGLALLI

IGIGSLQVMLDRGKELDWFSSNEIIILTIVAVVAISFLIVWELTDDNPIVDLSLFKSRNFTIGCLCISLA

YMLYFGAIVLLPQLLQEVYGYTATWAGLASAPVGVIPVILSPIIGRFAHKLDMRRLVTFSFIMYAVCFYW

RAWTFEPGMDFGASAWPQFIQGFAVACFFMPLTTITLSGLPPERLAAASSLSNFTRTLAGSIGTSITTTL

WTNREALHHAQLTESVTPFNPNAQQIYDQLQGMGMTQQQASGWIAQQITNQGLIISANEIFWISAAIFIL

LLGLVWFARPPFSAGGGGGGAH

>lcl|NZ\_FO834906.1\_prot\_WP\_016531940.1\_1116 [gene=emrA] [locus\_tag=BN49\_RS06905] [protein=multidrug efflux MFS transporter periplasmic adaptor subunit EmrA] [protein\_id=WP\_016531940.1] [location=complement(1148134..1149306)] [gbkey=CDS]

MSANAESQTPQQPGSKKGKRKGALLLLTLLFIIIAVAYGIYWFLVLRHYEETDDAYVAGNQVQIMAQVAG

SVTKVWADNTDYVQKGDPLVTLDQTDAQQAFEKAKTQLAASVRQTRQQMINSKQLQANIDVKKTALAQAQ

ADLNRRIPLGAANLIGREELQHARDTVASAQAELDVAIQQYNANQAIVLGTRLEQQPAVLQAATEVRNAW

LALQRTQIVSPISGYVSRRSVQPGAQIGTTTPLMAVVPATNLWIDANFKETQLAHMRIGQPATMISDIYG

DDVKYTGKVVGLDMGTGSAFSLLPAQNATGNWIKVVQRLPVRIELDEKQLAEHPLRIGLSTLVEVNTTDR

DGEMLASQVRSSPVYESNAREIALDPVNKLIDEIIQANAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002914337.1\_1117 [gene=mprA] [locus\_tag=BN49\_RS06915] [protein=transcriptional repressor MprA] [protein\_id=WP\_002914337.1] [location=complement(1149432..1149962)] [gbkey=CDS]

MDSSFTPIEQMLKFRASRHEDFPFQEILLTRLCMHMQGKLLENRNKMLKAQGINETLFMALITLESQENH

SIQPSELSCALGSSRTNATRIADELEKRGWIERRESDNDRRCLHLQLTEKGHQFLREVLPPQHNCLHQLW

SSLSTSEKDQLEHITRKLLSRLDQMEEEGVLADSLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914335.1\_1118 [gene=ygaH] [locus\_tag=BN49\_RS06925] [protein=L-valine transporter subunit YgaH] [protein\_id=WP\_002914335.1] [location=complement(1150053..1150388)] [gbkey=CDS]

MNSEVLLLGVIVGGVNYLFRYLPLRLRVGHARPARRGPVSVLLDTIGIASICALLVVSSVPEILADAHRL

APTLTGFLVLGAAFWKTRSIIVPTLLSAFAYGLAWKITNGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002914333.1\_1119 [locus\_tag=BN49\_RS06930] [protein=AzlC family ABC transporter permease] [protein\_id=WP\_002914333.1] [location=complement(1150378..1151124)] [gbkey=CDS]

MENPAPLTCALPERVATVGEGVKDSLPIVISYLPVAFAFGLNATRLGFTPLESLFFSCIIYAGASQFVIT

AMLAAGSSLWVAALTVMAMDVRHVLYGPSLRSRIRSALDKKKTALWAFGLTDEVFAAATARLVRDNRRWS

ENWMLGLAFTSWASWVCGTLAGAWSGNGLLVDYPAVEAALGFMLPALFMSFLLASFQRQQSLCVTAALAG

ALGGILLFSIPAAILAGIVCGCLTALLQAMLKGMPDEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002914330.1\_1120 [gene=proX] [locus\_tag=BN49\_RS06935] [protein=glycine betaine/L-proline ABC transporter substrate-binding protein ProX] [protein\_id=WP\_002914330.1] [location=complement(1151303..1152301)] [gbkey=CDS]

MRHSTMLATAAFATLLATSAFAADLPGKGITVKPAQSTISEESFQTLLVSRALEKLGYTVEKPSEVDYNV

AYTSIAAGDTTFIATNWQPLHDDMYAAAGGDNKFYRKGVYVSGAAQGYLIDKKTAEQYHITSIDQLKDPQ

IAKLFDTNNDGKADLTGCTPGWGCEAVINHQIDAYGLSKTVTHNQGNYAAMMADTIARYKEGKPVLYYTW

TPYWVSDVLKPGKDVVWLQVPFSSLPGEQKNIDTKLANGANYGFPVNTMHIVANKAWAEKNPAAATLFSV

MKLPIADINAENAMMHEGHASEADINGHVDGWIKAHQPLFDSWVKTALAAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042592.1\_1121 [gene=proW] [locus\_tag=BN49\_RS06940] [protein=glycine betaine/L-proline ABC transporter permease ProW] [protein\_id=WP\_046042592.1] [location=complement(1152380..1153447)] [gbkey=CDS]

MADQTNPWGSAPSTDSAAQAADAWGGASTAAPANGGGADWLHSAPAPQPEQFNIMDPFHKTLIPLDSWVT

HAIDWIVLHFRPLFQGIRVPIDYILSAFQQLLLGMPAPMAIIAFALIAWQISSLGMGVATLVSLIAIGAI

GAWSQAMVTLALVLTALLFCMVIGLPLGIWLARSPRAAKIIRPLLDAMQTTPAFVYLVPIVMLFGIGNVP

GVVVTIIFALPPIVRLTILGINQVPADLIEASRSFGASPRQLLFKVQLPLAMPTIMAGVNQTLMLALSMV

VIASMIAVGGLGQMVLRGIGRLDMGLATVGGVGIVILAIILDRLTQAVGRDARSRGNRRWYTTGPLGLIT

RPFCR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529305.1\_1122 [gene=proV] [locus\_tag=BN49\_RS06945] [protein=glycine betaine/L-proline ABC transporter ATP-binding protein ProV] [protein\_id=WP\_016529305.1] [location=complement(1153440..1154642)] [gbkey=CDS]

MAIKLEIKNLYKIFGEHPHRAFKYIEKGLNKAQILEKTGLSLGVKDASLAIEEGEIFVIMGLSGSGKSTM

VRLLNRLIEPTRGQVLIDGVDIAKMSDAELREVRRKKIAMVFQSFALMPHMSVLDNTAFGMALAGVPAAE

REQKAREALRQVGLENYAHAWPDELSGGMRQRVGLARALAINPDILLMDEAFSALDPLIRTEMQDELIKL

QAKHQRTIVFISHDLDEAMRIGDRIAIMQNGEVVQVGTPDEILNNPANDYVRTFFRGVDISQVFSAKDIA

RRSPVGLIRKTPGFGPRSALKLLQDEDREYGYVIERGNRFVGIVSIDSLKTALSAGQGIEAALIDAPLAV

EAQTPLSDLLSHVGHAPCAVPVVDEEQQYIGIISKRMLLQTLDREGVNHG

>lcl|NZ\_FO834906.1\_prot\_WP\_002914327.1\_1123 [gene=nrdF] [locus\_tag=BN49\_RS06950] [protein=class 1b ribonucleoside-diphosphate reductase subunit beta] [protein\_id=WP\_002914327.1] [location=complement(1154999..1155961)] [gbkey=CDS]

MTHLTRVSAINWNRIDDDKDLEVWNRLTSNFWLPEKVPLSNDIPAWQTLSAAEQQLTIRVFTGLTLLDTI

QNTVGAPALMADALTPHEEAVLSNISFMEAVHARSYSSIFSTLCHSKEVDAAFAWSESCDPLQRKAQLML

GYYQADEPLKKKIASVFLESFLFYSGFWLPMYFSSRGKLTNTADLIRLIIRDEAVHGYYIGYKYQKGLEI

VSPGKREELKNFALDLLMDLYDNELAYSRELYGESGWFDDVSAFLCYNANKALMNLGYEALFPAEMAAVN

PAILAALSPNADENHDFFSGSGSSYVIGKMEETADDDWDF

>lcl|NZ\_FO834906.1\_prot\_WP\_046042595.1\_1124 [gene=nrdE] [locus\_tag=BN49\_RS06955] [protein=class 1b ribonucleoside-diphosphate reductase subunit alpha] [protein\_id=WP\_046042595.1] [location=complement(1155972..1158113)] [gbkey=CDS]

MATTTAERITAAVDFHALNAMLNLYDSEGRIPFEKDRQAVEAFMATQVQPNALTFPSQEDKLSWLVSEGY

YDPQVLAGYDRGFVLALFAHARRAPFRFQTFLGAWKFYTSYALKTFDGKHYLEDFAERSVMVALTLARGD

EQQARQLTEEILSGRFQPATPTFLNAGKQQRGELISCFLLRIEDNMESIGRAVNSALQLSKRGGGVAFLL

SNLREAGAPIKRIENQSSGVVPVMKMLEDAFSYANQLGARQGAGAVWLHVHHPDILRFLDTRRENADEKI

RIKTLSLGVVIPDITFQLAKEDAQMALFSPYDVERLYGKPFADCAIGDLYPQLVADERVRKRWIRARDLF

QRLAEIQFESGYPYIMFEDTVNRASPVAGRVTMSNLCSEILQVSTPSAYNEDLSYAHIGEDISCNLGSLN

IAHTMDSPDFGRTIATAVRALTAVSDMSDIQSVPSVTAGNAASHAIGLGQMNLHGYLAREGIAYGSPEGL

DFTNIYFYTVTWHALHTSMQLARERGQRFAGFEQSRYASGAYFDKYLQEEWQPKTERVRTLFARAGISLP

DRESWRQLRDDVMRYGIYNRYLQAVPPTGSISYINHATSSIHPIVSKIEIRKEGKTGRVYYPAPFMNNDN

LALYQDAYEIGPEKIIDTYAEATRHVDQGLSLTLFFPDTATTRDINKAQIYAWKKGIKTLYYIRLRQLAL

EGTEIEGCVSCAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002914321.1\_1125 [gene=nrdI] [locus\_tag=BN49\_RS06960] [protein=class Ib ribonucleoside-diphosphate reductase assembly flavoprotein NrdI] [protein\_id=WP\_002914321.1] [location=complement(1158086..1158496)] [gbkey=CDS]

MSLIVYFSSRSENTHRFVQRLGLPAVRIPLNEREHLRVDEPYILIVPSYGGGGTAGAVPRQAIRFLNDVH

NRQLIRGVIAAGNRNFGDGWGRAGDVIAQKCAVPYLYRFELMGTPDDINTVRKGVSEFWQRQPQNV

>lcl|NZ\_FO834906.1\_prot\_WP\_002914320.1\_1126 [gene=nrdH] [locus\_tag=BN49\_RS06965] [protein=glutaredoxin-like protein NrdH] [protein\_id=WP\_002914320.1] [location=complement(1158493..1158738)] [gbkey=CDS]

MRIIIYTRNDCVQCHATRRAMESRGLAFEMVNVDQQPDAADTLREQGFRQLPVVIAGELRWSGFRPDMIN

RLRPSFTAASA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145727.1\_1127 [locus\_tag=BN49\_RS06970] [protein=carboxymuconolactone decarboxylase family protein] [protein\_id=WP\_004145727.1] [location=complement(1158922..1159353)] [gbkey=CDS]

MNQLRQPFSELSPEVYKGLVQASIALEKSELGNALVELVYLRVSQINGCAFCLEKHSQALRKGGMAQSKL

DALAGWRVSAHFTPAERAALAWAESVTDIATSHAEDEVYQPLREHFTPRQISDLTFAVSLMNAFNRLAVA

MRL

>lcl|NZ\_FO834906.1\_prot\_WP\_046042596.1\_1128 [locus\_tag=BN49\_RS06975] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_046042596.1] [location=1159442..1160794] [gbkey=CDS]

MEAINLPLYQRIARQLKSAIERGELTPGSRLPASRVYAQEQGVSRATIENAWGELVAQGWLERRGQAGTF

VSERLSPRQLAPVPPVQPAAPTEPLPFQMGLPALDLFPRGQWARVMGRRLRTQSRFDLAPGDPGGDPLLR

QAIVDYLRLSRSIDCQPDQVLITGSYAASMNLILRTLAQPGQHMWMEDPGYPFIRPVVEAGQLAVDAIPV

DDEGMDVGWGQRHHPQARFALLTPAHQSPLGGALSLPRRRQLLAWAAERDAWIIEDDYDSEFRYHGKPLP

PLKSLDAPQRVIYAGTFSKSMFPALRTAWLVVPTPLVARFHQTAERQSCTVPTLWQQTLADFIQQGHFWR

HLKKMRASYSQRRQWLESALQAQGFQVTPQLGGIQLVMSVSGDDRLLARRAVVAGLAVQALSDWRIRHAG

EGGLLMSFTNIRSPAMADGLARRLREAIAI

>lcl|NZ\_FO834906.1\_prot\_WP\_002914293.1\_1129 [locus\_tag=BN49\_RS06980] [protein=DUF883 domain-containing protein] [protein\_id=WP\_002914293.1] [location=complement(1160938..1161285)] [gbkey=CDS]

MANHVNRNNFDENAEDIHNDVSQLADTLEEVLKSWGSDAKEEAEAARVKAQSLLKETRARLNGHNRVQQA

ALDARQAACDALGCADTYVRNKPWHSVGAAAAVGVFIGVLLNLRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914291.1\_1130 [locus\_tag=BN49\_RS06985] [protein=DUF2002 family protein] [protein\_id=WP\_002914291.1] [location=1161435..1161797] [gbkey=CDS]

MYLRPDEVARVLEKAGFTMDVVTQKAYGYRRGDNYVYVNREARMGRTALVIHPALKERSNMLAEPASDIK

TCDHYEQFPLYLAGDAQQHYGIPHGFSSRMALERFLNGLFGEAQPAMSTN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530923.1\_1131 [locus\_tag=BN49\_RS06990] [protein=L-alanine exporter AlaE] [protein\_id=WP\_016530923.1] [location=complement(1161883..1162332)] [gbkey=CDS]

MFSAHSRLRHAVADTFAMVVYCTVVNMMIEIFLSGMTFEQSLSSRLVAIPVNIIIAVPYGIYRDFAMRQA

RRISPARWMKNMADVLAYVTFQSPVYVAILWSVGADWHQIVTAVSSNLAVSMMMGAAYGYFLDYCRRLFR

VAPYQQAKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914287.1\_1132 [gene=stpA] [locus\_tag=BN49\_RS07000] [protein=DNA-binding protein StpA] [protein\_id=WP\_002914287.1] [location=1163061..1163462] [gbkey=CDS]

MSSMLHKLNNIRSLRALSREFSIDVLEEMLEKLRIVTEEKRTQQQQAAQQQAEYQEKVNTWLELMRADGI

SPDELVADIQPPKAGGKKRQPRPAKYRYTDHTGAEKTWTGQGRMPKPIAEAVAQGKSLDSFLI

>lcl|NZ\_FO834906.1\_prot\_WP\_002914284.1\_1133 [locus\_tag=BN49\_RS07005] [protein=hypothetical protein] [protein\_id=WP\_002914284.1] [location=complement(1163535..1163714)] [gbkey=CDS]

MFAVGDLVQPRAGGPKLKVVEVQGEQLVVVQAAQEQGERYSLKSDEVTPYQEEGDFGVC

>lcl|NZ\_FO834906.1\_prot\_WP\_002914281.1\_1134 [gene=lpxO] [locus\_tag=BN49\_RS07010] [protein=lipid A hydroxylase LpxO] [protein\_id=WP\_002914281.1] [location=1163920..1164822] [gbkey=CDS]

MKYIILLIIVIAVLYVHYRGRVRYRFWRQLSDHSTFTAPLNGFMYLFSRVPNTPYLRPEMFPELAILQQN

WQVIRDEGLHLQQLEQIKAADKYNDAGFNSFFKTGWKRFYLKWYEDAHPSASQLCPQTTALLRDIPSVKA

AMFATLPDGSRLPRHRDPYAGSLRFHLGLATPNDDRCFIEVDGQRYSWRDGEGVLFDETYIHYAENTSGE

NRLILFCDIERPMRYRWAQKVNHWLGRHLMSAASAPNDIGDRTGGINRAFRYIYQIRIVGKRLKKWNKTV

YYIVKWLLFGGIAWLIWSAF

>lcl|NZ\_FO834906.1\_prot\_WP\_004185349.1\_1135 [locus\_tag=BN49\_RS07015] [protein=rhodanese family protein] [protein\_id=WP\_004185349.1] [location=complement(1164803..1165348)] [gbkey=CDS]

MTIATLTPAEAQAQIAQGARLIDIRDADEYAREHIPDAELVPLATLTSGAPLNARAGETVIFHCQAGSRT

QNNAIRLAAAAAPAQACLLAGGIQAWKAAGLPVVEDSSQPLPLMRQVQIAAGVLILLGVLLGYTVNGGFF

LLSGAVGAGLTFAGVTGFCGMARLLATMPWNRRQGVKTRSR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914277.1\_1136 [locus\_tag=BN49\_RS07020] [protein=metalloregulator ArsR/SmtB family transcription factor] [protein\_id=WP\_002914277.1] [location=complement(1165356..1165655)] [gbkey=CDS]

MTTPEDLQARAGEAAALMKAMSNPHRLLILCMLCDAPRASAGELARATGLSPSATSQHLARMRDEGLIDS

ERDAQRIHYFITHPAVQQVINTLKTLYCP

>lcl|NZ\_FO834906.1\_prot\_WP\_004212889.1\_1137 [locus\_tag=BN49\_RS07025] [protein=NAD(P)H-dependent oxidoreductase] [protein\_id=WP\_004212889.1] [location=complement(1165731..1166336)] [gbkey=CDS]

MANVLVLKSSINGETSLTNQLINEFLAARQAAGHGDRLTEHDLSAMALPTLDRPLFAALRGAVDPQPAIR

EAVALSDQLIAELKASDLLVIGAPMYNLNVPTDLKKWFDLVARARETFRYTESWPQGLVEGVRAVVVSSR

GGIHQGETTDAVTPYLRAVLGLMGIQEVEFIYAEGLDNRPHGRDAGIASARAQIARLAVPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145715.1\_1138 [locus\_tag=BN49\_RS07030] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004145715.1] [location=1166440..1167348] [gbkey=CDS]

MRDDLNAIPVFVTVVESGNFASAAAILHVTRSAVGKTIARLEARLGVALFQRTTRRQLLTEEGEQFYLQC

REALERIREAEETLQRGKDEVQGRLRVSLPVLFGQRCVAPLLFRLSQRYPLLKLELHYSDRQVNLLEEGF

DLAVRIGSLADTGSLRARALGEHGMVLCAAAEYLRQQPAPQTIAGLNEHRTLGYLHNGQLQKWQLYDPQQ

GEVRFSPQTWLIQDDFAAIAAAVQQGMGIAWLPDWLVAQALADGTLQQVLAPSAQVRFAIHAVWPEGPWL

PQKTRAAIDALREGLPLTATPG

>lcl|NZ\_FO834906.1\_prot\_WP\_023285477.1\_1139 [locus\_tag=BN49\_RS07035] [protein=sigma-54-dependent Fis family transcriptional regulator] [protein\_id=WP\_023285477.1] [location=complement(1167431..1169218)] [gbkey=CDS]

MAGNPFLLAPEVNANPLLSDSWSRCQRYGLDPATEDFPRLGAGELADRLASHRGLQQLAQPVVEALSRQV

ADLQSVVILSDPDGLVLHTLGDTQALQKAQRVALAPGNLWSESGRGTNAIGTALAIDDGCEIDGRQHFLT

RNQNLYCAAMPLQRPDGSIAGVLDISGPANFPHQHTFGWVKAAAKQIEYLWVKQSLHPEQWLMSLHRQVD

KLDSVEELLLVFSDNVLTAGNRLAMREFGLSAAQFGQLTFASLFPTLTQTAVSVPLPLTTPQGRYHYRLR

APTRRRVAVSAPPAMHLPFTSPREGEKLLRLLNAGIALCIEGETGSGKEYVSRTLHRHSRWRSGKFVAIN

CAAIPESLIESELFGYQPGAFTGASKNGYIGKIREADGGVLFLDEIGDMPLALQTRLLRVLQEKEVAPLG

ASRSVPVNFALICATHRNLTQRVSAGEFREDLLWRLREYALALPPLREWPALETFIATLWHDLGGASRRV

TLSNALLVHLSQLPWPGNVRQLQSVLKVMLALADEGDTLTTDALPEAYRAAPAPLPRGGLQARDEQLIVD

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042606.1\_1140 [locus\_tag=BN49\_RS07040] [protein=aldehyde dehydrogenase] [protein\_id=WP\_046042606.1] [location=1169474..1170994] [gbkey=CDS]

MRYAHPGQPGAVVSFKSAYGNFIDGRFVEPLSGEFFMNTSPVDGSNIAQFPRSDARDIDFALDAAHRAAP

AWGKTSVQQRSRLLLQVADRIEQHLEYLAVAESWDNGKPIRETLNADLPLAVDHFRYFAGCLRAQEGSTA

EIDETTVAYHFHEPLGVVGQIIPWNFPLLMAAWKLAPALAAGNCVVLKPAEQTPLSITLLLELIGDLFPA

GVLNVVQGFGKEAGEALATSKRIAKLAFTGSTPVGRHILACAAENIIPCTVELGGKSPNIYFADVMDGEE

EFIEKAVEGLVLGFFNQGEVCTCPSRALIHESIYEPFMARVMEKVAQIRRGDPLDTDTMIGAQASRQQFD

KILSYIQIAREEGGQILTGGERAAIAPALDNGFYIQPTLIKGRNDMRSFQEEIFGPVIGVTTFKDEAEAL

AIANETQFGLGAGVWTRDTNLAYRMGRGIKAGRVWTNCYHVYPAHAAFGGYKQSGVGRETHKMALDAYQQ

TKNLLVSYGTALLGLF

>lcl|NZ\_FO834906.1\_prot\_WP\_004145710.1\_1141 [locus\_tag=BN49\_RS07045] [protein=fimbrial protein] [protein\_id=WP\_004145710.1] [location=1171696..1172277] [gbkey=CDS]

MKKQPRFITILIGALLSGVALQATAANTINPDSGTSSEGAGGQVIFNGSITDSSCNVDSSSNGQKVDLGK

WASNYFTGTGFETTKTPFHIKVKDCPASVTTVAVLFDGARDQSDNSLLAINGGASGVAIKLYEHDRSTAV

SLGKTSAKQTVTPGTSGGTGSADLEFYADYISTAATVTAGKADGTANFNMIYN

>lcl|NZ\_FO834906.1\_prot\_WP\_042942767.1\_1142 [locus\_tag=BN49\_RS07050] [protein=molecular chaperone] [protein\_id=WP\_042942767.1] [location=1172472..1173134] [gbkey=CDS]

MMKKIIAVAAFLLCTTAAQAGIVMGGTRVIYQEGKREAAISVTNADTHTPYLVQSWVENYAENDKARVPF

IVTPPLFRLDPEQNNVLRINFIGASLPRDRESVFWLNVKSIAPTRQGEVNKLQVNIKSKFKIFYRPNDLA

GDPAKAWQQLKFSQSGGRLTVINPTPYFVSFYAVEVGGQSIDDPGMVAPFGEKTWPVNGHGTVKWRAIND

YGGVSDFAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046044021.1\_1143 [locus\_tag=BN49\_RS07055] [protein=fimbrial biogenesis outer membrane usher protein] [protein\_id=WP\_046044021.1] [location=1173171..1175726] [gbkey=CDS]

MKRITTARVREYALLPVTAGRAVALATVPTMMFCLSPLGRAMADDYFDPAALEFADPQQQTSDLHYFAKP

GGQQPGTYPVTVVVNDQELGQADITFVDDGGQLRPVLTPGQLAEYGVNVSAFPAFQALHEGETFTRIEKF

IPDASSRFSFANQRLTLSIPQAAMNVQSRGYVDPSRWDDGVPAAFVDYYFSGAQIKNADEGESSRSNYLN

LRSGLNLGAWRLRNISSMQYDQQRRHWDTQSTWLQRDVRSLKSLLRIGDTYTTGDVFDSIQFRGVQLMSD

DEMLPDSQRGFAPTIRGVAHSNAKVTVSQHGYVIYETFVSPGAFAISDLYPTSQSGDLEVKVTESNGAVR

TFTQPYSAVPYMLREGRGKFSLSAGRYHSGGESVRSPEFLQGTLFYGLTAGFTLYGGTQLARDYQAWALG

LGRGFGEFGSLGGDVTQAVTRTPSGKRYTGHSLRAQYQKNFVSSGTAFSLASYRYSSSGYYDFAEASALE

SAQGQVDNRRRREELSVSQSLGGLGSLAVSAWSQEYWHRQSRDETVHLGFYSAWKGISWGVGYYYTRTSG

QQKNDRSWSFNINIPLGGPLSDSAVSYNTTSDSNGYTSQQMSLYGAVPTRPNLFYSVQQGYGNQGRGSNS

SASLDYHGGFGNAQIGYRHDSASNQLTWGGAGSVVAHPHGVTFGQTVGESFAIVRAPGAAGVAVQNGNNV

HTDWRGYAVVPSLTAYRKNVITLDTESMADDTDVDQQGQTVIPGGGAVVMANYQTHIGNRVLFTLRNAQG

PLPFGASARLVEEEESGNPPGGMVADGGQVYLSGVPQEGTLAVSWNVNNQSQSCTLHFHLPDNPQQSLNT

VKTVTGLCQTR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532246.1\_1144 [locus\_tag=BN49\_RS07060] [protein=fimbrial protein] [protein\_id=WP\_016532246.1] [location=1175734..1176828] [gbkey=CDS]

MKSVFRLLPFLFLLGLSAYLPGVRAETCRANIGQTTVNIPNIKYLPTLPVNTQMTSAMADNGSGIPFSCD

LQLPTASAKRIVYKQLKTGGSPMVINGQHVYPSAIDGIGYALSFQCAGGPMRAIDGSHSAGGESVVICDS

ATLPALMTQQQTTVRIAVTFYKTGTVQLADGTHTNSPPLPQVGEMTIEQQTSASASFVASAPVSIDIAAL

NVDIGSSGSCQVATSTIQVSLGTVNRGEFHGKGTTGGQAKRFSIPVFCPTPTDVRIGFFGVSVESDTLAL

SQASNSASGVGVKLTYGNNPGAAVPDGTSVKINEASNLPILKRVTGASAGTAEAINFNAQYVQTDATVAA

GTANSMVTFALEYN

>lcl|NZ\_FO834906.1\_prot\_WP\_046042615.1\_1145 [locus\_tag=BN49\_RS07065] [protein=molecular chaperone] [protein\_id=WP\_046042615.1] [location=complement(1176743..1177513)] [gbkey=CDS]

MKTQLAVLLCAVTFQACAGITINATRVVYSGKEKVASLNIHNRSSTPYKVQIWLDAGLNTSRIGLPIVAT

PPQVYLSPQQSAQLRFIYLGGGLPGDRESVYWVNIQETPPAAVGTHTLQFVVRTRLKLFYRPPAITTTLA

REVQKLQWQQSGNNLRFTNLGPLHITLVNGALIDNKGHLSPIRNVMLRPCSSHTVMTTDSTRLYQLNYID

DYGAVVPIPLQNAHVPPQASYIPGRRSPCCWPCPPPRWRRFAHTAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145703.1\_1146 [locus\_tag=BN49\_RS07070] [protein=type 1 fimbrial protein] [protein\_id=WP\_004145703.1] [location=complement(1177550..1178101)] [gbkey=CDS]

MKIITLCLATVFAGLAAGSALAAEGKLNFIGKVVNASCKLEGVSDSGVIGVSMGAIPLSRLKNSQSGTGP

AVGIDIRVKDCEKGTYYIVVDGPSPAGTPENRVLALDGSGKPASNVGILLTDRTGTPLSLDERLDPQHDP

RIEISVDGGSGTFRLNAFYYTWDKAHADPGDGNATARFTIMQE

>lcl|NZ\_FO834906.1\_prot\_WP\_042942762.1\_1147 [locus\_tag=BN49\_RS07075] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_042942762.1] [location=1178551..1179411] [gbkey=CDS]

MNALARAADTVTDAAGHSGMKNDNFKDGEMRLTVGLALTLALTLAIMTCGAQARDMQSIEHSGELKVGVP

GDYAPLAFRNAAGELQGYDVDMARDLGRTLGLKVSFVYTSWPALAADLQADKFDIAMGGVTETPARAQAF

ALSHPVVANGKIALANCQAAPRLGSLEKIDRPDVKVIVNPGGTNQSFVDEHIKQAQIIRVQNNVDNLQAL

RQKTADMMVTDLIEGDYYQSKEPGVFCVANETPFAGTASNKVYMMSKDNPALLEKVNQWLDSQDKEVLKR

KWKIRG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042617.1\_1148 [locus\_tag=BN49\_RS07080] [protein=hypothetical protein] [protein\_id=WP\_046042617.1] [location=complement(1179467..1180087)] [gbkey=CDS]

MSLLRSLLFFFGAAVAAALAVLCLWVDIRVFGNDIPEVSLTEVVQESVLAVIVLVHLLLARKYAHLRYSN

ILIGGFFLAMLIRELDGLFDLLSHGSWVWFALLATAGSLLLPLRHLHQTLSQLAAYTRTPYYGMMISGLL

AILVFSRLFGMHGLWYAVLEENYARVVKNTVEEGSESFGYMLCLTATLGYACYFRSLAQQALSPQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145699.1\_1149 [locus\_tag=BN49\_RS07085] [protein=SDR family oxidoreductase] [protein\_id=WP\_004145699.1] [location=complement(1180243..1181037)] [gbkey=CDS]

MKIDLAGKVALVTASTAGIGFAIAKGLAESGAEVILNGRSEQSVNAAIARLQNEVPGAKARPAIADLSDA

DGAAQLLRAVTGVDILVNNAGIYGPQDFYATDDATWDNYWQTNVMSGVRLSRGLLPAMVSKGWGRVVFIS

SESARNIPADMIHYGVTKTAQLSLARGLAKYVAGSGVTVNSVLPGPTISDGFAEMLKDEVAKTGQSLEEL

AKAFVMTHRPSSVIQRAASVAEVANMVVYVCSPQASATSGAALRVDGGVVDDIL

>lcl|NZ\_FO834906.1\_prot\_WP\_015958846.1\_1150 [locus\_tag=BN49\_RS07090] [protein=glyoxylate/hydroxypyruvate reductase A] [protein\_id=WP\_015958846.1] [location=complement(1181098..1182030)] [gbkey=CDS]

MSDITIVVDCNDADFARDICAALQQFPDVTALLPHHQAARDAQYASCWFPDPQLLTRSPGLKLIQAASAG

VDHLPPALFASEIPLCRVIDEDFRHGMFEYALWSVLWFQRHFDRALAHQRTQTWKLYPQRAAADFHIGIM

GLGEIGGYIADQLARLGYRVSGWSRSEKQLAGVTCYRGEEALDSFLGSLDGLINLLPLTAQTRGILAAPL

FNRLPAGAVLINCGRGEHMVNEDVLAALESGQLAGAVLDVFPQEPLPADDPLWRHPQVVITPHMASAASA

EVIARQLLENIQRQRRGLPLKNLVNKHAGY

>lcl|NZ\_FO834906.1\_prot\_WP\_004180964.1\_1151 [locus\_tag=BN49\_RS07095] [protein=class II aldolase/adducin family protein] [protein\_id=WP\_004180964.1] [location=complement(1182036..1182764)] [gbkey=CDS]

MATEQHLRQQLAAAYRLAALFGWEDTLYTHFSVRLPGDGEPRFLINPFGMMFDEVTASNLIVVDMQGKVV

AGDAPANSAGFTIHSAVHMAREDAHCVIHTHTLPGMAVAACEDGLLQLNQISTEFYQRVGYHPYEGVAFD

LDERARIQRSLGNNIAMILQSHGLLSVGRTVADAFYIMYYLNRACEIQMAAAQLAALSPIHTIAPHLSQH

ACEQLMGVEHERQQVWQAWLRRLDRLDTSYKD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151026.1\_1152 [locus\_tag=BN49\_RS07100] [protein=amino acid ABC transporter permease/ATP-binding protein] [protein\_id=WP\_004151026.1] [location=complement(1182765..1184285)] [gbkey=CDS]

MAFDWGYFFSLFSIGAFWQACVTVIVISTLSWGIGLVVGFLLACAKLSAPRWVKIPVELYIWFFRSVPLM

VLLVFVYNLPQLFPVTQPLLGVPFIAGLVSMTVTEAAYMAEIHRGGLLSVAKGQSEAGHALSFSFIGIQR

LIVIPQAFRISLPTLINEYITIIKLSSILSVVSLPELLLTGQRLYAQNFLVMETLLAVAVYYVMVVTVFT

WLFRALENRLDIQRKRPQTLSEAECQALRQSLPALSEESNTPAVNGAPPALDLRGIRKSWGQHEVLKGID

LQVENGEVISIIGPSGSGKTTLIRTINALESLDGGEIILYGEDYLKGGAIVDKRQMRAGVRRIGMVFQSF

NLFPHRTVLDNVMLAPRYHQLLDQPVAREQALALLDRVGLLAHAHKYPGQLSGGQQQRVAIARALALKPD

IMLFDEPTSALDPELVGEVLKVIQSLAREGMTMLIVTHEMDFALSISDRVVLMENGVVQADIAPQVIRSP

LEAPSLQRIREFMGVR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042620.1\_1153 [locus\_tag=BN49\_RS07105] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_046042620.1] [location=complement(1184316..1185119)] [gbkey=CDS]

MTSTLKKISRRVALTLAVSACFSPVTQAAELLTEGVFKVGMEVTYPPFESYDSNNNIVGLDPEFAALIAQ

HLQAKPQLIDTKFTSLILGIGKKYDAVISGMYVTPERQKQADAIPYALSGASIIALKGGAVQPKTEDELC

GVKVGLQAGTTWVTSLKKHSDEWCLKNGKPAITIQEFPTAPEASQALLSKNIGAQLEIAPAAQIIVDKSR

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531987.1\_1154 [locus\_tag=BN49\_RS07110] [protein=isopenicillin N synthase family oxygenase] [protein\_id=WP\_016531987.1] [location=complement(1185139..1186206)] [gbkey=CDS]

MTAVKHAFTELPTIDIRDLVGDDLARRQAVADAIGRAAREVGFFYITGHGIDPALIAGVREAAKQIFALP

MEEKMNYYIGHSKSHKGYVPEGEEIYGSGKPDHKEAFDIGFQAADDHPLVLAGTPLIGANEWPDLPDFRA

RVLAYYDAVFALGHRLFDAFALALGLPEGYFKPMVTCPPAKLRLIHYPFDASVEDVPGIGAHTDYECFTL

LLADQPGLEVLNEESVWIDAPPVKNAAGEEAFVINIGDMLEVLSAGTFVATAHRVRRVPQERYSFPLFFA

CDYHTLIRPLPTFLAAGEAGEYQELSIGEHMWSQALQTYRYLREKVNRGELQLPERARGTNTFGHLKKQA

QQKTP

>lcl|NZ\_FO834906.1\_prot\_WP\_004174773.1\_1155 [locus\_tag=BN49\_RS07115] [protein=TIM barrel protein] [protein\_id=WP\_004174773.1] [location=complement(1186203..1187066)] [gbkey=CDS]

MELKCFRTLWGVTTPWPQTLDELQRVGCCGIEARVPLTVAERRQLADRLQASGLEYIAILFSGGGVLPAQ

HETPEQHLARLQTRFAEASGLNPRFVNLLAGNDRWPLAQQVDFLGKAHELAAGFGLTCSFETHRATSLYS

PWLTLEIIQQLPQLRFTADISHWVVVSERLLDDPSDDFSAFIDRVHHVQARVGYDQGPQVPHPAAPEYQP

ALAFAERFWQQIWRSQRQRGYPQTTLTPEFGADGYLHHLPFTNVPVADLWSLNAWMATRQQAHFQQFLSL

TEQEPQP

>lcl|NZ\_FO834906.1\_prot\_WP\_004145693.1\_1156 [gene=speB] [locus\_tag=BN49\_RS07120] [protein=agmatinase] [protein\_id=WP\_004145693.1] [location=complement(1187077..1188027)] [gbkey=CDS]

MDNLFHQPQGGNEMPRFAGRATMMRLPFIEDLQGLDAAFVGIPLDIGTSQRSGTRYGPRYIRAESVMIRP

YNMATGAAPFDSLSVADIGDVPINTYSLLKSVQIIEDYYTGLNSYPLIPLTLGGDHTITLPILRALTKKH

GPVGLIHVDAHTDTNDEMFGEKIAHGTTFRRAVEEGLLDLKRVVQIGQRAQGYAAGDFQWGVDQGFRLVQ

AEQCWHTSLAPLMAEVRQQMGDGPVYLSFDIDSLDPIWAPGTGTPEVGGLTSIQALEIVRGCRGLNLIGA

DLVEVSPPYDVSGNTSQLAANLLYEMLCVLPGVKYA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914199.1\_1157 [locus\_tag=BN49\_RS07125] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002914199.1] [location=1188143..1189054] [gbkey=CDS]

MHHDASLNIRQLQVFEAVARLESYSRAQQELGISVSAISNAMSQLEGQLGFTLCQRGRGGFSLTEKGQQF

LQQAIRVLSELNELERQSALLKGEHSGTLCISTLDSIETETALSLPVVLRSFSDKFPHVHIKLIIRTPAE

QLNGVLNNHIDLAIGSYNSQVHNIISEPLYREQHWLYCSDLHPMFFSRQLDKEQISQCPLVTRSYWNTSD

LRRRGFSKGSATVETVDAQLLLILSGKYIGYLPEHYAWPWIKENRLRVLLPNEFGFQSPFSAICKRGRSN

EPYLKAFRDLLKKNTVARPKWNY

>lcl|NZ\_FO834906.1\_prot\_WP\_000888203.1\_1158 [locus\_tag=BN49\_RS07130] [protein=Rrf2 family transcriptional regulator] [protein\_id=WP\_000888203.1] [location=1189468..1189947] [gbkey=CDS]

MLDYRFPTALQMVLSVAMAEQMGERSTSAILAYGLEANPSFIRKLMVPLTRDGIIVSTLGRNGSIHLGRP

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DTSGCDPVPEMIARFKKAH

>lcl|NZ\_FO834906.1\_prot\_WP\_046042624.1\_1159 [gene=oqxB] [locus\_tag=BN49\_RS07135] [protein=multidrug efflux RND transporter permease subunit OqxB] [protein\_id=WP\_046042624.1] [location=complement(1190017..1193169)] [gbkey=CDS]

MDFSRFFIDRPIFAAVLSILIFITGLIAIPLLPVSEYPDVVPPSVQVRAEYPGANPKVIAETVATPLEEA

INGVENMMYMKSVAGSDGVLVTTVTFRPGTDPDQAQVQVQNRVAQAEARLPEDVRRLGITTQKQSPTLTL

VVHLFSPNGKYDSLYMRNYATLKVKDELARLPGVGQIQIFGSGEYAMRVWLDPNKVAARGLTASDVVTAM

QEQNVQVSAGQLGAEPLPQESDFLISINAQGRLHTEEEFGNIILKTAQDGSLVRLRDVARIEMGSGSYAL

RSQLNNKDAVGIGIFQSPGANAIDLSNAVRAKMAELATRFPEDMQWAAPYDPTVFVRDSIRAVVQTLLEA

VVLVVLVVILFLQTWRASIIPLIAVPVSVVGTFSILYLLGFSLNTLSLFGLVLAIGIVVDDAIVVVENVE

RNIEEGLAPLAAAHQAMREVSGPIIAIALVLCAVFVPMAFLSGVTGQFYKQFAVTIAISTVISAINSLTL

SPALAALLLKPHGAKKDLPTRLIDRLFGWIFRPFNRFFLRSSNGYQGLVSKTLGRRGAVFAVYLLLLCAA

GVMFKVVPGGFIPTQDKLYLIGGVKMPEGSSLARTDAVIRKMSEIGMNTEGVDYAVAFPGLNALQFTNTP

NTGTVFFGLKPFDQRKHTAAEINAEINAKIAQIQQGFGFSILPPPILGLGQGSGYSLYIQDRGGLGYGAL

QSAVNAMSGAIMQTPGMHFPISTYQANVPQLDVQVDRDKAKAQGVSLTDLFGTLQTYLGSSYVNDFNQFG

RTWRVMAQADGPYRESVEDIANLRTRNNQGEMVPIGSMVNISTTYGPDPVIRYNGYPAADLIGDADPRVL

SSSQAMTHLEELSKQILPNGMNIEWTDLSFQQATQGNTALIVFPVAVLLAFLVLAALYESWTLPLAVILI

VPMTMLSALFGVWLTGGDNNVFVQVGLVVLMGLACKNAILIVEFARELEIQGKGIMEAALEACRLRLRPI

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042626.1\_1160 [gene=oqxA] [locus\_tag=BN49\_RS07140] [protein=multidrug efflux RND transporter periplasmic adaptor subunit OqxA] [protein\_id=WP\_046042626.1] [location=complement(1193193..1194368)] [gbkey=CDS]

MSLQKTWGNIHLTALGAMMLSFLLVDCDDSVAQNAAPPAPTVSAAKVLVKSISQWDSFNGRIEAVESVQL

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SREEWEQRRSAAVQAQADIRAAQAAVDAAQLNLDLTKVTAPIDGRASRALITSGNLVTAGDTASVLTTLV

SQKTVYVYFDVDESTYLHYQNLARRGQGASSDNQALPVEIGLVGEEGYPHQGKVDFLDNQLTPSTGTIRM

RALLDNSQRLFTPGLFARVRLPGSAEFKATLIDDKAVLTDQDRKYVYIVDKDGKAQRRDITPGRLADGLR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002914181.1\_1161 [locus\_tag=BN49\_RS07145] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_002914181.1] [location=1194702..1195064] [gbkey=CDS]

MNTGAIIQDLIDWIDNHLDSRLDIDTVARRAGYSKWHLQRIFKEHTGQPLGEYIRAKKLQKSIERLAHSN

EPILNVAIALGFDSQQSFNRSFKRQYGQAPGVWRRSISRSVAQTSRQRSA

>lcl|NZ\_FO834906.1\_prot\_1162 [locus\_tag=BN49\_RS07150] [protein=flavin reductase] [pseudo=true] [partial=5'] [location=complement(1195075..>1195266)] [gbkey=CDS]

IQQQHNLFMGDIVAAWSNDRVFRNGHWIFDDAPDELRTVHYVAGGQFYAIGKGSKFDHGPGQD

>lcl|NZ\_FO834906.1\_prot\_1163 [locus\_tag=BN49\_RS30265] [protein=LysR family transcriptional regulator] [pseudo=true] [partial=5',3'] [location=<1195252..>1195404] [gbkey=CDS]

VLLLNRSTRRVSFTPQGMQYPAQSQDISALIEHSESSLSESVARPQGRLRV

>lcl|NZ\_FO834906.1\_prot\_WP\_002914164.1\_1164 [gene=smpB] [locus\_tag=BN49\_RS07155] [protein=SsrA-binding protein SmpB] [protein\_id=WP\_002914164.1] [location=complement(1196033..1196515)] [gbkey=CDS]

MTKKKAHKPGSATIALNKRARHEYFIEDEYEAGLALQGWEVKSLRAGKANIGDSYVILKDGEAFLFGANF

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DLKDREWALDKARIMKHAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004174798.1\_1165 [locus\_tag=BN49\_RS07160] [protein=type II toxin-antitoxin system RatA family toxin] [protein\_id=WP\_004174798.1] [location=1196665..1197102] [gbkey=CDS]

MPQISRTALVPFSAEQMYQLVNDVKSYPDFLPGCTGSRVLELGPTQMTAAVDVSKAGISKTFTTRNTLTS

NQSILMSLVDGPFKKLIGGWKFIPLSPEACKIEFHLDFEFTNKLIEMAFGRIFKELAANMVQAFTSRAKE

VYSAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004145682.1\_1166 [locus\_tag=BN49\_RS07165] [protein=RnfH family protein] [protein\_id=WP\_004145682.1] [location=1197092..1197382] [gbkey=CDS]

MPANIRVEVAYALPEKQYLQRVTLDEGATVEQAIIASGLLALRDDIDLAKNKLGIYSRPVKLHDEVHDGD

RVEIYRPLIADPKELRRQRAEKSAAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002914160.1\_1167 [gene=bamE] [locus\_tag=BN49\_RS07170] [protein=outer membrane protein assembly factor BamE] [protein\_id=WP\_002914160.1] [location=complement(1197449..1197790)] [gbkey=CDS]

MRCKTLTAAAAVLLMLTAGCSTLERVVYRPDINQGNYLAPNDVAKIRVGMTQQQVAYALGTPMMTDPFGT

NTWFYVFRQEPGHQKVTQQTLTLTFNSGGVLTNIDNKPALTSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004174799.1\_1168 [gene=recN] [locus\_tag=BN49\_RS07180] [protein=DNA repair protein RecN] [protein\_id=WP\_004174799.1] [location=complement(1197938..1199599)] [gbkey=CDS]

MLAQLTISNFAIVRELEIDFHSGMTAITGETGAGKSIAIDALGLCLGGRAEADMVRRGATRADLCARFAL

KDTPAAQRWLEENQLESGRECLLRRVISADGRSRGFINGTAVPLSQLRELGQLLIQIHGQHAHQLLTKPE

HQKTLLDGYTGEYALTQRMAEHYRQWHQSCRELAQHQQQSQERAARADLLQYQLKELNEFNPLPGEFEQI

DEEYKRLANSGQLLSTCQHALTVLADGEEANLQSQLYTAKQLVSELVGMDSKLSGVLDMLEEAAIQLSEA

SDELRHYHDRLDLDPNRLFELEQRISRQIALARKHQVMPEELPAVYQAMLEEQRLLDDSAGSLESLSQQV

VEHHQLALETARQLHALRQASADELTQLITESMHSLSMPHGVFAIEVAFDERHLTADGADHIEFRVTTNP

GQPLQPIAKVASGGELSRIALAIQVITARKMETPALIFDEVDVGISGPTAAVVGKLLRQLGESTQVMCVT

HLPQVAGCGHHHFFVCKETDGEMTETHMQPLDKRARLQELARLLGGSEVTRNTLANAKELLAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002914158.1\_1169 [gene=nadK] [locus\_tag=BN49\_RS07185] [protein=NAD(+) kinase] [protein\_id=WP\_002914158.1] [location=complement(1199686..1200564)] [gbkey=CDS]

MKNHFKCIGIVGHPRHPTALTTHEMLWRWLCSKGYEVLVEQQIAHELQLSNVKTGTLAEIGQQADLAVVV

GGDGNMLGAARTLARYDINVIGINRGNLGFLTDLDPDNALQQLADVLEGHYIAEKRFLLEAQVCQQDCQK

RISTAINEVVLHPGKVAHMIEFEVYIDEVFAFSQRSDGLIISTPTGSTAYSLSAGGPILTPSLDAITLVP

MFPHTLSARPLVINGDSTIRLRFSHRCSDLEISCDSQIALPIQDGEDVLIRRCDYHLNLIHPKDYSYFNT

LSTKLGWSKKLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002914155.1\_1170 [gene=grpE] [locus\_tag=BN49\_RS07190] [protein=nucleotide exchange factor GrpE] [protein\_id=WP\_002914155.1] [location=1200689..1201279] [gbkey=CDS]

MSSKEQKTPEGQAPEEIITEQHDDVEAVEPEVSAEQVDPRDEKIANLEAQLAEAQKREREVMLRAKADED

NLRRRTEQDIEKAHKFALEKFVNELLPVIDSLDRALEVADKANPELAPMVEGIELTLKSMLDVVRKFGVE

VIADTNVPLDPNVHQAIAMVESEDVAAGNVLSVMQKGYTLNGRTIRAAMVTVAKAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004149392.1\_1171 [locus\_tag=BN49\_RS07195] [protein=HlyC/CorC family transporter] [protein\_id=WP\_004149392.1] [location=complement(1201399..1202685)] [gbkey=CDS]

MEHISTTTLIITLIVMVIISAYFSGSETGMMTLNRYRLRHMAKQGNRPAKRVEKLLRKPDRLISLVLIGN

NLVNILASALGTIVGMRLYGDAGVAIATGVLTFVVLVFAEVLPKTIAALYPEKVAYPSSFLLAPLQVLMM

PLVWLLNTITRILMRMMGIRTDTVISSALSKDELRTIVNESRSQISRRNQDMLLSVLDLEKVSVNDIMVP

RNEIVGIDINDDWKSIVRQLTHSPHGRIVLYRDSLDDAISMLRVREAYRLMTEKKEFTKEIMLRAADEIY

FVPEGTPLSTQLVKFQRNKKKVGLVVDEYGDIQGLVTVEDILEEIVGDFTTSMSPTLAEEVTPLNDGTVI

IDGSANVREINKAFNWHLPEDEARTVNGIILEALEEIPVPGTRVRIEQYDIDILDVQDNMIKQVKVMPVK

SLRESVAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002914153.1\_1172 [locus\_tag=BN49\_RS07200] [protein=inner membrane protein YpjD] [protein\_id=WP\_002914153.1] [location=complement(1202705..1203496)] [gbkey=CDS]

MPVFALLALVAYSVSLALIIPGLLQKNSSWRRMAILSATIALICHAFALEARIFPGGESGQNLSLLNVGS

LVSLMICTVMTIVASRNRGWLLLPIVYAFALINLAFATFVPNEYITHLETTPGMLVHIGLSLFSYATLII

AALYALQLAWIDYQLKNKKLAFSSEMPPLMSIERKMFHITQVGVVLLTLTLCSGLFYMHNLFSSENIDKA

VLSIIAWFVYIVLLWGHYHEGWRGRRVVWFSVAGAGLLTLAYFGSRVLQQFVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002914152.1\_1173 [gene=ffh] [locus\_tag=BN49\_RS07205] [protein=signal recognition particle protein] [protein\_id=WP\_002914152.1] [location=1203660..1205024] [gbkey=CDS]

MFDNLTDRLSRTLRNISGRGRLTEDNIKDTLREVRMALLEADVALPVVRDFISRVKESAVGHEVNKSLTP

GQEFVKIVRNELVAAMGEENQTLDLAAQPPAVVLMAGLQGAGKTTSVGKLGKFLREKHKKKVLVVSADVY

RPAAIKQLETLAEQVGVDFFPSDVGQKPVDIVNAALKEAKLKFYDVLLVDTAGRLHVDEAMMDEIKHVHA

AINPVETLFVVDAMTGQDAANTAKAFNEALPLTGVVLTKVDGDARGGAALSIRHITGKPIKFLGVGEKTE

ALEPFHPDRVASRILGMGDVLSLIEDIESKVDRAQAEKLASKLKKGDGFDLTDFLEQLRQMKNMGGMASL

MGKLPGMGQIPDNVKAQMDDKVLVRMEAIINSMTLKERAKPEIIKGSRKRRIAAGCGMQVQDVNRLLKQF

DDMQRMMKKMKSKGGMMKMMRGMKGMMPPGFPGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914149.1\_1174 [gene=rpsP] [locus\_tag=BN49\_RS07210] [protein=30S ribosomal protein S16] [protein\_id=WP\_002914149.1] [location=1205284..1205532] [gbkey=CDS]

MVTIRLARHGAKKRPFYQVVVTDSRNARNGRFIERVGFFNPIANGAEEETRLDLDRIAHWVGQGATVSDR

VAALIKAANKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150977.1\_1175 [gene=rimM] [locus\_tag=BN49\_RS07215] [protein=ribosome maturation factor RimM] [protein\_id=WP\_004150977.1] [location=1205551..1206099] [gbkey=CDS]

MSKQHTAQAPVDPIVLGKMGSSYGIRGWLRVFSSTEDAESIFDYQPWLIQKAGQWQVVELESWRHHNQDI

IIKLKGVDDRDAANLLTNCEIIVDSSQLPELEEGDYYWKDLMGCQVVTTEGYSLGKVIDMMETGSNDVLV

IKANLKDAFGIKERLVPFLDGQVIKKVDLTTRTIEVDWDPGF

>lcl|NZ\_FO834906.1\_prot\_WP\_002914147.1\_1176 [gene=trmD] [locus\_tag=BN49\_RS07220] [protein=tRNA (guanosine(37)-N1)-methyltransferase TrmD] [protein\_id=WP\_002914147.1] [location=1206131..1206898] [gbkey=CDS]

MWIGIISLFPEMFRAITDYGVTGRAVKNGLLSIESWSPRDFTHDRHRTVDDRPYGGGPGMLMMVQPLRDA

IHAAKAAAGEGAKVIYLSPQGRKLDQAGVSELATNQKLILVCGRYEGIDERVIQTEIDEEWSIGDYVLSG

GELPAMTLIDSVSRFIPGVLGHEASATEDSFADGLLDCPHYTRPEVLEEMEVPPVLLSGNHAEIRRWRLK

QSLGRTWLRRPELLENLALTEEQAKLLAEFKTEHAQQQHKHDGQA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529466.1\_1177 [gene=rplS] [locus\_tag=BN49\_RS07225] [protein=50S ribosomal protein L19] [protein\_id=WP\_016529466.1] [location=1206938..1207285] [gbkey=CDS]

MSNIIKQLEQEQMKQDVPSFRPGDTVEVKVWVVEGSKKRLQAFEGVVIAIRNRGLHSAFTVRKMSNGEGV

ERVFQTHSPVVDSIAVKRRGAVRKAKLYYLRERTGKSARIKERLN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529467.1\_1178 [locus\_tag=BN49\_RS07235] [protein=DUF2946 domain-containing protein] [protein\_id=WP\_016529467.1] [location=1207405..1207863] [gbkey=CDS]

MVSNSFQQTTPKRRAAWLALLAILLIVVAPLISVSLQKDPMSAMPGMHHAMMMDSSSANMAQMPGHKMAM

MHSIDGATHTGHEMPLDHAEACGYCVLLAHVPGLLFALALFVAMLLRRIRLPVSRPVLKHWHYFPWLYPE

TRAPPRLSAFSL

>lcl|NZ\_FO834906.1\_prot\_WP\_046042634.1\_1179 [locus\_tag=BN49\_RS07240] [protein=PepSY domain-containing protein] [protein\_id=WP\_046042634.1] [location=1207920..1209290] [gbkey=CDS]

MTTCTSRAAWLNLLRRLHFYIGLFIGPFIFVAALTGTLYVATPQLENWLYHDALHGLAEGTPQPLSAQIA

VAEEATQGNLRLLAVRPAPALGETTRIMFADPGLGESESRAIFVDPIALRVKGDMTVYGTSGILPLRQWI

DYAHRSLLLGDSGRLYSELAASWMWVAALGGIALWAMTRPKRRLNNALQNHRRLHVTLGWGLLVGMLLFS

ATGLTWSQWAGGNVDKMRAAFGWLTPQVNTQLHGEMTMTHDPHAGHHMDAMAMAQHQPALQLAQFDQALA

AARQAGLNASRLEIRPPVSDDRAWTVNEIDRRWPTQVDAVAIDGATMQVVDRTRFADFPLMAKLTRWGVD

FHMGILFGLANQLLLVGFGCALCVTIGVGYRLWWIRRPPQAAWDPAHSLLQAWLSLAWPARSLVLGLAFA

LGLAMPLMGASLLLFIAVDYLRWRAATAMRMMKSSD

>lcl|NZ\_FO834906.1\_prot\_WP\_004145671.1\_1180 [locus\_tag=BN49\_RS07245] [protein=OmpA family protein] [protein\_id=WP\_004145671.1] [location=complement(1209299..1209781)] [gbkey=CDS]

MIRKYFVPALMAAALLTGCQAPQGKFTPEQVAAMKSYGFTESNGDWSLGLSDSILFDKNDYRLRPDSRQQ

ITTMASRLAATGITHSRLEGHTDNYGEDSYNEALSLKRANSVADAWAEGAHVPRSNLVTRGLGKKYPIAS

NDTAAGRAENRRVTVVISTP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531065.1\_1181 [gene=dgcN] [locus\_tag=BN49\_RS07250] [protein=diguanylate cyclase DgcN] [protein\_id=WP\_016531065.1] [location=complement(1209795..1211018)] [gbkey=CDS]

MNKDFSQTPRPTFKRSLRRISVISVVISMTLVWLLLSTASIFTLKQYAQKNLELTAATMGRSLEAALVFG

DSAAAEETLASLGKQGQISQAIVLNGQMQHFAAWRHEPLANKEQVSGLISKWLFPEPTVQPIWHQGKQIG

KLRLTALDELISHFLGISILVLTGSILLASFIALLLTHSLHRGIVAALQSITEVVHDIRENRHFSRRVPE

ERIEEFHLFAQDFNSLLGEMEDWQRQLQAKNAQLLRSSLHDPLTGLANRAAFRNALAELMQNEVDHQTSA

LLFLDGDNFKLINDNWGHAAGDKVLMEVASRLMTFAGKRHLAWRLGGDEFAVLLREVRSEAEVQALCQAL

TEQFLPPFNLHNGHSATLSLSVGYALAWEHATAESLQELADQNMYRMKNQRIQQTLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004174804.1\_1182 [locus\_tag=BN49\_RS07255] [protein=YfiR family protein] [protein\_id=WP\_004174804.1] [location=complement(1211011..1211520)] [gbkey=CDS]

MTVLHRLLLTVFFLIAVSPVFAAGPSEHVRAIVSGIVTYTRWPSLTGAPKLCIFASSRFTHSLAHEDPDA

LPYQPVIVRNREEALKTTCDGFYFGSESPTEQSELTRRYGPRPLLLIAEQNTDCSIGSAFCLIINDDRVR

FSVNLDVLTHSGVRVNPDVLMLARKKPHE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529712.1\_1183 [gene=aroF] [locus\_tag=BN49\_RS07260] [protein=3-deoxy-7-phosphoheptulonate synthase AroF] [protein\_id=WP\_016529712.1] [location=1211863..1212933] [gbkey=CDS]

MQKDALNNVHITDEHVLMTPEQLKAEFPLSVEQEAQIAYARQTISDIIAGRDPRLLVVCGPCSIHDPEAA

IEYARRFKALAAEVSDSLYLVMRVYFEKPRTTVGWKGLINDPHMDGSFDVEGGLKIARRLLVELVNMGLP

LATEALDPNSPQYLGDLFSWSAIGARTTESQTHREMASGLSMPVGFKNGTDGSLATAINAMRAAAMPHRF

VGINQAGQVCLLQTQGNPNGHVILRGGKAPNYGPEDVAKCEKEMAQAGLKPSLMVDCSHGNSNKDFRRQP

AVAESVVAQIKDGNRSIIGLMIESNIHEGNQSSEQPREAMKYGVSVTDACISWETTEALLRELDKDLRGH

LAARLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002914113.1\_1184 [gene=tyrA] [locus\_tag=BN49\_RS07265] [protein=bifunctional chorismate mutase/prephenate dehydrogenase] [protein\_id=WP\_002914113.1] [location=1212943..1214064] [gbkey=CDS]

MVAELTALRDQIDEVDKALLSLLAKRLELVAEVGEVKSQYGLPIYVPERESAMLASRREEAAALGVPPDL

IEDVLRRVMRESYSSENDKGFKTLQPNLRPVVIVGGGGQMGRLFEKMLTLSGYQVRILEKNDWARAADIV

ADAGMVIVSVPIHTTVETIGRLPPLPADCILVDLASVKAEPLQAMLAAHQGPVLGLHPMFGPDSGSLAKQ

VVVYCDGRQPEAYQWFLEQIQVWGARLHRISAVEHDQNMAFIQALRHFATFAYGLHLAEENVRLEQLLAL

SSPIYRLELAMVGRLFAQDPQLYADIIMSSENNLALIKRYYQRFGEAIGLLEQGDKQAFIDSFRKVEHWF

GDYAQRFQSESRTLLRQANDNRQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529713.1\_1185 [locus\_tag=BN49\_RS07270] [protein=SMP-30/gluconolactonase/LRE family protein] [protein\_id=WP\_016529713.1] [location=1214127..1214999] [gbkey=CDS]

MAEPQPLFDYTGYLPECPTWSEAEQALYWADIMECEIHRYDIRSGEHQVLQFPEEVGCFALREKGGFIVA

LRSGIWLTDAHGLLRRKVCDNPSNPELARFNDGGTDRDGRFYAGTFWGPGDYNGALLMRVDNDLQPKVIQ

CDIHGANGLAFSADRRWMYTSDTPNAVIYRTPLDEQGEPGRREVFRRFQPGEGIPDGAAIDVEGCYWSAM

FDGWRIARFSPQGEALESYPMPVRCPTMVCFGGADMKTLYITTTRENMEDDELAQYPLSGAIFTLPVAVA

GMKKLPFREC

>lcl|NZ\_FO834906.1\_prot\_WP\_016529714.1\_1186 [gene=pheA] [locus\_tag=BN49\_RS07275] [protein=bifunctional chorismate mutase/prephenate dehydratase] [protein\_id=WP\_016529714.1] [location=complement(1214996..1216156)] [gbkey=CDS]

MTEENPLLALRDKISALDEKLLALLAERRGLAVEVGKAKLASHRPVRDIDRERDLLERLMTIGKHHNLDA

HYITRLFQLIIEDSVLTQQTLLQQHLNKINPHSARVAFLGPKGSYSHLAARQYAARHFEQFIESGCAKFA

DIFNQVETGQADYAVVPIENTSSGGINDVYDLLQHTSLSIVGELTIPIDHCVLVSTSTDADKIQTVYSHP

QPFQQCSQYLSRYPHWKIEYTESTSAAMEKVAQANSPAVAALGSEAGGALYGLQVLEHCQANQTQNITRF

LVLARKAVNVSDQVPAKTTLLMATGQQAGALVEALLVLRNHNLIMTKLESRPIHGNPWEEMFYLDIQANL

DSLPMRKALKELADITRSMKVLGCYPSENVVPVDPV

>lcl|NZ\_FO834906.1\_prot\_WP\_100250063.1\_1187 [gene=pheL] [locus\_tag=BN49\_RS30270] [protein=pheA operon leader peptide PheL] [protein\_id=WP\_100250063.1] [location=complement(1216257..1216304)] [gbkey=CDS]

MKLVPFFFAFFFTFP

>lcl|NZ\_FO834906.1\_prot\_WP\_002914111.1\_1188 [gene=raiA] [locus\_tag=BN49\_RS07280] [protein=ribosome-associated translation inhibitor RaiA] [protein\_id=WP\_002914111.1] [location=complement(1216411..1216746)] [gbkey=CDS]

MTMNITSKQMEITPAIRQHVADRLAKLDKWQTHLINPHIILSKEPQGFIADATINTPNGHLVASARHEDM

YAAINELINKLERQLNKVQHKGEARRAATSVKEAGFVEEEE

>lcl|NZ\_FO834906.1\_prot\_WP\_004145664.1\_1189 [gene=bamD] [locus\_tag=BN49\_RS07285] [protein=outer membrane protein assembly factor BamD] [protein\_id=WP\_004145664.1] [location=complement(1217017..1217754)] [gbkey=CDS]

MTRMKYLVAAATLSLALVGCSGSKEEVPDNPPNEIYATAQQKLQDGNWKQAITQLEALDNRYPFGPYSQQ

VQLDLIYAYYKNADLPLAQAAIDRFMRLNPTHPNIDYVIYMRGLTNMALDDSALQGFFGVDRSDRDPQHA

RDAFNDFSKLVRGYPNSQYATDAYKRMVFLKDRLAKYELSVVDYYTDRGAWVAVVNRVEGMMRNYPDTQA

TRDALPKMENAYRQMQMNAQADKVAKIIAANSKNT

>lcl|NZ\_FO834906.1\_prot\_WP\_002914110.1\_1190 [gene=rluD] [locus\_tag=BN49\_RS07290] [protein=23S rRNA pseudouridine(1911/1915/1917) synthase RluD] [protein\_id=WP\_002914110.1] [location=1217886..1218866] [gbkey=CDS]

MAQRVQLTATVTENQLGQRLDQALAELFPDYSRSRIKEWILDQRVLVNGTIGDKPKEKVLGGERIAIDVE

IEEEARFQPQDIPLNIVYEDDDIIVINKPRDLVVHPGAGNPDGTVLNALLHYYPPIADVPRAGIVHRLDK

DTTGLMVVAKTIPAQTRLVESLQLREITREYEAVAIGHMTAGGTVEEPISRHPTKRTHMAVHPMGKPAVT

HYRIMEHFRIHTRLRLRLETGRTHQIRVHMSHITHPLVGDQVYGGRPRPPKGASEEFITALRKFDRQALH

ATMLRLYHPISGIEMEWHAPIPQDMVELIEAMRADFEAHKDDIDWL

>lcl|NZ\_FO834906.1\_prot\_WP\_004212956.1\_1191 [gene=pgeF] [locus\_tag=BN49\_RS07295] [protein=purine nucleoside phosphorylase YfiH] [protein\_id=WP\_004212956.1] [location=1218863..1219594] [gbkey=CDS]

MTKLIVPQWPMPGSVAACSSTRIGGVSLPPYDSLNLGAHCGDNLQDVEENRRRMFAAGGLPSYPVWLEQV

HGTEVLTLDGGPYPSKRADASYSRTPGTVCAVMTADCLPVLFCNRDGTEVAAAHAGWRGLCEGVLEATVA

RFADKAENIMAWLGPAIGPQAFEVGPEVRDAFMAKDENAHRAFRPAGEKYFADIYQLARQRLANVGVEQI

FGGDRCTLSEKDDFFSYRRDKTTGRMASFIWLI

>lcl|NZ\_FO834906.1\_prot\_WP\_004150973.1\_1192 [gene=clpB] [locus\_tag=BN49\_RS07300] [protein=ATP-dependent chaperone ClpB] [protein\_id=WP\_004150973.1] [location=1219724..1222297] [gbkey=CDS]

MRLDRLTNKFQLALADAQSLALGHDNQFIEPLHLMSALLNQEGGSVRPLLTSAGVNAGKLRTDIEQALSR

LPQVEGTGGDVQPSQDLVRILNLCDKLAQKKKDNFISSELFVLAALESRGTLTDLLKSAGATTANVTQAI

EQMRGGESVNDQGAEDQRQALKKFTVDLTERAEQGKLDPVIGRDEEIRRTIQVLQRRTKNNPVLIGEPGV

GKTAIVEGLAQRIVNGEVPEGLKGRRVLALDMGALVAGAKYRGEFEERLKGVLTDLSKQEGNVILFIDEL

HTMVGAGKADGAMDAGNMLKPALARGELHCVGATTLDEYRQYIEKDAALERRFQKVFVAEPSVEDTIAIL

RGLKERYELHHHVQITDPAIVAAATLSHRYIADRQLPDKAIDLIDEAASSIRMQIDSKPEELDRLDRRII

QLKLEQQALKKESDEASLKRLDMLNEELADKERQYSVLEEEWKAEKASLSGTQTIKAELEQAKIAIEQAR

RVGDLARMSELQYGKIPELEKQLAAATQSEGKTMRLLRNKVTDAEIAEVLARWTGIPVSRMMESERDKLL

RMEQELHHRVIGQDEAVEAVSNAIRRSRAGLSDPNRPIGSFLFLGPTGVGKTELCKTLANFMFDSDDAMV

RIDMSEFMEKHSVSRLVGAPPGYVGYEEGGYLTEAVRRRPYSVILLDEVEKAHPDVFNILLQVLDDGRLT

DGQGRTVDFRNTVVIMTSNLGSDLIQERFGELDYGHMKDLVLGVVSQNFRPEFINRIDEVVVFHPLGEKH

IASIAQIQLQRLYKRLEERGYEVQMSDEALKLLSANGYDPVYGARPLKRAIQQQIENPLAQQILSGELVP

GKTIELVVKDDRIVAVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530595.1\_1193 [gene=dkgB] [locus\_tag=BN49\_RS07330] [protein=2,5-didehydrogluconate reductase DkgB] [protein\_id=WP\_016530595.1] [location=1228158..1228961] [gbkey=CDS]

MAIPAFGLGTFRLKDDVVIASVKTALELGYRAIDTAQIYDNEAAVGQAIAESGVPRDELFITTKIWIENL

SKDKLIASLQESLQKLRTDYVDLTLIHWPAPNDAVAAEEFMAALMEAKKLGLTRQIGISNFTIPLMERAI

AAVGAENIATNQIELSPYLQNRKVVDWAREHGIHITSYMTLAYGKALKDEVIARIAAKHNATPAQVILAW

AMGEGYAVIPSSTKRDNLASNLKALDLQLEDEDRQAIAALDCNDRLVSPQGLAPQWD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530596.1\_1194 [locus\_tag=BN49\_RS07335] [protein=DNA-binding transcriptional regulator YafC] [protein\_id=WP\_016530596.1] [location=complement(1229007..1229912)] [gbkey=CDS]

MRATSEEIAIFVAVVESGSFSRAAEQLGQANSAVSRAVKKLESKLGVSLLNRTTRQLSLTEEGERYFRRM

QVVLQEMAAAENDLLETRTTPRGLLRVDAATPVMLHFLMPLVKPFRERYPEMTLSLVSSETFINLIERKV

DVAIRAGTLADSSLRARPLFTSYRKIVASPVYVARYGMPQHPSDLKQHHCLGFTEPVSLNTWPVSCCDGQ

LLEIEAAVSSNSGETLKQLCLTGNGIACLSDYMVDKEIASGEFVELLADKRLPVEMPFSAVYYSDRAVST

RIRAFIDFLSDHVKQLPKELS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530597.1\_1195 [locus\_tag=BN49\_RS07340] [protein=MFS transporter] [protein\_id=WP\_016530597.1] [location=1230017..1231207] [gbkey=CDS]

MPLALFALTIGAFAIGTTEFVIVGLVPTIAQQLSISLPSAGLLVSIYALGVAIGAPVLTALTGRMPRKQL

LLALMVLFTAGNVLAWQAPGYETLILARLLTGLAHGVFFSIGSTIATSLVAKEKAASAIAIMFGGLTVAL

VTGVPFGTFIGQHFGWRETFLAVSILGVIALISSLILVPNNIPGRASASLRDQMKVLTHPRLLMIYAITA

LGYGGVFTAFTFLAPMMQELAGFSPSAVSWILLGYGVSVAIGNVWGGKLADKHGAVSALKFIFAALVVLL

LVFQLTASVHYAALATVLVMGVFAFGNVPGLQVYVVQKAEQYTPGAVDIASGLNIAAFNVGIALGSIVGG

QTVERYGLAQTPWIGAMIVLVALLLVVLSGRLDKLPRRSAALSPEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889629.1\_1196 [locus\_tag=BN49\_RS07345] [protein=endonuclease/exonuclease/phosphatase family protein] [protein\_id=WP\_002889629.1] [location=1231310..1232107] [gbkey=CDS]

MRKNTYAMRYVAGQPAERILPPGAFAGVSPVYPAGTPLSSDEKIRVLVWNIFKQQRAEWQSVLKNFGKDA

HLVLLQEAQTTPELVRFATSNYLAADQVPALVLPQHPSGVMTLASAHPIYCCPLREREPILRLPKSALVT

VYPLPDARLLMVVNIHAVNFSLGVDVYSKQLLPIGDQIAHHSGPVIMAGDFNAWSRPRMNALYRFAREMS

LREVRFSDDQRRRAFGRPLDFVFYRGLSVHDASVLVTRASDHNPLLVEFSPGKPD

>lcl|NZ\_FO834906.1\_prot\_WP\_021314673.1\_1197 [locus\_tag=BN49\_RS07350] [protein=class I SAM-dependent methyltransferase] [protein\_id=WP\_021314673.1] [location=1232199..1232969] [gbkey=CDS]

MTTRSHHDNVEKQFGSQASAYLTSAVHASGRDLQRLAERLADFPQAKVLDMGCGAGHASYTAAGQVAEVT

AYDLSSQMLEVVAAAAKEKGFSNIVTQQGYAETLPFADASFDVVISRYSAHHWHDVGQALREVKRVLKPG

GVIIVMDVMSPGHPVRDVWLQTVEALRDTSHVRNYSSGEWLTLATEAGLVVNQLLTDRLPLEFSSWVARM

RTPEPLVEAIRLYQQSASAEVKAYFELQEDGSFTSDTILFEAHKAV

>lcl|NZ\_FO834906.1\_prot\_WP\_002889632.1\_1198 [gene=mltD] [locus\_tag=BN49\_RS07355] [protein=murein transglycosylase D] [protein\_id=WP\_002889632.1] [location=complement(1233027..1234394)] [gbkey=CDS]

MKARAILLASVLLVGCQASKHDGTVEQRAQSLSAAGQGEAGKFTSQARWLDDGTFYAQDQDLWTSIGDEL

KMGIPDNPRIREQKQKYLRNKSYLHDVTLRAEPYMYWIAGQVKKRNMPMELVLLPIVESAFDPHATSGAN

AAGIWQIIPSTGRNYGLKQTRSYDARRDVVASTTAALDMMQRLNKMFDGDWLLTVAAYNSGEGRVMKAVK

ANRSRGKPTDFWSLSLPHETKIYVPKMLALSDILKNSKRYGVKLPTADESRALARVRLDSPVDISQLADM

AGMPVSKLKTFNAGVKGSTLGASGPKYVMVPQKHAAQLRESLASGDIAAVQPTQLADNTPLTSRSYKVRS

GDTISGIASRLGVTTRDLQQWNNLRGSGLKVGQNLVIGAGSSAQRLANNSDSITYRVRKGDSLSSIAKRH

GVNIRDVMRWNSDTDNLRPGDQLTLFVKNSDRPES

>lcl|NZ\_FO834906.1\_prot\_WP\_016530024.1\_1199 [gene=gloB] [locus\_tag=BN49\_RS07360] [protein=hydroxyacylglutathione hydrolase] [protein\_id=WP\_016530024.1] [location=complement(1234466..1235221)] [gbkey=CDS]

MNLISIPAFQDNYIWVLSENNGRCIIVDPGEAAPVLAAIEENQWQPEAILLTHHHQDHVGGVKQLREQFP

SIVVYGPAETQDKGVTQVVGDGDRLSILGHDFSIFSTPGHTLGHICYYSEPYLFCGDTMFSGGCGRLFEG

TAEQMYQSFMKINALPEETLICCAHEYTLANMKFALSILPDDRDINDYYHKVNELRAKKQKTLPVTLKNE

RRINLFLRVNDIDLIDKINKETNLQHSVARFAWLRSKKDDF

>lcl|NZ\_FO834906.1\_prot\_WP\_002889685.1\_1200 [locus\_tag=BN49\_RS07365] [protein=class I SAM-dependent methyltransferase] [protein\_id=WP\_002889685.1] [location=1235254..1235976] [gbkey=CDS]

MKPARIPHTVTAPEHWSSMPWGEYYRETLEQQMKPWLAKLYGFHLLKIGNLSAEINTEACAISHQVNVSL

AGNPMQVRADPLHLPFAEKSVDACLLAHTLPWCSDPHRLLREADRVLIDDGWMILTGFNPVSLMGLRKLV

PVLRKGTPYNSRMFTLMRQLDWLALLNFEVLHYGRYQVLPWSRHGGKLLSTHLPALGCLQLIVARKRTIP

LTLNPMKSGKAKTQLRPAVGATRQWRKGQN

>lcl|NZ\_FO834906.1\_prot\_WP\_002889686.1\_1201 [gene=rnhA] [locus\_tag=BN49\_RS07370] [protein=ribonuclease HI] [protein\_id=WP\_002889686.1] [location=complement(1235973..1236440)] [gbkey=CDS]

MLKQVEIFTDGSCLGNPGPGGYGAIMRYRQHEKTFSAGYRLTTNNRMELMAAIVALEALKEHCEVVLSTD

SQYVRQGITQWIHNWKKRGWKTAEKKPVKNVDLWQRLDAALGQHKIKWEWVKGHAGHPENERCDELARAA

ASHPTLDDVGYLPES

>lcl|NZ\_FO834906.1\_prot\_WP\_004152034.1\_1202 [gene=dnaQ] [locus\_tag=BN49\_RS07375] [protein=DNA polymerase III subunit epsilon] [protein\_id=WP\_004152034.1] [location=1236505..1237236] [gbkey=CDS]

MSTAITRQIVLDTETTGMNQIGAHYEGHKIIEIGAVEVINRRLTGNNFHVYLKPDRLVDPEAFGVHGIAD

EFLLDKPTFADVADEFMDYIRGAELVIHNASFDIGFMDYEFSKLNRGIGKTETFCKITDSLALARKMFPG

KRNSLDALCSRYEIDNSKRTLHGALLDAQILADVYLMMTGGQTSMAFSMEGESQQQAGEMGIQRVVRAGS

QLRVVYASDEELANHESRLDLVQKKGGSCLWRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530025.1\_1203 [locus\_tag=BN49\_RS07385] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530025.1] [location=complement(1237506..1238387)] [gbkey=CDS]

MDLRRFITFKTVVEEGSFLRAAQKLCCTQSTVTFHIQQLEQELAIPLFEKIGRRMCLTAAGKKVLPHVYD

LTKVMASIRQAARQDDEPGGELRVATGETLLAYKMPRVLQRFKQRAPKVRLSLQSLNCYSIRDALLADEV

DLGVFYRVGNDDALTIMELGQQSLALVASVEQAPVDFMRPRQHIPLSFIINEPQCVFRQIFESTLRQREI

TLENTIELWSIESIKQCVAGNLGVSFLPRFAVEDELKRGTLVELPFSETPLTIHALCAHHAGKAISPAMR

VFMQCMQEEQEVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002889688.1\_1204 [gene=eamB] [locus\_tag=BN49\_RS07390] [protein=cysteine/O-acetylserine transporter] [protein\_id=WP\_002889688.1] [location=1238491..1239081] [gbkey=CDS]

MTPTLISAFLTYTLITALTPGPNNILALSSVTSHGLRRSLRVLAGMSVGFIITMLICAALTFSLVELDSR

FTLVLGWIGAAYILWLAWQIAKSKPATGMPSVEPVGFWASLGLQFVNVKIILYGITALSTFVLPVTREPV

WLISVSLLLAAIGALGNLCWALAGHLFQRLFLLYGRQLNWMLAALLVYCAVRIVVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002889689.1\_1205 [locus\_tag=BN49\_RS07395] [protein=amidohydrolase] [protein\_id=WP\_002889689.1] [location=complement(1239112..1239882)] [gbkey=CDS]

MPGLKISLLQQPLVWMDGPANLRHFDRQLEGITGRDVIVLPEMFTTGFAMEAAKQSLPEADVVEWMHARA

AQSQALIAGSAALQTEHGAVNRFLLVEPDGTVHHYDKRHLFRMADEHHHYEAGNQRVVFEWRGWRILPLV

CYDLRFPVWSRNQNDYDLALYVANWPAPRSLHWQSLLIARAIENQAYVAGCNRVGTDGNGHHYRGDSRII

NPQGEIIATADPHQATRLDAELSLSALQEYREKFPAWRDADPFTIG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889690.1\_1206 [gene=fadE] [locus\_tag=BN49\_RS07400] [protein=acyl-CoA dehydrogenase FadE] [protein\_id=WP\_002889690.1] [location=complement(1240061..1242505)] [gbkey=CDS]

MMILSIVATVVLLGALFYHRVSLLLSSVILLAWTAALGAAGVWNIWLLLPLAIILLPFNFAPMRKSMISA

PAFRTFRKVMPPMSRTEKEAIDAGTTWWEGDLFRGNPDWQKLHNYPQPRLTAEEQAFLDGPVEEACRMAN

DFAITHEMADLPPELWAYLKEHRFFAMIIKKEYGGLEFSAYAQARVLQKLSGVSGILAITVGVPNSLGPG

ELLQHYGTEEQKNHYLPRLARGLEIPCFALTSPEAGSDAGAIPDTGVVCMGDWQGQQVLGMRLTWNKRYI

TLAPIATVLGLAFKLSDPDRLLGGEEELGITCALIPTSTPGVEIGRRHFPLNVPFQNGPTRGKDIFVPID

YIIGGPSMAGQGWRMLVECLSVGRGITLPSNATGGLKSVAMATGAYAHIRRQFKISIGKMEGIEEALARI

AGNAYVMDAAASLITYGIMLGEKPAVLSAIVKYHCTHRGQRSIIDAMDITGGKGIMLGEGNFLARAYQGA

PIAITVEGANILTRSMMIFGQGAIRCHPYVLEEMAAAQNNDLNAYDKLLFKHIGHVGSNKVRSFWLGLTG

GRTSSAPTRDATRRYYQQMNRLSANLALLSDVSMAVLGGSLKRRERISARLGDVLSQLYLASAVLKRYDD

EGRNEADLPLVHWGVQDALHQAEQAIDDLLDNFPNRLVAGVMRLVIFPTGRHHHAPSDRLDHQVAKILQV

PSATRSRIGRGQYLTPSEHNPVGLLEEALLEVMAADPIHQRICKELGKNLPFTRLDELAHNALAKGLISQ

DEAAILTRAEHSRLRSINVDDFAPEELATKPVKLPEKVRKVEAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145825.1\_1207 [gene=lpcA] [locus\_tag=BN49\_RS07405] [protein=D-sedoheptulose 7-phosphate isomerase] [protein\_id=WP\_004145825.1] [location=1242745..1243326] [gbkey=CDS]

MYQDLIRNELNEAAETLANFLQDEANIHAIQRAAVLLADSFKAGGKVLSCGNGGSHCDAMHFAEELTGRY

RENRPGYPAIAISDVSHLSCVSNDFGYEYVFSRYVESVGRAGDVLLGISTSGNSGNVIKAIEAARAQGMK

VITLTGKDGGKMAGSADVEIRVPHFGYADRIQEIHIKVIHILIMLIEKEMAKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889696.1\_1208 [locus\_tag=BN49\_RS07410] [protein=class II glutamine amidotransferase] [protein\_id=WP\_002889696.1] [location=1243401..1244168] [gbkey=CDS]

MCELLGMSANVPTDICFSFTGLVQRGGGTGPHKDGWGITFYEGKGCRTFKDPQPSFQSPIAKLVQDYPIK

SCSVVAHIRQANRGRVALENTHPFTRELWGRNWTYAHNGQLKGYKSLKTGNFHPVGETDSEKAFCWLLHR

LTERYPRTPGNMLGVFKYIATLAGELREKGVFNMLLSDGRYVMAFCSTNLHWITRRAPFGVAKLLDQDVE

IDFQRETTPNDVVTVIATQPLTANETWHKIMPGEWALFCLGERVV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530028.1\_1209 [locus\_tag=BN49\_RS07415] [protein=peptidoglycan meso-diaminopimelic acid protein amidase] [protein\_id=WP\_016530028.1] [location=complement(1244139..1244879)] [gbkey=CDS]

MRKIALFIAMLLLPCVSFAGLLSSNSPTTPISKEYKQQLMGSPVYIEIFKEERMLDLYVKMGETYQLLDS

YRICNYSGGLGPKQRQGDFKSPEGFYNVTRSQLKPDSRFYKAINIGFPNAYDRAHGYEGKYLMIHGDCVS

VGCYAMTDSGIDEIFQFVTGALVFGQPSVQVSIYPFRMTNANMERHKYSYYADFWKQLKPGYDYFQQTHK

PPVVSVTDGRYVVSKPLSHEVVQPQLASNYTLPETK

>lcl|NZ\_FO834906.1\_prot\_WP\_002889702.1\_1210 [locus\_tag=BN49\_RS07425] [protein=Na(+)-translocating NADH-quinone reductase subunit A] [protein\_id=WP\_002889702.1] [location=1245291..1246634] [gbkey=CDS]

MIKITKGLDLPIAGMPLQQISPAPAVKRVALLGEEYVGMRPAMAVKEGDRVKKGQILFEDKKIPGVCFTA

PASGIVSAIHRGERRVLQSVVIDIEGNDAVAFTRYAADALAELPRDTVQQQLLASGQWTALRTRPFSKTP

LPGSTPAAIFVNAMDTNPLAAEPQPIILAERAAFDAGLTVLTRLTDGKVHVCQPSGGKLGGHPLGQVCFN

QFSGPHPAGLPGTHIHFLEPVSLNKQVWHLNYQDAIAIGKLFLDGELYCERIIALGGPQVTSPRLVKTTL

GASLEDLLAGELQEGENRVISGSVLSGARAHGPHAFLGRFHLQVSVVKEGREKELFGWVMPGKEKFSITR

TTLGHFFKRKRFHFSTDTNGGERAMVPIGNYERVMPLDILPTILLRDLLAGDTDSAQALGCLELDEEDLA

LCTYVCPGKYEYGPALRSVLTRIEQEG

>lcl|NZ\_FO834906.1\_prot\_WP\_004147186.1\_1211 [locus\_tag=BN49\_RS07430] [protein=NADH:ubiquinone reductase (Na(+)-transporting) subunit B] [protein\_id=WP\_004147186.1] [location=1246638..1247876] [gbkey=CDS]

MGLKHLIEKLEPHFTHGGKLEKYYPLYEAAATIFYTPGQVTRGAAHVRDAIDLKRMMILVWFAVFPAMFW

GMYNVGLQTIPALHKLYGAEQLQQAIANNWHYSVAQWLGVSFSADAGWLSMMTLGAVFFLPIYITVFIVG

GFWEVLFAIVRKHEINEGFFVTSILFALIVPPTLPLWQAALGISFGVVIAKEIFGGTGRNFLNPALAGRA

FLFFAYPAQISGDLVWTAADGFSGATPLSQWASGGGEALVNVATGVPVSWMDAFLGNIPGSIGEVSTLMI

FIGGAIILFGRVASWRIVAGVMIGMIATATLFNVIGSDTNPMFAMPWYWHLVLGGFAFGMMFMATDPVSA

SFTDKGKWSYGVLIGVMCVLIRVVNPAYPEGMMLAILFANLFAPLFDYLVVQANIKRRKSRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177336.1\_1212 [locus\_tag=BN49\_RS07435] [protein=Na(+)-translocating NADH-quinone reductase subunit C] [protein\_id=WP\_004177336.1] [location=1247869..1248663] [gbkey=CDS]

MAEKKSNDSIGKTLLVVLVLCLVCSIVVAGSAVGLKSRQQAQRALDKQRNILAVSGLMHPGMDADAVADT

FAARITPRLVNLATGELLEKDPGKFNQAQALKDPQQSMALDASQDPAGIKRRSNLAEIYLVRDAQQKIEQ

VVLPIYGNGLWSMMYAFVALDVDGRTVKGITYYDQGETPGLGGEVENPNWRQQFVGKQVLDDNGMPALKV

VKGGARAGDLHAVDGLSGATLTSNGVQHSFDFWMGELGFGPFLKKVREGELNNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889716.1\_1213 [locus\_tag=BN49\_RS07440] [protein=NADH:ubiquinone reductase (Na(+)-transporting) subunit D] [protein\_id=WP\_002889716.1] [location=1248656..1249294] [gbkey=CDS]

MAEQSDMKEVKRVLVGPLIANNPIALQVLGVCSALAVTTKLETAFVMTIAVTLVTAFSSMFISMIRHHIP

NSVRIIVQMAIIASLVIVVDQLLRAFAYETSKQLSVFVGLIITNCIVMGRAEAYAMKSPPLASFMDGIGN

GLGYGAILIIVGFLRELIGSGKLFGITVLETVQNGGWYQPNGLFLLAPSAFFIIGLLIWALRSWKPEQQE

KE

>lcl|NZ\_FO834906.1\_prot\_WP\_004177335.1\_1214 [gene=nqrE] [locus\_tag=BN49\_RS07445] [protein=NADH:ubiquinone reductase (Na(+)-transporting) subunit E] [protein\_id=WP\_004177335.1] [location=1249301..1249897] [gbkey=CDS]

MAHYISLFVRAVFVENMALAFFLGMCTFLAVSKKVSTAFGLGVAVTVVLGLAVPINNLVYNLVLRDGALV

EGVDLSFLNFITFIGVIAALVQILEMILDKYFPALYNALGIFLPLIAVNCAIFGGVSFMVQRDYNFPESI

VYGFGSGIGWMLAIVAMAGIREKMKYANVPAGLRGLGITFITTGLMALGFMSFSGVQL

>lcl|NZ\_FO834906.1\_prot\_WP\_002889720.1\_1215 [gene=nqrF] [locus\_tag=BN49\_RS07450] [protein=NADH:ubiquinone reductase (Na(+)-transporting) subunit F] [protein\_id=WP\_002889720.1] [location=1249910..1251133] [gbkey=CDS]

MEIILGVVMFTLIVLVLSGLILAARSKLVNAGDVVIEINNEADKQIRTPAGDKLLNTLSSNGIFVSSACG

GGGSCGQCRVTVKEGGGDILPTELSHITKRDAKAGCRLACQVAVKQNMKIELPEEIFGVKKWECEVISND

NKATFIKELKLRIPEGEVVPFRAGGYIQIECPPHKVAYADFDVPDEYRSDWDKFNLFRYVSEVKEPTLRA

YSMANYPEEKGIIMLNVRIATPPPKVPDAPPGIMSSYIWSLKPGDKVTISGPFGEFFAKETDAEMVFIGG

GAGMAPMRSHIFDQLKRLHSTRKISFWYGARSLREMFYDEEFEQLARDNPNFTFHVALSDPLPEDNWTGH

TGFIHNVLYENYLRDHPAPEDCEFYMCGPPVMNAAVIKMLKDLGVEDENILLDDFGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004178678.1\_1216 [gene=nqrM] [locus\_tag=BN49\_RS07455] [protein=(Na+)-NQR maturation NqrM] [protein\_id=WP\_004178678.1] [location=1251136..1251351] [gbkey=CDS]

MLTVFIATFVIFALVIFGMSLGYLVKRKSIQGSCGGISALGLEKVCDCPEPCDARKKRLAREAQRQQRRI

L

>lcl|NZ\_FO834906.1\_prot\_WP\_016530032.1\_1217 [locus\_tag=BN49\_RS07460] [protein=glycerophosphoryl diester phosphodiesterase] [protein\_id=WP\_016530032.1] [location=complement(1251574..1252434)] [gbkey=CDS]

MKKILTALCLLATAGAWAAPQLIAHRGGTGDAPENTLPAIKLALENNAEAIWVTVQLSRDGVPVLYRSSD

LSALTNSEGKVSGLTAAELAKVDAGWKWGDDSHPWRGKQATIPTLQSVLQQWPHTFFYIDIKSPDADPTV

MGQRLLEVLKTTDSLDRVRVYSTEDRYIAALPPAIPRFVTRSETRTRLANISLSHQCQPASQRDGEQWYG

LELKRKVEVVEKFTLGEGISPATLTWDKEAMDCFRSQDKAHIIFFGINSAEDYRTAIELGADGVMVDSPA

QAKSWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002889726.1\_1218 [gene=dinB] [locus\_tag=BN49\_RS07465] [protein=DNA polymerase IV] [protein\_id=WP\_002889726.1] [location=1252594..1253649] [gbkey=CDS]

MRKIIHVDMDCFFAAVEMRDNPALRDIPLAIGGSRVQRGVISTANYPARKFGVRSAMPTATALKLCPHLT

LLPGRFDAYKEASNHIREIFSRYTSRIEPLSLDEAYLDVSDSEHCHGSATLIAQEIRQTIERELRLTASA

GVAPVKFLAKIASDMNKPNGQFVIAPHQVAEFVRALPLAKIPGVGKVSAAKLENMGLRTCGDVQNSDLAM

LLKRFGKFGRILWERSHGIDEREIHNDRQRKSVGVERTLAEDIHEWPECEAIIENLYPELERRLAKVKPD

LLIARQGIKLKFNDFQLTTQEHVWPRLNKEDLIATAHKAWDERRGGRGVRLVGLHVTLLDPQLERQLLLG

I

>lcl|NZ\_FO834906.1\_prot\_WP\_016530033.1\_1219 [locus\_tag=BN49\_RS07470] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_016530033.1] [location=1253652..1254104] [gbkey=CDS]

MHIRAYRDSDLPLLCQIFLRAVRETASRDYTPGQIAAWAQVDETRWRQKLADSIGLVAMVNSQPVGFITA

IGTHIDLLFVSPDRARQGIGGALIEALCVQYPAQILTVDASITAKPCFTAHGFKVVAEQRVAAHGEWFIN

YRMEKRVALW

>lcl|NZ\_FO834906.1\_prot\_WP\_016530034.1\_1220 [gene=pepD] [locus\_tag=BN49\_RS07475] [protein=cytosol nonspecific dipeptidase] [protein\_id=WP\_016530034.1] [location=complement(1254147..1255604)] [gbkey=CDS]

MSELSQLSPQPLWDIFAKICSIPHPSYHEEQLAEHIMGWAKEKGLHAERDQVGNILIRKGATAGMENRKP

VALQAHLDMVPQKNNDTVHDFVKDPIQPYIDGEWVKARGTTLGADNGIGMASALAVLADDSVAHGPLEVL

LTMTEEAGMDGAFGLQANWLQADILINTDSEEEGEIYMGCAGGIDFTSNLALTREAIPAGFQSFKVTLKG

LKGGHSGGDIHLGLGNANKLLSRFLAGHADELDLRLVDFNGGTLRNAIPREAYATVAVAADKADALKALV

NTYQALLKNELEAKEKNLVVLLEAVDNDKAALTQASRDTFIRLLNATPNGVIRNSDVAKGVVETSLNVGV

VTMTDDNVQIHCLIRSLIDSGKDYVVSMLDSLGKLAGAKTEAKGAYPGWQPDANSPVMHLVRETYQRLFN

KTPNIQIIHAGLECGLFKKPYPEMDMVSIGPTITGPHSPDEQVHIESVGQYWTLLTELLKAIPAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002889733.1\_1221 [gene=gpt] [locus\_tag=BN49\_RS07480] [protein=xanthine phosphoribosyltransferase] [protein\_id=WP\_002889733.1] [location=1255862..1256320] [gbkey=CDS]

MSEKYVVTWDMLQIHARKLASRLLPVEQWKGIIAVSRGGLVPGALLARELGIRHVDTVCISSYDHDNQRE

LKVLKRAEGDGEGFIVIDDLVDTGGTAVAIREMYPKAHFVTIFAKPAGRPLVDDYVVDIPQDTWIEQPWD

MGVVFVPPIAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002889742.1\_1222 [gene=frsA] [locus\_tag=BN49\_RS07485] [protein=esterase FrsA] [protein\_id=WP\_002889742.1] [location=1256426..1257670] [gbkey=CDS]

MSQANLSETLFKPRFKHPETSTLVRRFSAGKPQAMQSALSGNHVDHWYRLINRLMWIWRGVTPQEILDVQ

ARIVMSEAERTDPELFDTVIGYRGGNWIFEWAKEAMQWQQKAGQEADPLLSGRHWLHASNLYSIAAYPHI

KGDELAEQAQALANRAYEEAAQRLPGSLRELEFTIPGGSPITGFLHMPKGEGPFPTVLMCGGLDSLQTDY

YNLYENYFSPLGIAMLTIDMPSIGFSSKWTLNQDTSLLHQHALRHLENVPWIDHTRVAAFGFRFGANIAV

RLGYLEPQRLKAVACLGPVVHGLLVDPLHQGRVPEMYLDVLASRLGMHDASDEALRVELNRYSLKTQGLL

GRRCPTPMLSGFWKDDPFSPEEESRLITSSSADGKLLEIPFNPVYRNFDHALRQIARWINHRFG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177332.1\_1223 [gene=crl] [locus\_tag=BN49\_RS07490] [protein=sigma factor-binding protein Crl] [protein\_id=WP\_004177332.1] [location=1257728..1258126] [gbkey=CDS]

MTLPSGHLKSKLIKKFTALGPYIREEQCHDNRFFFDCLAVCVNVKPAPEKREFWGWWMEMEAQESRFTYS

YQFGLFNKEGSWQAVDIGDPEVSDRLEKTLREFHERAAALLTTFNLKLEPADDFSEPVRLRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177331.1\_1224 [gene=csiR] [locus\_tag=BN49\_RS07495] [protein=DNA-binding transcriptional regulator CsiR] [protein\_id=WP\_004177331.1] [location=complement(1258212..1258904)] [gbkey=CDS]

MTAIPQATAIDGYRWLKNDIIRGVYHPDEKLRMSLLTSRYGLGVGPLREALSQLVAERLVTVVNQKGYRV

APMSEQELLDIFDARANMEAMLVRLAIERGGDEWEAELLARTHLLNKLESCEASEHLLDEWDQRHQAFHT

AIVAGCGSQYLLQMRERLFDLAARYRFIWLRTTVLSVEMLEDKHVQHQTLVDAILARDAEQASALMREHL

LTPIPIIQQAMAGKLSPQAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889795.1\_1225 [gene=gabP] [locus\_tag=BN49\_RS07500] [protein=GABA permease] [protein\_id=WP\_002889795.1] [location=complement(1258950..1260350)] [gbkey=CDS]

MGQLSQSQDLGAGLKSRHVTMLSIAGVIGASLFVGSSVAIAEAGPAVLLAYLFAGLLVVMIMRMLAEMAV

ATPDTGSFSTYADKAIGRWAGYTIGWLYWWFWVLVIPLEANIAAIILHSWVPGVPVWLFSLVITLALTGS

NLLSVKNYGEFEFWLALCKVIAILAFIVLGAVAITGFYPYAEVSGISRLWDHGGFMPNGFGAVLSAMLIT

MFSFMGAEIVTIAAAESDTPDKHIVRATNSVIWRISIFYLCSIFIVVALIPWNMPGLKSIGSYRSVLELL

HIPYAKLIMDGVILLSVTSCLNSALYTASRMLYSLSRRGDAPAIMGRTNRSKTPYVAVLLSTGAAFLTVV

VNYYAPAKVFKFLIDSSGAIALLVYLVIAVSQLRMRKILQAQGGEIRLRMWLYPYLTWLVIAFITFVLVV

MLFRPAQQLEVISTGLLALGIICTVPIMSRWKKLVLWQKLPLQNTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004147193.1\_1226 [gene=gabT] [locus\_tag=BN49\_RS07505] [protein=4-aminobutyrate--2-oxoglutarate transaminase] [protein\_id=WP\_004147193.1] [location=complement(1260486..1261769)] [gbkey=CDS]

MNSNKAMMARRSDAVPRGVGQIHPIFAERAENCRVWDVEGREYLDFAGGIAVLNTGHLHPQVVAAVEDQL

KKLSHTCFQVLAYEPYLALCEKMNQKVPGDFAKKTLLVTTGSEAVENAVKIARAATGRSGAIAFTGAYHG

RTHYTLSLTGKVNPYSAGMGLMPGHVYRALYPCALHGVSDDEAIASIHRIFKNDAAPEDIAAIIIEPVQG

EGGFYAASPAFMQRLRALCDEHGIMLIADEVQSGAGRTGTLFAMEQMGVAADITTFAKSIAGGFPLAGVT

GRAEVMDAIAPGGLGGTYAGNPIACAAALAVLQIFEQENLLEKANQLGDTLRQGLLAIAEDHPEIGDVRG

LGAMIAIELFEEGDRSRPNARLTADIVARARDKGLILLSCGPYYNVLRILVPLTIEEAQIEQGLKIIADC

FSEAKQA

>lcl|NZ\_FO834906.1\_prot\_WP\_032104723.1\_1227 [gene=gabD] [locus\_tag=BN49\_RS07510] [protein=NADP-dependent succinate-semialdehyde dehydrogenase] [protein\_id=WP\_032104723.1] [location=complement(1261782..1263230)] [gbkey=CDS]

MQLNDMTLFRQQAMIDGQWRDAPNGDVIAVTNPANGEQLGSVPKMGADETREAIEAANRALPAWRALTAK

ERANILRRWFDLMMENQDDLARLMTLEQGKPLAEAKGEISYAASFIEWFAEEGKRIYGDTIPGHQADKRL

LVIKQPIGVTAAITPWNFPAAMITRKAGPALAAGCTMVLKPASQTPFSALALAELANRAGIPAGVFNVVT

GSAGAVGGELTSNPLVRKLSFTGSTEIGRQLMEQCAKDIKKVSLELGGNAPFIVFDDADLDKAVEGALAS

KFRNAGQTCVCANRLYVQDGVYERFAEKLQQAVEKLRIGDGLQDGVTTGPLIDEKAVAKVEEHIADAIAK

GAKVVTGGKPHALGGNFFQPTILVNVPDSAKVAKEETFGPLAPLFRFKDEADVIAQANDTEFGLAAYFYA

RDLSRVFRVGEALEYGIIGINTGIISTEVAPFGGVKASGLGREGSKYGIEDYLEIKYMCIGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002889846.1\_1228 [gene=lhgO] [locus\_tag=BN49\_RS07515] [protein=L-2-hydroxyglutarate oxidase] [protein\_id=WP\_002889846.1] [location=complement(1263255..1264523)] [gbkey=CDS]

MYDFVIIGGGIIGMSTAMQLIEIYPDARIALLEKEAGPACHQTGHNSGVIHAGVYYTPGSLKAQFCLAGN

RATKAFCEQNGIRYDVCGKMLVATSPLEMERMRALWDRTAANGLQREWLSAGELREREPNITGLGGIFVP

SSGIVSYREVAAAMAKNFEAKGGTIVYNAEVSALKEHASGVVIRTRQGGEYEASTLIACSGLMADRLVKM

LGVDPGFIICPFRGEYFQLAPQHNQIVNHLIYPIPDPAMPFLGVHLTRMIDGSVTVGPNAVLALKREGYR

KRDISLADTLEILTSPGIRRVLQNNLRSGLGEMKNSLCRSGYLRLVQKYCPSLTLSDLRPWPAGVRAQAV

SPQGKLIDDFLFVTTARSIHTCNAPSPAATSAIPIGAHIVSKVQSLLASQSNPGRTLRAARSVETLHAAF

TR

>lcl|NZ\_FO834906.1\_prot\_WP\_002889847.1\_1229 [gene=csiD] [locus\_tag=BN49\_RS07520] [protein=glutarate dioxygenase GlaH] [protein\_id=WP\_002889847.1] [location=complement(1264551..1265528)] [gbkey=CDS]

MNALTAVKPTPAPVAQQYPGFSFTPSAQSPRLLELTFSAETTTQFLQQVAQWPVQALEYKSFLRFQVGKI

LDDLCGNQLQPLLIKTLLDRAEGALLINGEGIDHVSQAEEMVKLATAVAHLIGRSNFDAMSGQYYARFVV

KNVDNSDSYLRQPHRVMELHNDGTYVEEQTDYVLMMKIDEQNMQGGNSLLLHLDDWEHLDEFFRDPLARR

PMRWAAPPSKNVSKDVFHPVFDVDSLGRPVMRYIDQFVQPKDFEEGTWLSRLSDALETSKNILSIPVPVG

KFLLINNLFWLHGRDRFTPHPDLRRELMRQRGYFAYSTNHYQTHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002889848.1\_1230 [locus\_tag=BN49\_RS07525] [protein=YjhX family toxin] [protein\_id=WP\_002889848.1] [location=1265989..1266246] [gbkey=CDS]

MNLSRQEQRTLHVLAKGGRIAHVRDTSGRITAVECYTREGLLLSDCTLAVFKKLKTKKLIKSVNGQPYRI

NTTGLNNVRAQADNR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531937.1\_1231 [locus\_tag=BN49\_RS07530] [protein=class I SAM-dependent methyltransferase] [protein\_id=WP\_016531937.1] [location=1266304..1267053] [gbkey=CDS]

MIDIPRIFTISESEHRIHNPFTPEKYATLGRALRMAPGTTILDLGSGSGEMLCSWARDHQIVGTGVDMSL

LFSQQAAARAEELGVSDRVTFVHQDASGYVASQPCDIAACVGATWIGGGVAGTIELLKQSLTPGGMLLIG

EPWWRKRPATAEEAVACGAQSPDDFLTLPALVAHFGELGYDVVEMVLADQEGWDRYEAAKWLTMRRWLEA

NPHDDFAPEVRQQLTTAPLHHVTWTREYLGWGVFVLMAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004222817.1\_1232 [locus\_tag=BN49\_RS07535] [protein=HNH endonuclease] [protein\_id=WP\_004222817.1] [location=1267325..1267789] [gbkey=CDS]

METLVILAVVVWVLFKLVQKVTSKLYPPDSVKVQEKPDTTPATDAWGNYPKAEGHVVLFEQYRHEQALRQ

QAAKEADTFYRSREWRRLRYQAFQRYGNKCCVCGRGASDGMVMHVDHIKPRSLYPHLALDIANLQIMCNE

CNVSKGNRDEVAWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004147204.1\_1233 [gene=lpdA] [locus\_tag=BN49\_RS07540] [protein=dihydrolipoyl dehydrogenase] [protein\_id=WP\_004147204.1] [location=complement(1268131..1269528)] [gbkey=CDS]

MHDKYDVLIIGGGPGGYVAAIRAGQLGLRTVLVEKQHLGGICLNWGCIPTKALLHGAEVAHTITHASQLG

ISVGEVNVDLQKLVQFSRTVSQQLTAGVAYLLKKNGVRVIDGTARLRGKGQITVEDARGEARDYRADHVI

LATGARPRALPGIAPDGEHIWTYFEALRPKLLPKSLLIIGSGAIGVEFASLYNDLGCKVTLVELASQILP

VEDAEVSAAVRKSFEKRGIQIHTQTLVTQVQLTDIGVRCTLNNTGGEYSQDVERVLLAVGVQPNIEDLGL

EALGVELDRGFIKTDAACRTNVFGLYAIGDVAGPPCLAHKASHEGVICVETLAGVEGAHPLDRDYVPGCT

YARPQVASLGLTESTALARGRPVRIGKFSYQSNGKALASGETEGFVKTIFDAETGELLGAHMVGAQVTEQ

IQGFGIARHLEATDESLLSMIFAHPTLSEAMHESILAACDQPLHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004222820.1\_1234 [locus\_tag=BN49\_RS07545] [protein=2-oxo acid dehydrogenase subunit E2] [protein\_id=WP\_004222820.1] [location=complement(1269518..1271053)] [gbkey=CDS]

MSEIKTLEMPKWGLSMEEGLLARWAIQEGDDFTRGQEICEIETSKIVNVLEAPFAGTLRRIIAREGETLQ

VGAVLALAADASVSDAELDEFAASLATVKPAAPGPEAAAPDVAAQAGAKPPSVVSPPSNSPEPPVGQTVI

PVSLQGVTDVTQVNATPHALRLSARWGVDLKKVRGSGRGERISVSDLESAIVAAGGRLASPTPPVRPSKA

PRSHADDSQVSATPLARRLAGKLGINLHDCRSSGSRGRVSRDDVLAASLLLDGPPQTSPVQESAPAPFES

IPMSGMRRAIASRLQTSKQQSPHFRLSVDLDLERLLAFRQEINREVPGVKISVNDLLVKACALALVAVPD

VNIQFDEAAQSIRRFTDADISVAVALPAGLITPIVRSANRKSISDISNEIHSLVTRAKAGTLKPEEFQGG

TFSLSNLGMLGVRQFDAIINPPQSAILAIGAGEVRAVVRDGQIVARQQMTVSLSCDHRVIDGAAGAAFLR

ELKRLIETPTLMFIQETSYAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002889881.1\_1235 [locus\_tag=BN49\_RS07550] [protein=alpha-ketoacid dehydrogenase subunit beta] [protein\_id=WP\_002889881.1] [location=complement(1271057..1272076)] [gbkey=CDS]

MTIKTYREAVKEALAQEMERDERVVLIGEDLRGGHGGNAPEEAKIEAFGGVLGVTKGLWTQFGSDRVIDT

PITESAIIGMAAGAAATGLRPVAELMFMDFFGVSHDALYNQAAKFRYMFGGKARAPLVMRGMIGAGFSAA

AQHSQSPYNIFATTPGLKVVVPSTPYDVKGLLIQSIRDDDPVVFCEHKMLYDLKGEVPDEIYTIPLGVAN

YTREGEDVTIIALSAMVHKANQVADKLAREGISVEVVDPRTISPLDEEGILESVASTGRVVIVDESAARF

GFAHDVAALIASQAFHFLKAPVLLVTPPHTPVPFSPALEKLWIPGVERIEAAVRQVLED

>lcl|NZ\_FO834906.1\_prot\_WP\_002889884.1\_1236 [locus\_tag=BN49\_RS07555] [protein=thiamine pyrophosphate-dependent dehydrogenase E1 component subunit alpha] [protein\_id=WP\_002889884.1] [location=complement(1272088..1273047)] [gbkey=CDS]

MLSKQALLQAYRKMREIRTFEERLHQENTSGDIPGFIHLYTGEEAIAVGVCENLTSADFIGSTHRGHGHC

IAKGCDIHGMMAEIFGKDSGLCRGKGGSMHIADLSKGMLGANAIVGGAPPLAIGAALTAKTLKTGNVGVS

FTGDGGSNQGLVFEAINMAVVLQLPAVFIFENNGYGEGTGHDYAVGGRDIARRAAGFGLPAVTVDGTDFF

AVYEATSEAVKRAREGGGPSVIEAKAFRWHGHFEGDPALYRAEGEVQRLREQHDPLKIFTAKVKQHITQE

ELAAIDEEVEALVNDAVLKARAAAYPAPEDLLTDVYVSY

>lcl|NZ\_FO834906.1\_prot\_WP\_171819490.1\_1237 [locus\_tag=BN49\_RS07560] [protein=LuxR C-terminal-related transcriptional regulator] [protein\_id=WP\_171819490.1] [location=1273421..1276066] [gbkey=CDS]

MLERPRLLQLLNPVQQCRLGVVCAGAGFGKTTLLAQWHQQMVAQGERIAWLSLDEDDDDVWQFIPYLLQA

LRPLYADWDADFWRDMEEQKLSSSEQLLAGLINQLHYCPHDVYLIIDDFHVINDRGVYEAVGYLIKHAPA

ALHLIIGSRFHPNLALSQLQAQDQLVEIYDRDLQFTLEETKHYFSRTVALPLSNHHAQRLQSVTEGWIAG

MKIASLSAELQHDPEHLLRNMHGGIRSIARYLKEVVLDPLPEEILDFLVKTSFLSRLNAELCNAVTGRDD

SKAMLTWIERHNLFLSALDEQGYWFRYHPLLQENLRTMLQQNNDIDRKQLHELASHWFVEQKLWSEAVRH

ALSAGKPVHSPVQDGASAQSLAEEGDIDTLISWMHHLPPSTDPSRIDLQINLAWALAHYFHFDESRQLLD

NLDQMVLHHREDLTRSTWCKLRVVRAICEAFAENIPESLAIVQPLLAEVPCGDTWVDGLICNILSYCHVV

NQRYHDALEVQQHMPSPESPLDNLFVSVYRAFIIAQCHLCQGDLGKAGWYAEKTLRQAECYTGTQSTSGA

TLAPLLAEIAYECQSGDSPEHLLADRLEFIDRFSPPDALSRCYTYLARQALDGNMPYEAERLLEHAQRLA

VSRGWQRLQAMMLAEQVRVRLQRGNVTGAEQLQRQLEQMAASFRMDAEHPCQRAIALSASLSHCRLLLAR

GQAPQACILLADMVPDQENRGDRLTAARLRTLWSLALWNSGKTAAARTTFQPVVQLAEQQHLKGLFLEAG

DTLQPLLAGMNETSSACTEEGIVHEPWAGKRAPADGTPFNSGSPDIHGELSEREFQILQLIAEGQMNKEI

ARSLAISAETVKWHIKNIYAKLKVNSRTQAMSRALEMKLLD

>lcl|NZ\_FO834906.1\_prot\_WP\_009485120.1\_1238 [gene=accB] [locus\_tag=BN49\_RS07565] [protein=acetyl-CoA carboxylase biotin carboxyl carrier protein] [protein\_id=WP\_009485120.1] [location=1276439..1276894] [gbkey=CDS]

MDIASIEKLIALVEASGIGELEIAEGASSVRISRAISSPTAVGSSAVSAAVVQPQLDIPIQAAQARAIAS

DPATEHITSSPMVGTFYLSPGPGAAPFVAVGQQVNIGDTLCIVEAMKMMNQISAENSGIVKAILATDGQP

VEFDQPLIVIE

>lcl|NZ\_FO834906.1\_prot\_WP\_004222829.1\_1239 [gene=accC] [locus\_tag=BN49\_RS07570] [protein=acetyl-CoA carboxylase biotin carboxylase subunit] [protein\_id=WP\_004222829.1] [location=1276903..1278249] [gbkey=CDS]

MLDKIVIANRGEIALRILRACRELNIRSVAVHSTADRELKHVLLADESVCIGPPSSAKSYLNIPAVISAA

EVTGAAAIHPGYGFLAENADFAEQVERSGFVFIGPKAETIRLMGDKVSAIQAMKQAGVPCVPGSDGPLDD

NHEKNRRLAAGIGYPIIVKASGGGGGRGMRVVREEKELAQAIDMTRAEAKAAFNNDMVYMEKYLENPRHI

EIQILADGQGQAIYLAERDCSMQRRHQKVVEEAPAPGITAEIRQAIGERCAKACLDIGYRGAGTFEFLYQ

QGEFYFIEMNTRIQVEHPVTEMITGIDLIKEQLRIASGLPLSISQQQVSLRGHAIECRINAEDPHTFMPS

PGKITRFHAPGGFGVRWESHIYAGYCVPPYYDSMIGKLIVIGDSRNEAIARMEHALSELVIDGIKTNAEL

QRRIMADDHFRAGGCNIHYLEKKLELNR

>lcl|NZ\_FO834906.1\_prot\_WP\_004222831.1\_1240 [locus\_tag=BN49\_RS07575] [protein=Glu/Leu/Phe/Val dehydrogenase] [protein\_id=WP\_004222831.1] [location=1278330..1279601] [gbkey=CDS]

MSALSYVTGESHCAWAIYLSQVERVLPLPGDLNRWANTLRHPERALIVDVPLEMDDGTIRHFEGFRVQHN

LSRGPGKGGVRYHPDVSLQEVMALAAWMTVKCAALNLPFGGAKGGVRVDPSTLSDRELERLTRRYTCEIS

RVIGPRQDIPAPDVGTNAQVMAWMMDTWSRNAGTAATGVVTGKPVHLGGSLGRVQATGRGVFITGCHIAE

KMGLPVAQSRVAVQGFGNVGSVSAGLFHAAGARVVAVQDHRATLYQHNGLDIPALQAWQQEHGTIAGFPG

ADNVTEEAFWRLEYEILIPAALEGQISAELAAGLRCRLILEGANGPTLPEADDVLAERGIVLVPDVIANA

GGVTVSYFEWVQDLSSLFWSEEEIDARLDTIMRHAIESVWQKAQALAIPLRTAAWALACERILQASKDRG

LYS

>lcl|NZ\_FO834906.1\_prot\_WP\_012968872.1\_1241 [locus\_tag=BN49\_RS07580] [protein=DMT family transporter] [protein\_id=WP\_012968872.1] [location=complement(1279662..1280582)] [gbkey=CDS]

MNARLGIYLKILSALCATLMLACVKGLQGAIPTGEVIFFRSFIAMFPLLIWLKIQGNVLASIKTKNIFGH

LIRGFSGTGGMYFNYLALVSISLADATALSYAAPLFTVIMAALLLKERVRFSRWLGVIVGFSGILFMLSA

SLTASGSLFAGGHLQSGMALGVAFALLAALCTATSNIQIRFLNGIEKPGAIVFYFSLMTTLIGLATSLFG

WVRPTPSQLLLLVGCGFFGGMAQILVTLSLRFTDASLLAPFDYTTLVWSMVIGYLFLNSLPGSSTLIGAG

IVALAGIFTLWCDQRQRRAHIARASS

>lcl|NZ\_FO834906.1\_prot\_WP\_004222836.1\_1242 [locus\_tag=BN49\_RS07585] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004222836.1] [location=1280880..1281719] [gbkey=CDS]

MKLKRNAGLALVLTLVAVSGAARADMLADIHARGELKCAVYSDVPPFSAPDPKTRQLVGMDVELCHALAK

QMGVKAQLVPTSVEARIAIIATGRADVLIANLAYTKTRGRQIQFSDPYYVAKEMLLVKEANADKTLADFK

GKRISATKGTTSEQSIVLKGGKPVTFQDAASAFLALEQNKVLGFVTNTMTGIKMIGQAKKDGINLAMIKE

PMALEPIGVGMKQGEPQLLASVNESLKVMDDDGTIDKIWNTWIGPNTEYKMVREERVQPLSSLTFEPLE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529972.1\_1243 [gene=pxpB] [locus\_tag=BN49\_RS07590] [protein=5-oxoprolinase subunit PxpB] [protein\_id=WP\_016529972.1] [location=1281722..1282429] [gbkey=CDS]

MTPTSKTLLPERRVEIHASAPARISMMGSRAWLIEAPGAFDLPAQRRIWSMAQNLQQWPAVESLIPGVTN

LLVLLHDTPEEPTAVERRLHEYWLSAQALNLEGRQIDIPVCYGGEHATDLEAVCRHTGFSAREVIRRHSQ

GVYTVVALGSAPGFGYLHGLDPRLATPRKKVPSLNMLKGTVTIGGPQAGVSVLTGPNGWNAIGYAEIEVF

NPHAAIPALMAPGDIIRFLPERVEL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529973.1\_1244 [locus\_tag=BN49\_RS07595] [protein=biotin-dependent carboxyltransferase family protein] [protein\_id=WP\_016529973.1] [location=1282426..1283412] [gbkey=CDS]

MIEIEQSGSLNTIQDLGRPAWRHLGVSVSGVMDPLALRAGNTLLGNEENAAVIEVQMFPFRVRFLADSWI

ALTGADCRARLDGDELPAWWGCAVRKGQVLELRFPRRGARGYLCVAGGIDVPLVLGSRSTALRGGFGGLE

GRQLQRGDVLSCGPWQGAPLPDSGIGIEPPEVALNAFFPRNAQGDVQIRAIPAGEYPLFAADASRFWSQA

WKISQHSNRTGYRLAGEPILPAETVEMRSYGLIPGIVQVPPAGEPIIQLSDANTAGGYPKIACVIEEDLW

RLGQLQAGQSIQLVQADTSTAIAVRQEIERWLQRLRVSIAPLVKVVGL

>lcl|NZ\_FO834906.1\_prot\_WP\_021312346.1\_1245 [locus\_tag=BN49\_RS07600] [protein=LamB/YcsF family protein] [protein\_id=WP\_021312346.1] [location=1283423..1284193] [gbkey=CDS]

MKIDVNSDMGEGFGVYQLCDDSALMDKVSSANIACGFHAGDPAIMTRMVRLAKVRGVGIGAHPGLPDRQG

FGRKEMAFSADEICQQVVYQLGALSAIARAEGTRVVHLSFHAAMGNMINRDDALALQVMQAVARIDSQLI

IFCQPDTIIERAAQAAGLPTLTLFLADRAYDDRGQLVPRGIAGSLIKEEAAVRARVRQFLQQGTVTTFSG

NTLSIRARSILVHSDTPGSLALATLVRSEIEACGATVASAAEVLAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530498.1\_1246 [locus\_tag=BN49\_RS07605] [protein=pyridoxal phosphate-dependent aminotransferase] [protein\_id=WP\_016530498.1] [location=complement(1284417..1285619)] [gbkey=CDS]

MPDIADRLKNVTVSASVAMTQKARDLAAQGIDVVGLSTGEPDFPTPPHVIDAAYAAACAGDTRYPPTDGT

PALRAAIQRKFLRDNELRYDISQILTAGGARQIIFNAMMATINPGDEVLIPMPSWISYADIVKFAGGTPV

PVPCHEEYGFKPLPQDVEAAITPKTKWLLLNYPSNPTGSVATHAELLALGETLLRHPHIWIMTDDIYEHL

LYDGVKFWPLAQVEPRLYDRVLTVNGVSKAYSMTGWRLGFCGGPLTLIKAMSNVNTQNSGGVTTLAQAGS

VAALDGPQDLLAERAEIYRQRRDYVLERLAGIHGLRCHKPQGAFYLFVNIEAFIGKTSASGHFIASDSDF

VMALIEEQHVVTVQGAAYGMSPYFRLSYATSMERLQTGCDRLAAFCAGCR

>lcl|NZ\_FO834906.1\_prot\_WP\_004222846.1\_1247 [gene=nac] [locus\_tag=BN49\_RS07610] [protein=nitrogen assimilation transcriptional regulator NAC] [protein\_id=WP\_004222846.1] [location=1285975..1286898] [gbkey=CDS]

MNLRRLKYFIKIVDVGSLTQAADILHIAQPALSQQLATLEGEVDQQLLIRTKRGVTPTNAGKILYTHAQA

ILRQCEQAQSAIDGAGQALSGQVSVGLAPGTAAQLLAIPLLTEVQRQHPGIVLYFNENFGTTLSELIMSG

RMDMAVIYGDRDIHGLRFLPLMKEELFFVCPHALGESRREISLAEVARYDLFLPRIYNIMRKAADDAFTL

AGLSYRVKCEIESLTTLNAALAADLGGTIMPESAARTMLQPANAWMARIVEPNVLTSLSFCMSDHLPLSQ

PAEAVKGILLSLMAQRTEDNRPLTLVG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530499.1\_1248 [locus\_tag=BN49\_RS07615] [protein=acetyl-CoA carboxylase biotin carboxyl carrier protein subunit] [protein\_id=WP\_016530499.1] [location=1287016..1287456] [gbkey=CDS]

MMEKELIAFEDVRQLAQKMHNAGLRELEWRGADWSVRLRYPSGKTMAEPPPLPPLAAETRPLSVCSPMPG

RLLLSHPSHGEAFVSEGQHVAPNDILALVQVGPLYLPVRSPVAGTLKSLMAPAGSRLEYGSEIALLLPTD

AASAKL

>lcl|NZ\_FO834906.1\_prot\_WP\_046042675.1\_1249 [locus\_tag=BN49\_RS07620] [protein=SDR family oxidoreductase] [protein\_id=WP\_046042675.1] [location=1287570..1288322] [gbkey=CDS]

MPFSDYKVALVTGASAGMGEAIVERLCQEGIEVHAVARRHEQLAALADRTGCIPHAVDVGDLSALTALCQ

GLQVDILVNNAGVSHPGSILDAEADWVNTQVDVNLRAVLHLCRLLVPGMVARDCGHVINITSIAAIYNFN

GNSIYHATKAGVHALSRQLRVDCYGKRVRITEICPGRVATEIFGNVSGDHEEARRRFIDGFELPEAKDIA

DCVAFALAAPVAVNIGNIEITPTLQVPGGLSTMRPGDRES

>lcl|NZ\_FO834906.1\_prot\_WP\_016531274.1\_1250 [locus\_tag=BN49\_RS07625] [protein=amino acid ABC transporter permease] [protein\_id=WP\_016531274.1] [location=1288346..1289041] [gbkey=CDS]

MALDFSNVMTGHYGQMIIDGTVVTLELALGAWLLAMFIALVLVMIRLSNKRFAQLFVAAYVSYHRNVPTL

IQLMMWYFAIPTLLPESLQMWVNEMNAEFLFSLVALGLCQAAYFSEDIRSGLRAIPEGQNEAARALGMGY

LRAMWLVILPQGIRNALPSVINHTVLLFKNTSLAMVIGVTELTYVTRDIENQTFRTFEAYMVATVGYLAF

SLLLMGMGALLARRFQRAYAR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531275.1\_1251 [locus\_tag=BN49\_RS07630] [protein=amino acid ABC transporter permease] [protein\_id=WP\_016531275.1] [location=1289047..1289808] [gbkey=CDS]

MFDFFTILHDNGLLLLMGQYPDGPLGGVLCTLLVSLLAVLFAFPVGVLLCLARLSPWRWLSWPVTCWIYL

LRGIPLMMVVFWTYFCVPLLIGHNISGFSTMLCTLVIYESTYIAEIVRGGIQALPSGQYEASRALGMGHV

RALRLVILPQALYNALPSLVSQLVSIIKDSTLGYVINVPELTYAANQVSNQLLTKPFQVFAIVALSYYII

NFSLTWLANRLELRIASRRQRAQSAMGKPVTPLILDPSPSQTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016531276.1\_1252 [locus\_tag=BN49\_RS07635] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_016531276.1] [location=1289827..1290555] [gbkey=CDS]

MILFNQVNKWYGEYQALTDVSAEIKSGEVVVVCGPSGSGKSTLIRTVNRLEPIEQGQILFDGVDIHGSST

RLNQLRTRIGFVFQSFNLFPHVSVLENIMMSPVKVLGEKRSEARRHAGELLERVGLSHKADVYPAQLSGG

QQQRVAIARALAMKPPVMLFDEPTSALDPEMVGEVLSVMRGLAQEGMTMMCVTHEMNFARDVADTIWFMD

QGQILEKSAPDKFFTAPQHPRARRFLNDLLLH

>lcl|NZ\_FO834906.1\_prot\_WP\_046042694.1\_1253 [gene=proA] [locus\_tag=BN49\_RS07645] [protein=glutamate-5-semialdehyde dehydrogenase] [protein\_id=WP\_046042694.1] [location=complement(1291576..1292829)] [gbkey=CDS]

MLEQMGIAAKAASWQLALLSSREKNQVLEKIADYLEAQTDDILRANAEDLAEARTNGLSEAMLDRLALTP

ARLSGIASDVRQVCNLADPVGQVIDGGLLDSGLRIERRRVPLGVIGVIYEARPNVTVDVASLCLKTGNAA

ILRGGKETWRTNAATVKVIQQALQECGLPAAAVQAIESPDRALVGEMLKMDKYIDMLIPRGGAGLHKLCR

EQSTIPVITGGIGVCHIFVDETAEIAPALKIIVNAKTQRPSTCNTVETLLVHRNIADTFLPALSKQMAES

GVTLHAAPSALPALQNGPAKVEPVKAEQYDDEYLSLDLNVKVVADMDEAIAHIREHGTQHSDAILTRTLR

NANRFINEVDSSAVYVNASTRFTDGGQFGLGAEVAVSTQKLHARGPMGLEALTTYKWIGFGDDTIRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144574.1\_1254 [gene=proB] [locus\_tag=BN49\_RS07650] [protein=glutamate 5-kinase] [protein\_id=WP\_004144574.1] [location=complement(1292840..1293943)] [gbkey=CDS]

MSESQTLVVKLGTSVLTGGSRRLNRAHIVELVRQCAQLHAMGHRIVIVTSGAIAAGREHLGYPELPATIA

SKQLLAAVGQSRLIQLWEQLFSIYGIHVGQMLLTRADMEDRERFLNARDTLRALLDNSIVPVINENDAVA

TAEIKVGDNDNLSALAAILAGADKLLLLTDQPGLFTADPRSNPQAELIKDVYGIDDALRAIAGDSVSGLG

TGGMGTKLQAADVACRAGIDTIIAAGNRPDVIGHAMAGLPVGTCFHAQESPLENRKRWIFGAPPAGEITV

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GYEYGPVAVHRDDMIIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004144576.1\_1255 [gene=phoE] [locus\_tag=BN49\_RS07660] [protein=phosphoporin PhoE] [protein\_id=WP\_004144576.1] [location=1294233..1295285] [gbkey=CDS]

MKKSTLALMMMGFVASTATQAAEVYNKNANKLDVYGKIKAMHYFSDYDSKDGDQTYVRFGIKGETQINDD

LTGYGRWESEFSGNKTESDSSQKTRLAFAGVKLKNYGSFDYGRNLGALYDVEAWTDMFPEFGGDSSAQTD

NFMTKRASGLATYRNTDFFGLVDGLDLTLQYQGKNEGREAKKQNGDGVGTSLSYDFGGSDFAVSAAYTSS

DRTNDQNLLARGQGSKAEAWATGLKYDANNIYLATMYSETRKMTPISGGFANKAQNFEAVAQYQFDFGLR

PSLGYVLSKGKDIEGVGSEDLVNYIDVGLTYYFNKNMNAFVDYKINQLKSDNKLGINDDDIVALGMTYQF

>lcl|NZ\_FO834906.1\_prot\_WP\_004222859.1\_1256 [locus\_tag=BN49\_RS07665] [protein=NlpC/P60 family protein] [protein\_id=WP\_004222859.1] [location=complement(1295330..1295896)] [gbkey=CDS]

MKPKLTHALFLIPFLLLAGCSSSPKQAKNTKSHADMTIDGGSDDLIPVVAALHDQMHTWQGTPYEWGGTE

QSGVDCSGFVWRTLKDRFNLPMERITTRELLHMGVRVNKRDLRPGDLVFFRTRAGMHVGFYDTDHNFLHA

SSSQGVMRSSLDNPYWESAFYQARRLPKEYNAQITMNSDTLHLAKNRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529192.1\_1257 [locus\_tag=BN49\_RS07670] [protein=DMT family transporter] [protein\_id=WP\_016529192.1] [location=1296309..1297178] [gbkey=CDS]

MHVRYSLLASQATTALFVLLWGSAAIFTRWGLDNASPMALLVFRFLVALVALAPLAIVRRRWLPAPGTRL

QTAATGLMLIGGYSVCYFEAMANGVTPGLIATIMGIQSILTLCVVERRLHGRRLSGLLLALAGLVLLVWR

SLAASPMATVGILFALAALLLMTFGALWQKRSRQAPADVLPLQYAVSLGLCLLIAPVSGFRFTVNAGLII

PVLFLGLLISVVAQLLLYRLLSAGNIVNVTSLFYLVPAITALLDYLLLGNRLPAAAMIGMMAIVGGIVLV

FRTAKVRAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177299.1\_1258 [locus\_tag=BN49\_RS07675] [protein=HAD-IB family hydrolase] [protein\_id=WP\_004177299.1] [location=1297274..1297939] [gbkey=CDS]

MGNTLTIFDLDNTLIQGDSSTVWSQFMVREGLATQKGYLAREARLMADYDRGEMNIADYVALIQAPLAGI

PKSDVDALVARCVREAILPRVYPQAWELIRRLRAEGEQMLIISASVSLLVQAVAAALEIDQALGIDVAMV

DGGYSGEITGIPSYQQGKVARLAQWREAHPQYDGEVTFYTDSINDLPLCLHADRVRLVNPCPQLQAAGAG

YGWPVLSWRLE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529191.1\_1259 [locus\_tag=BN49\_RS30710] [protein=hypothetical protein] [protein\_id=WP\_016529191.1] [location=complement(1298244..1298447)] [gbkey=CDS]

MASGTELRLCRVAATPYPAYSPKSPLAQGLLKLPVLAASTSLRRSRKAGGTGGGGDWPPPVRSQRHE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531458.1\_1260 [gene=phnE] [locus\_tag=BN49\_RS07685] [protein=phosphonate ABC transporter, permease protein PhnE] [protein\_id=WP\_016531458.1] [location=complement(1298991..1299875)] [gbkey=CDS]

MSVWHMQPDIAASRRQHKQLYQVQGRYLRYVGLVALACLLYYVWFFLQFGVSGEQLTTGLQQIGRYLARM

FVWHDFWNWPFGYYFTQIGVTLAIVFAGTLTATVLALLLSFFAARNIMRGVVLGTLALLMRRLFDVLRGI

DMAIWGLIFVRAVGLGPLAGVLAIIMQDTGLLGRLYAEGHEAVDRSPGRGLTAVGANGLQKHRFGIFTQS

FPTFLALSLYQIESNTRSAAVLGFVGAGGIGLIYAENMRLWNWDVVMFITLLLVAVVMIMDTLSAWLRRR

YIGGAAVPLYQGGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002890001.1\_1261 [gene=phnE] [locus\_tag=BN49\_RS07690] [protein=phosphonate ABC transporter, permease protein PhnE] [protein\_id=WP\_002890001.1] [location=complement(1299872..1300744)] [gbkey=CDS]

MKTTHTEFERYYQQVRSRQKRDAVCWSLLLLALYFAAGSAAEFNLLTIWHSLPHFFDYMAETIPPLSAGN

LFADVQTKGSLAWWGYRLPIQLPLIWETLQLALASTLVAVAIATVFAFLAANNAWSPAPVRFAIRVLVAF

LRTMPELAWAVIFVMAFGIGAIPGFLALMLHTVGSLTKLFYEAVESAQNKPVRGLAACGASPLQKIRFAL

WPQVKPLFLSYGFMRLEINFRSSTILGLVGAGGIGQELMTNIKLDRYDQVSITLLLIILVVSALDMLSGR

LRLWVLEGKK

>lcl|NZ\_FO834906.1\_prot\_WP\_023284714.1\_1262 [gene=phnD] [locus\_tag=BN49\_RS07695] [protein=phosphonate ABC transporter substrate-binding protein] [protein\_id=WP\_023284714.1] [location=complement(1300811..1301749)] [gbkey=CDS]

MKKYMTGAVRLSAMVAGIMMAWQAAAAQPKELNLGILGGQNATQQIGDNQCVKAFLDKELNVDTKLRNSS

DYSGVIQGLLGGKVDVVLSMSPSSYASVYLNNPKAVDIVGIAVDDKDQSRGYHSVVIVKADSPYKTLDDL

KGKAFGFADPDSTSGYLIPNHAFKEKFGGNADNKYNNTFSSVTFSGGHEQDILGVLNGQFAGAVTWASMV

GDYNTGYTTGAFNRLIRMDHPDLMKQIRIIWQSPLIPNGPILVSNALPADFKAKVVAAVKKLDTEDHACF

IKAMGGTQHIGPGSVADFQQIIDMKRELVSAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004177295.1\_1263 [gene=phnC] [locus\_tag=BN49\_RS07700] [protein=phosphonate ABC transporter ATP-binding protein] [protein\_id=WP\_004177295.1] [location=complement(1301772..1302614)] [gbkey=CDS]

MNSSLAAVAETDFQPFTDLAAGRQRKVLSVRNLSKAYQAQHKVLDGISFDLHAGEMVGVIGRSGAGKSTL

LHVLNGTHSASGGEILSYPEVGTPHDVSQLKGRALNAWRSHCGMIFQDFCLVPRLDVLTNVLLGRLSQTS

TLKSLFKIFPAADRARAIALLEWMNMLPHALQRAENLSGGQMQRVAICRALMQNPGILLADEPVASLDPK

NTQRIMDVLREISEQGISVMVNLHSVELVRAYCTRVIGVASGQLIFDDHPSRLTQDVLQRLYGDEVSQLH

>lcl|NZ\_FO834906.1\_prot\_WP\_004144585.1\_1264 [locus\_tag=BN49\_RS07705] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004144585.1] [location=1303463..1304005] [gbkey=CDS]

MEYKSCSDKYIWSADDSYFYKGLSELIVDIDELIYLSLEKIRKDFVFINLNTASLNEFIRRDSEWLSAVK

GKQVVLIAARKSEALANYWYYNSDIRGVVYVGLSRDIRKELAYVINGRFLRKDIKKDKITDREMKIIRMT

AQGMQPKSIARIENCSVKTVYTHRRNAEAKLYSKIYKLVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002890053.1\_1265 [gene=ecpA] [locus\_tag=BN49\_RS07710] [protein=common pilus major fimbrillin subunit EcpA] [protein\_id=WP\_002890053.1] [location=1304080..1304667] [gbkey=CDS]

MKKKVLAIALVTAFTGMGVAQAADVTAQAVATWSATAKKDTTSKLVVTPLGSLAFQYAEGIKGFNSQKGL

FDVAIEGDTTATAFKLTSRLITNTLTQLDTSGSTLSVGVDYNGAAVEKTGDTVMIDTANNIMGGNLSALA

NGYNASGRTTAQDGFTFSIISGTTNGTTAVTDYSTLPEGIWSGDVSVQFDATWTS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529018.1\_1266 [locus\_tag=BN49\_RS07715] [protein=hypothetical protein] [protein\_id=WP\_016529018.1] [location=1304726..1305394] [gbkey=CDS]

MKKHLLALGLLLAGVSPAQALDVGDISSFMNSGSSTLSKTIKNSTDSGRLINIHLERLSSPLDGGQVIPM

DKPDEVLLTPASLLLPAQASDVIRFFYKGPADDKERYYRIVWFDQALSDAQRDNANRSAVVTASARIGTI

LVVAPRQVNYRFQYANGSLTNTGNATLRILAYGPCLKAADGKECKENYYLMPGKSRRFTRVDTADKKGRV

ALWQGEQFVPVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529017.1\_1267 [locus\_tag=BN49\_RS07720] [protein=fimbrial biogenesis outer membrane usher protein] [protein\_id=WP\_016529017.1] [location=1305420..1307945] [gbkey=CDS]

MPQRWITPGLKTRLAFGMIFLFVQPDVSAAAAGAQQIGGVIIPQAFSQALQDGMSVPLYIHLAGSQSTRD

DQRIGSAFIWLDGGQLRVRQIQLEESEGNASVSEQTRQQLIGLANAPFSEALTIPLTDSAQLDLSLRQLL

LQLVVKREALGTVLRSRSEDIGQSSVNTLSSNLSYNLGVYNNQMRNGGSNTSSYLSLNNVTALREHHVVL

DGSLYGIGSGQQDSELYKAMYERDIAGHRFAGGMLDTWNLQSLGPMTAISAGKIYGLSWGNQASSTVFDN

SQSATPVIAFLPAAGEVHLTRDGRLLSVQNFAMGNHEVDTRGLPYGIYDVEVEVIVNGRVVSKRTQRVNK

LFSRGRGAGAPLAWQVWGGSFHMDRWSESGKKTRPAKESWLAGLSASGSLSTLSWAATGYGYDNQAVGET

RLTLPLGESINVNLQNMLASDSSWSSVGSISATLPGGFSSVWVNQERTRIGDQLRRSDADNRAIGGTLNL

NVLWSKLGTFSVSYNDDRRYNSHYYTADYYQTVYSGAFGSLGLRAGIQRYNNGDSSANTGKYIALDLSLP

LGNWFSAGMTHQNGYTMANLSARKQFDEGTIRTIGANLSRAISGDTGDDKTLSGGAYAQFDARYASGTLN

VNSAADGYVNTNLTASGSVGWQGKNIAASGRTDGNAGVIFNTGLEDDGQISARVNGRIFPLSGKRNYLPL

SPYGRYEVELQNSKNSLDSYDIVSGRKSHLTLYPGNVAVIEPEVKQMVTVSGRIRAEDGTLLANARINNH

IGRTRTDENGEFVMDVDKKYPTIDFSYGGNKTCEVALELSQARGAVWVGDVVCSGLSSWAAVQQSGEENE

S

>lcl|NZ\_FO834906.1\_prot\_WP\_002890060.1\_1268 [gene=ecpD] [locus\_tag=BN49\_RS07725] [protein=fimbrial adhesin EcpD] [protein\_id=WP\_002890060.1] [location=1307935..1309578] [gbkey=CDS]

MKVNALMALAILALLWPAAALRAAVTKTTWSDAPAREFVFVENNSDDNFFVTPGGALDPRMTGANRWTGL

KYTGSGTIYQQSLGYIDNGYNTGLNANWKFDMWLENSPVSHPLTGLRCINWYAGCDMATSLILPQTTDAS

GFYGATVTSGGAKWMHGMMSDAFYQYLQQMPVGGSFTMTINACQTSVNYDASSGARCKDQASGNWYVRNV

THTKAANLRLINTHSLAEVFINSDGVPTLGEGNADCRTQTIGSRSGLSCKMVNYTLQTNGLSNTSIHIFP

AIANSSLASAVGAYDMQFSLNGSSWKPVSNTAYYYTFNEMKSSDSIYVFFSSNFFKQMVNLGISDINTKD

LFNFRFQNTTSPESGWYEFSTSNTLIIKPRDFSISIISDEYTSAPSREGYVGSGEPALDFGYIVTTSGKT

AADEVLIKVTGPAQVIGGRSYCLFSSDDGTAKVPFPATLSFITRSGTTQTYDAGCDDSWRDMTDALWLTT

PWTDISGEVGQMDKTTVKFSIPMDNAISLRTVDDNGWFGEVSASGEIHVQATWRNIN

>lcl|NZ\_FO834906.1\_prot\_WP\_002890061.1\_1269 [locus\_tag=BN49\_RS07730] [protein=fimbria/pilus periplasmic chaperone] [protein\_id=WP\_002890061.1] [location=1309547..1310257] [gbkey=CDS]

MSRRRGATLTKALLTVGCLLAAPLAQAISVGNLTFSLPAEADFASKRVVNNNKSARLYRIAVSAIDRPGG

SEVRSRPVDGELLFAPRQLVLQAGESEYFKFYYHGPRDNRERYYRVSFREIPTRNLTRRSPTGGEVSMEP

VVVMDTILVVRPREVQFKWSFDKVAGTVSNTGNTWFKLLIKPGCDSTEEEGDAWYLRPGDVVRQPALRQP

GNHYLVYNDKFIKISDTCPLKPRPAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004177292.1\_1270 [locus\_tag=BN49\_RS07735] [protein=amino acid ABC transporter permease] [protein\_id=WP\_004177292.1] [location=complement(1310261..1310950)] [gbkey=CDS]

MNANLAVIADNLDYLLWGRLAEGQPGGVALTLLMAIGATLLALPGGIALAGLAWRYGGLVRRLLFLWAEI

IRGIPLIFVIFWLWYLLPMLTGGDLPGAVTVTLALAWFTAASVMHSVLAGLQSLPKGQYEAALTQGFAPG

QTLRLVLLPQALRNVQPSLVGIFIGLLKDTSLAFIVNVPELTTVAGQVNNRVQIYPLAIFVFTGAVYYLL

CCGLSLLASRRFTRRAATR

>lcl|NZ\_FO834906.1\_prot\_WP\_004178715.1\_1271 [locus\_tag=BN49\_RS07740] [protein=amino acid ABC transporter permease] [protein\_id=WP\_004178715.1] [location=complement(1310940..1311692)] [gbkey=CDS]

MTPMLDWHGVLSGQPLQWIISGFLTTVWVSVAGILLATLLAVLLLALRLGGGRAGRGLVAAWVSLFRNTP

LLVQLLFWYFAAWNLLPLAVKEVVNDEHAWSILPGNVWWLTPEFLCSMWGLGVFTSAFLVEEIASGLRAV

SHGQREAALSQGFTPWQELRFILLPQGLANAWQPIVGQYLNLMKLSSLASGIGFAELTYQVRQIESYNAH

ALEAFAVGTALYLALGVAMGVALTRLGPGRKLQRSARHER

>lcl|NZ\_FO834906.1\_prot\_WP\_016530262.1\_1272 [locus\_tag=BN49\_RS07745] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_016530262.1] [location=complement(1311689..1312507)] [gbkey=CDS]

MFSGLLSHSAAPAADFSRLQRASITFRDVAKRYGDHQVLNAIILQVEPGEVVAILGPSGSGKSTLIRLIN

QLESLSGGEILIDGKPTSRLSGSALRQLRSRVGFVFQQFNLYAHLTAQENITLALERVHGWEKSAAQARA

LALLRQVGLEEKAQQMPAQLSGGQQQRVAIARALASSPQIILFDEPTSALDPEMIGEVLQVMKTLAHSGI

TMLVVTHEMQFAREIADRVVFIDGGDILEVAPPAEFFAHPQHARARRFLQKVLDPLHQESLE

>lcl|NZ\_FO834906.1\_prot\_WP\_002890106.1\_1273 [locus\_tag=BN49\_RS07750] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_002890106.1] [location=complement(1312509..1313318)] [gbkey=CDS]

MRNKTTKIALALGMLLLASQAQADQLADIKAAGVVKVATFDANPPFGSVDAKTHHIVGYDVDFAQALAKA

LGVKLELVATNPANRIPLLQSGKADLIVADITITPERAQVIDFSTPYFVTGQQFLVPAGSPDKLDEYSKA

RIGAVKGTTGEQALHQRFPQARVLSYDDIPLALTALRNGNVQAITQDSTILAGLLAEAPDKAKFKILPDL

LSKEEIGVGVKKGEPALLKAVNDELVKLEKTGEAAKIYDVWFGPATKTPQPRAFTIEAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002890108.1\_1274 [locus\_tag=BN49\_RS30290] [protein=hypothetical protein] [protein\_id=WP\_002890108.1] [location=1313653..1313823] [gbkey=CDS]

MALWQRLTGWLAFLSNGEAGQQDTQRVMEAILPVASLYGVDIGNVETRWFRHDKTY

>lcl|NZ\_FO834906.1\_prot\_WP\_002890126.1\_1275 [locus\_tag=BN49\_RS07760] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_002890126.1] [location=complement(1313940..1314635)] [gbkey=CDS]

MLNARELKVFYGVIQGLKGVDIDVYDREIVTLIGSNGAGKTSTLNGIVNLVRSSGRVSFLNDDISRSQTH

QIVRRGLALVPEGRRVFTNLTIEENLRMGAYNNLAGYARLRDRMYALFPRLKERRHQMAGTMSGGEQQML

AIARALMSEPVLLMLDEPSLGLAPKIVGELFGIIKQLREENMTVLLVEQNATAALAIADRAYVLENGRIT

LSGAAREMLTNPEIKRMYLGG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530261.1\_1276 [locus\_tag=BN49\_RS07765] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016530261.1] [location=complement(1314628..1315410)] [gbkey=CDS]

MAENNVILQVQDVTMQFGGLRAIDNVSFHVDEAEIFGLIGPNGAGKTTLFNVITANYKPTSGSVTLAGTS

LKGLKPNQVVNAGIARTFQNIRLFNSMTVLENVMVGLDRASRYSLLEAALHIGRYFPAERAVKAKAMAIL

EDIGIAHFAHMQATNLSYGNQRKVEIARALATAPKLLLLDEPAAGMNPKETEDLAELIFRMRHDYQLSVL

LIEHDMPFVNRLCERVMVLEYGKPLFSGLMAEAIQHPDVISAYLGEANYA

>lcl|NZ\_FO834906.1\_prot\_WP\_004183134.1\_1277 [locus\_tag=BN49\_RS07770] [protein=branched-chain amino acid ABC transporter permease] [protein\_id=WP\_004183134.1] [location=complement(1315397..1316446)] [gbkey=CDS]

MLNATTTAGAQLRNLVIIVICIALLAGINVVFNDYIVRVISTIFIFMILAVSYNLINGVTGQLSLEPNGF

VAVGAYVTALLILSSDSKVDMFEMAAPSPWILSLHAGFLPALLISGLCAAALAVCLAVPVFRVRGDYLAI

VTLGFGFIIKILAINNPQITNGAIGLNDIPQQPHLLFWCGLFALLATGMILQLVWSKYGRMMKAIRDDED

AAIAMGVNTFRIKTCAFATSAFFEGIGGGLLASLLTTISPGLFDFMLTFQLLIIIVLGGLGSTTGALLGT

VLVVGSGEWLRFLDQPLQFFGHDLGAYPGLRMVVFSLLLLIIMLFAREGLLGKKEIWQMGRRNSSYGGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002890128.1\_1278 [locus\_tag=BN49\_RS07775] [protein=branched-chain amino acid ABC transporter permease] [protein\_id=WP\_002890128.1] [location=complement(1316446..1317345)] [gbkey=CDS]

MDGAIFLQQVVNGMSLGGMYALIAIGYTMVYGVLRLINFAHADVMMVGAFSTLFLFSSVGLPFGVAVFLT

LGLCGLFGMLIDRVAYRPLRQASKISMLITAIGVSFFLENLFNVLFGGSSRFFSAPDFFNQTRAFGSVII

TNVAWIVPLITVLLLLAILWLLYRTRYGMAIRAVAFDVNTVRLMGIDANRIISLVFALGSSLAALGGVFY

SISYPTIDPLMGVLIGLKAFAAAVLGGIGSVTGAVLGGFILGFTEVVAVAIFPELGGYKDAFAFLFLILV

LLFRPVGIMGDERLERSRF

>lcl|NZ\_FO834906.1\_prot\_WP\_004147267.1\_1279 [locus\_tag=BN49\_RS07780] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004147267.1] [location=complement(1317365..1318471)] [gbkey=CDS]

MATLVAALVGASSAQAAEIKIGVVLPLSGALSGYGQPSQKGLDIIQAITPTLKNGDTIKLIVIDDKSDKV

EAANAMQRLVSSDKVDAVIGEVTSSNTLAMTKIADDSKTPLVSSTATNDRVTRNHPYVSRVCFSDSFQGV

VGANLASRDLKAKTAAIVFDSSNDYSVGLAKAFRTQFLKNGGTIPIEVQAPGGSKDFKAQLASVKAKNVD

MIYMPIYYTEGALIAVQSKQLGLNKPVVGGDGLAADQVFFDVGKDAVNGYMTTDYYSPNAKEQTPAGETF

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VINEVKDGKLAFRTVVNP

>lcl|NZ\_FO834906.1\_prot\_WP\_004144596.1\_1280 [locus\_tag=BN49\_RS30890] [protein=hypothetical protein] [protein\_id=WP\_004144596.1] [location=1318464..1318607] [gbkey=CDS]

MAIKDAFPENDFIGISPSVDYLSLTINDCITLRNNAPAYPANYWLLC

>lcl|NZ\_FO834906.1\_prot\_WP\_016532555.1\_1281 [gene=eutC] [locus\_tag=BN49\_RS07790] [protein=ethanolamine ammonia-lyase subunit EutC] [protein\_id=WP\_016532555.1] [location=complement(1319047..1319823)] [gbkey=CDS]

MNRPDAWNPLREFTDARIALGRSGASLPTREVLNFGLAHARARDAIHQPFASQQLVAPLAALGLEALTVH

SAAPDRHTYLRRPDLGRQLADESRADLAASGVRPADLLLVIGDGLSSWAVERQAVPLIRALLPYLRTLGI

GLAPVVLAHQSRVALGDDIGETLKARAVAILIGERPGLSSPDSLGVYLTWQPHRQRLESERNCISNIRPE

GLSHDAAAFKLAWLLEQAFWRRLTGVGLKDESDNPALHGKIKPLPPLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177286.1\_1282 [locus\_tag=BN49\_RS07795] [protein=ethanolamine ammonia-lyase subunit EutB] [protein\_id=WP\_004177286.1] [location=complement(1319820..1321208)] [gbkey=CDS]

MYKTTLSGQVWRFDSLKTLMAKASPARSGDALAGIIATSAEERMAAKMALAEVPLTDILDNPLIPYEQDE

VTRLILDTHDAQGFAALRHLTVGDFRDWLLDDATDTATLQRVARAITPEMAAAVSKLMRNQDLILAASKC

QVVTRFRNTIGLPGHLSVRLQPNHPTDDLKGIAASMLDGLLYGAGDAVIGINPASDSLPVLAQLNIMLDD

IIQRFAIPTQSCILTHVTNTLQLIERGAPVDLVFQSVAGTEAANSGFGINLAMLQEAREAALSLRRGTLG

NNVMYFETGQGSCLSANAHHGVDQQTCEARAYAVARHFEPLLVNTVVGFIGPEYLYDGKQIIRAGLEDHF

CGKLMGLPIGCDVCYTNHAEADQDDMDTLLTLLCAAGLTFLIGVPGADDIMLNYQSTSFHDALYARRLLG

LKHAPEFADWLAKMQIIDPHGALRLTDARHPLLSVLPQGASV

>lcl|NZ\_FO834906.1\_prot\_WP\_004177284.1\_1283 [gene=eat] [locus\_tag=BN49\_RS07800] [protein=ethanolamine permease] [protein\_id=WP\_004177284.1] [location=complement(1321218..1322597)] [gbkey=CDS]

MTEHTTTLKRTLGSFRLWGIAVGLVISGEYFGWSYGWSQAGTMGFMVVALAVAAMYCAFIFSFTELTTAI

PHAGGPFAYAYRAFGPTGGFIAGFATLIEFVFAPPAIAMAIGAYLNVQFPALDPKWVACGAYVIFMTLNI

LGVGIAATFELIVTLLAIFELLVFMGVVAPGFSWSHFTTNGWAGADSFSGLALPGMFAAIPFAIWFFLAI

EGASMAAEEAKDPQRTIPRALGGGILTLTVLAIGVMVFAGGVGDWRALSNINDPLPQAMKTVVGNGSGWL

HMLVWLGLFGLVASFHGIIMGYSRQIYSLARAGYLPAGLASLNRRTRTPHLAILAGGVVGIAAIFSDSLI

TISGMPLTACIVTMSVFGAIVMYITSMAALFKLRRSEPKLIRPFRAPLYPLAPAFALGMAVLCLVAMVWY

NLLLALIFAAMMLGGYLWFRKTAAARERAPVDPQLRTVS

>lcl|NZ\_FO834906.1\_prot\_WP\_072143245.1\_1284 [locus\_tag=BN49\_RS30895] [protein=hypothetical protein] [protein\_id=WP\_072143245.1] [location=1322660..1322788] [gbkey=CDS]

MSAAIRRQSVARPLALRKNGAGCTLSARTLVQRLCFFSGGTV

>lcl|NZ\_FO834906.1\_prot\_WP\_046042715.1\_1285 [gene=mmuP] [locus\_tag=BN49\_RS07810] [protein=S-methylmethionine permease] [protein\_id=WP\_046042715.1] [location=1322871..1324280] [gbkey=CDS]

MQSTTQQQGGQLKRTMKTRHLIMLSLGGVIGTGLFFNTGYIISTTGAAGTLLAYLIGALVVWLVMQCLGE

LSVAMPETGAFHVYAARYLGPATGYTVAWLYWLTWTVALGSSFTAAGFCMQYWFPQVPVWIWCVVFCAVI

FGLNIISTRFFAEGEFWFSLVKVITIVAFIILGGAAIFGIIPMQDGSPAPGLRNITAEGWFPHGGLPILM

TMVAVNFAFSGTELIGIAAGETEKPHKVIPVAIRTTIARLIIFFIGTVFVLAALIPMQQAGVEKSPFVLV

FEKVGIPYAADMFNFVILTAILSAANSGLYASGRMLWSLSNEKTLPACFAKVNKRGVPVTALSVSMLGGV

LALFSSVVAPDTVFVALSAISGFAVVAVWLSICASHFMFRRRHLQQGKALSDLQYRAPWYPVVPVLGFVL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004144601.1\_1286 [gene=mmuM] [locus\_tag=BN49\_RS07815] [protein=homocysteine S-methyltransferase] [protein\_id=WP\_004144601.1] [location=1324267..1325199] [gbkey=CDS]

MSQTNPFTALLAAQPFVLLDGAMATELEARGCDLADSLWSAKVLLENPQLIRDVHLDYFRAGAQVAITAS

YQATPAGFAARGLDEAQSRALIGKSVELARKAREAYLAENPQAGTLLVAGSVGPYGAFLADGSEYRGDYQ

RSAAEFQAFHRPRVEALLDAGADLLACETLPSFAEIQALAALLQEYPRARAWYSFTLRDAEHLSDGTPLR

EVMAALADNPQVVAVGINCIALENTPAALAHLHSLTALPLVVYPNSGEHYDAVSKTWHHHGEACASLADY

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>lcl|NZ\_FO834906.1\_prot\_WP\_002890192.1\_1287 [gene=tauA] [locus\_tag=BN49\_RS07820] [protein=taurine ABC transporter substrate-binding protein] [protein\_id=WP\_002890192.1] [location=1325439..1326401] [gbkey=CDS]

MAFTSRITLLAALAVAAFQAQAVNVTVAYQTSAEPAKVAQADNTFAKTSGATVDWRKFDSGASVVRALAS

GDVQIGNIGSSPLAVAASQQVPIEVFLLASKLGNSEALVVKKSITKPEDLIGKRIAVPFISTTHYSLLSA

LKHWGIKPGQVQIINLQPPAIIAAWQRGDIDGAYVWAPAVNELEKEGKVLTDSSQVGEWGAPTLDVWVVR

KDFAEQHPEIVKAFAKSAIDAQQPYIANPEAWLKQPDNISKLARLSGVPEADVPGLVKGNTYLTAAEQAQ

ALNGPVNQAIVDTARFLKEQGKVPAAGTDYRQYVTDRFVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530986.1\_1288 [gene=tauB] [locus\_tag=BN49\_RS07825] [protein=taurine ABC transporter ATP-binding subunit] [protein\_id=WP\_016530986.1] [location=1326413..1327180] [gbkey=CDS]

MLQISHLSADYGGKPALADINLTLESGELLVVLGPSGCGKTTLLNLIAGFVPYQHGSITLEGQRVTGPGA

ERGVVFQNEGLLPWRNVQDNVALGLQLAGVDKAQRRQAAAQMLKTVGLEGAEKRFIWQLSGGQRQRVGIA

RALAANPQLLLLDEPFGALDAFTREQMQTLLLKLWHETGKQVLLITHDIEEAIFMATELVLLSPGPGRVV

ERLPLDFSRRFVAGESCRSIKSDPRFIEQREYILSRVFDQREAFS

>lcl|NZ\_FO834906.1\_prot\_WP\_004144603.1\_1289 [gene=tauC] [locus\_tag=BN49\_RS07830] [protein=taurine ABC transporter permease TauC] [protein\_id=WP\_004144603.1] [location=1327177..1328004] [gbkey=CDS]

MSVVLNDKPRQSTLKWRWPLSRQLTLSVATLAVLLAVWWAVAALQLISPLFLPPPGQVLQKLITIAGPQG

FMDATLWQHLAASLTRIVIALLAAVLIGVPVGIAMGLNSTVRGILDPLIELYRPVPPLAYLPLMVIWFGI

GETSKILLIYLAIFAPVAMSALAGVKSAQQVRIRAARSLGASRAQVLWLVILPGALPEILTGLRIGLGVG

WSTLVAAELIAATRGLGFMVQSAGEFLATDVVLAGIAVIAIIAFLLELGLRALQRRLTPWHGEVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004147277.1\_1290 [gene=tauD] [locus\_tag=BN49\_RS07835] [protein=taurine dioxygenase] [protein\_id=WP\_004147277.1] [location=1328001..1328852] [gbkey=CDS]

MSERLSITPLGPYIGAQVSGADLTRPLSDNQFEQLYHAVLRHQVVFLREQNITPAQQRDLALRFGDLHIH

PVYPHAPGVEEIIVLDTHNDNPPDNDNWHTDVTFIDTPPAGAILAAKELPTTGGDTLWTSGIAAWEALSE

PFRQLLSGLHAEHDFRKSFQEYKYNKTEAEHRRWQEAVAKHPPLLHPVVRTHPVTGKQALFVNEGFTTRI

VEVSEKESAALLNFLFAHVTKPEFQVRWRWQPNDVAIWDNRVTQHYANADYLPQRRIMHRATILGDKPYY

RAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004183143.1\_1291 [locus\_tag=BN49\_RS07840] [protein=lysophospholipid acyltransferase family protein] [protein\_id=WP\_004183143.1] [location=complement(1329015..1330733)] [gbkey=CDS]

MFSLDNVLDDLWPQARPAPWQKKLLKKLFYEEEFQQFADRHRHLKGLDTVEQVLEYLNIRCAIPAHDLEQ

IPEYGPLVIIANHPTGTLDGLALLYAVSRVRRDVKVVTNRMLTHLEPLSSLFIPVDNIHGRTAKAALQQM

DQQLQAGGVLIFFPAGEVSRLTRRGIRDKKWHSGFIKLAAKYRAPLLPAWINARNSALFYASTLISDNLP

LLLLMQQMFRRRNSSLPVRIGQQIPWSNWFDAQSSARELTGRCYQHLEQLRKGLPGRFKTESAIARPEDR

ALLKRELHKAECLGRTADGKAIYLWQRNGQEDAPLLRELGRLREIAFRAVGEGSGKRRDIDGYDDDYLHL

ILWDEEDLEIVGAYRFMPTAIQLAKRGLEGIYSYSLFHYDGRMDDVLQHGIELGRSFIQPRYWGRRGLDY

LWSGIGAYLARYPHYRYLFGPVSISGGLPPAARDLLVAFYRMWFPATHPLAESRRPYPASLPDVLAQFGG

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YIGAHLGAQKSA

>lcl|NZ\_FO834906.1\_prot\_WP\_002890201.1\_1292 [gene=hemB] [locus\_tag=BN49\_RS07845] [protein=porphobilinogen synthase] [protein\_id=WP\_002890201.1] [location=complement(1331187..1332161)] [gbkey=CDS]

MTDLITRPRRLRQSAALRALFEETTLSLNDLVLPIFVEEEIDDYKAIEAMPGVMRIPEKYLAREIERIAN

AGIRSVMTFGISHHTDATGSDTWNENGLVARMSRICKSTVPEMIVMSDTCFCEYTSHGHCGVLCDHGVDN

DATLENLGKQAVVAAAAGADFIAPSAAMDGQVQAIRRSLDAAGFTNTAIMSYSTKFASSFYGPFREAAGT

ALKGDRKTYQMSPMNRREAIRESLLDEAQGADCLMVKPAGAYLDILRDIRERSDLPLGAYQVSGEYAMIK

FAAQAGAIDEEKVVLESLGAIKRAGADLIFSYFALDLAEKKILR

>lcl|NZ\_FO834906.1\_prot\_WP\_004178722.1\_1293 [gene=ampH] [locus\_tag=BN49\_RS07850] [protein=D-alanyl-D-alanine-carboxypeptidase/endopeptidase AmpH] [protein\_id=WP\_004178722.1] [location=complement(1332268..1333428)] [gbkey=CDS]

MKRSLLIFAALCAASWTSVQAAQPTVDPVFASDVVDRYANHIYYGSGATGMALVVIDGNQRVFRSFGETR

PGNNQHPQLDSVIRIASLSKLMTSEMLVKLLDQGVVKLNDPLSKYAPPGARVPDWQGKPITLVNLATHTS

ALPREQPGGAAHRPVFVWPTRQQRWNWLSTATLKTAPGSQAAYSNLAFDLLADALSTAAGKPYPQLFEEQ

ITRPLGMKDTTFTPSPDQCQRLMIPEKGASPCNNTLAAIGSGGVYSTPGDMMRWMQQFLSSDFYTRSQQA

DRMQTLIYQRNQLTRVIGMDVPGRADALGLGWVYMKPKNGHPGIIQKTGGGGGFITYMAMNPQANVGAFV

VVTRSPLTRFNNMSDGINDLVSELSGAQPNMQTASQ

>lcl|NZ\_FO834906.1\_prot\_WP\_072145332.1\_1294 [locus\_tag=BN49\_RS07855] [protein=isochorismatase family protein] [protein\_id=WP\_072145332.1] [location=1333647..1334159] [gbkey=CDS]

MVVDMQNGVFATPRLARERCVAQINRLVRAADRVIFIQHDEAGGLEAGSEGFALLPELEQPAGALYVTKT

ACDAFYHTSLAQVLDEHDIQQFVICGCATDYCLDTTIKNGASRGYGIVIAEDAHTTADRPAAQAATLIAH

YNEVWRTLTIPGNPLQVKPTETILHAWQQN

>lcl|NZ\_FO834906.1\_prot\_WP\_016531799.1\_1295 [gene=sbmA] [locus\_tag=BN49\_RS07860] [protein=peptide antibiotic transporter SbmA] [protein\_id=WP\_016531799.1] [location=1334277..1335497] [gbkey=CDS]

MFKSFFPKPGPFFISAFIWSMLAVIFWLAGGGDWLLRVTGASQNVAISAARFWSLNYLVFYAYYLFCVGV

FALFWFVYCPHRWQYWSILGTSLIIFVTWFLVEVGVAINAWYAPFYDLIQSALATPHKVSINQFYQEIGV

FLGIAIIAVIIGVMNNFFVSHYVFRWRTAMNEHYMAHWQHLRHIEGAAQRVQEDTMRFASTLEDMGVSFI

NAVMTLIAFLPVLVTLSEHVPDLPIVGHLPYGLVIAAIVWSLMGTGLLAVVGIKLPGLEFKNQRVEAAYR

KELVYGEDDETRATPPTVRELFRAVRRNYFRLYFHYMYFNIARILYLQVDNVFGLFLLFPSIVAGTITLG

LMTQITNVFGQVRGSFQYLISSWTTLVELMSIYKRLRSFERELDGKPLQEAIPTLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004183146.1\_1296 [locus\_tag=BN49\_RS07865] [protein=DUF1615 domain-containing protein] [protein\_id=WP\_004183146.1] [location=1335516..1336622] [gbkey=CDS]

MAARLSRIIPVSLTLLAAMALSACTSQQAPALKEGEKPVDVASVVRQKMPASVKDREAWAQAIATAFDSQ

KLAPTEENVCSVLAVAQQESNYQSDPVVPGLNKIAWQEIDRRAEKMHIPPFLVHTALKITSPNGKSYSDR

LDNVKTEKQLSAIFDDFIGMVPMGQKLFGSLNPVHTGGPMQVSIAFAEQHTSGYPWKMNGTVRQEVFSLR

GGLWFGTYHLLNYPASYSAPLYRFADFNAGWYASRNAAFQNAVVKASGVKLALDGDLIRYDSEEPGSTEL

AVRRLASQLGMSDSEIHRQLKKGDSLAFEKTDLYQQVFRLAEKKAGKTLPREMLPGIQLESPKITRNLTT

AWFAKRVDERRANCMARR

>lcl|NZ\_FO834906.1\_prot\_WP\_002890210.1\_1297 [locus\_tag=BN49\_RS07870] [protein=YaiY family protein] [protein\_id=WP\_002890210.1] [location=complement(1336619..1336921)] [gbkey=CDS]

MAEFSFSKSLLGNKKRGALTGSHVAYGLFVLICCWAGAQMLSMLIHAPGVFERLMQAQDASRPQVDISLA

VGTLFGLIPFLIGCTFIGVLALIVRWRQRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002890215.1\_1298 [locus\_tag=BN49\_RS07875] [protein=DUF2754 family protein] [protein\_id=WP\_002890215.1] [location=1337174..1337377] [gbkey=CDS]

MKLTDKIRRDWHYYAVALGLIFILNGVVGLLGFETQGWQSYAVGLITWVISFWIAGFVIRRRPAEEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151348.1\_1299 [gene=ddlA] [locus\_tag=BN49\_RS07880] [protein=D-alanine--D-alanine ligase] [protein\_id=WP\_004151348.1] [location=complement(1337410..1338507)] [gbkey=CDS]

MAKMRVGIVFGGKSAEHEVSLQSAKNIVEAIDKSRFDVVLLGIDKQGLWHINDAGNYLLNAQDPARIALR

PSTVTLAQIPGREAQQLINAESGQPLAAIDVIFPIVHGTLGEDGSLQGMLRMANLPFVGSDVLGSAACMD

KDVTKRLLRDAGLAVAPFITLTRANRAQFSFADVEAKLGLPLFVKPANQGSSVGVSKVKNEEQYHQAVAL

AFEFDHKVVVEQGIKGREIECAVLGNDHPQASTCGEIVLNSEFYAYDTKYIDDQGAQVVVPAAIAPEIND

KIRAIAVQAYQTLGCSGMARVDVFLTADNEVVINEINTLPGFTNISMYPKLWQASGLDYTSLITRLIELA

LERHAADRALKTSMN

>lcl|NZ\_FO834906.1\_prot\_WP\_042942438.1\_1300 [locus\_tag=BN49\_RS07885] [protein=extensin family protein] [protein\_id=WP\_042942438.1] [location=1338607..1339290] [gbkey=CDS]

MRGKTLLVLAGLLGAGLLGYRNLPPHLNPLAPLALDDPPGWLTSFKLRRLTADQCASLLAEANRRRLTAS

RPVADSEGSCPLRNVVRVANFGSVQLSSSFLASCPLALSSALYIEQQAKPLTRQLMASDLRQIDHLGSFA

CRNIYHRQQARRSEHATADALDVSGIRLADGRRVSVLQGWRSETSRPWLAALLSSSCHYFGNALGPEYNA

AHANHFHFGMRGQGFCF

>lcl|NZ\_FO834906.1\_prot\_WP\_002890219.1\_1301 [locus\_tag=BN49\_RS07890] [protein=multidrug efflux MFS transporter] [protein\_id=WP\_002890219.1] [location=1339460..1340659] [gbkey=CDS]

MESWKVNLISVWFGCFFTGLAISQILPFLPLYVSQLGVTSHEALSMWSGLTFSVTFLVSAIVSPMWGSLA

DRKGRKLMLLRASLGMAIAILLQAFATNVWQLFILRAIMGLTSGYIPNAMALVASQVPRERSGWALSTLS

TAQISGVIGGPLLGGFLADHVGLRMVFFITAILLTISFLVTLFLIKEGVRPQVSKSERLTGKQVFASLPY

PGLVISLFFTTLVIQLCNGSIGPILALFIKSMAPDSNNIAFLAGMIAAVPGVSALISAPRLGKLGDRIGT

SRILLATLCCAVVMFFAMSFVTTPLQLGTLRFLLGFADGAMLPAVQTLLLKYSSDSVTGRIFGYNQSFMY

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>lcl|NZ\_FO834906.1\_prot\_WP\_002890221.1\_1302 [gene=iraP] [locus\_tag=BN49\_RS07895] [protein=anti-adapter protein IraP] [protein\_id=WP\_002890221.1] [location=1340959..1341219] [gbkey=CDS]

MKNLIAELLVKLAQKEEEAKELTVQVEALEIVVTALLRHMEHDAQQALIQDIEQAIDQVTPCPPVNDHDA

MLLQQYLKKLLRHPRS

>lcl|NZ\_FO834906.1\_prot\_WP\_004232385.1\_1303 [gene=phoA] [locus\_tag=BN49\_RS07900] [protein=alkaline phosphatase] [protein\_id=WP\_004232385.1] [location=1341309..1342739] [gbkey=CDS]

MEMTKVKLSALFIALIPLLGSPVIHAETTAAPVLENRAAQGDITTPGGARRLTGDQTEALRASLINKPAK

NVILLIGDGMGDSEITAARNYAEGAGGFFKGIDALPLTGQYTHYSLDKKTGKPDYVTDSAASATAWTTGV

KTYNGALGVDIHENAHQTILELAKAAGLATGNVSTAELQDATPAALVAHVTSRKCYGPTVTSEKCPSNAL

EKGGKGSITEQLLNARPDVTLGGGAKTFAETATAGEWQGKTLREQAQARGYQIVTDAASLAAATEASQDK

PLLGLFADGNMPVRWEGPKASYHGNIDKPPVTCTPNPKRDASVPTLAQMTEKAIDLLSRNEKGFFLQVEG

ASIDKQDHAANPCGQIGETVDLDEAVQKALEFARKDGNTLVIVTADHAHASQIIPADSKAPGLTQALNTH

DGAVMVMSYGNSEEESMEHTGTQLRIAAYGPHAANVVGLTDQTDLFTTMKAALSLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002890225.1\_1304 [locus\_tag=BN49\_RS07905] [protein=PsiF family protein] [protein\_id=WP\_002890225.1] [location=1342831..1343148] [gbkey=CDS]

MKITLLMTLLFGLIFISAVGAAEKTPTPQQQRMTDCNQQASAKMLKGEERKTFMSQCLKKETTTSQGKAL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002890227.1\_1305 [gene=proC] [locus\_tag=BN49\_RS07910] [protein=pyrroline-5-carboxylate reductase] [protein\_id=WP\_002890227.1] [location=complement(1343216..1344025)] [gbkey=CDS]

MDKKIGFIGCGNMGKAILGGLIASGQVQPGQIWVYTPSPDKVAALRDQYGINAASSAQEVAQIADIVFGA

VKPGIMTKVLGDIASSLNKESLVVSIAAGVTLEQLARALGHDRKIIRAMPNTPSLVNAGMTSVTPNALVS

SEDVAEVLTIFRCFGQAEQIAEPMIHPVVGVSGSAPAYVFMFIEAMADAAVLGGMPRAQAYKFAAQAVMG

SAKMVLESGEHPGALKDMVCSPGGTTIEAVRVLEEKGFRSAVIEAITQCMEKSEKLSRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002890230.1\_1306 [locus\_tag=BN49\_RS07915] [protein=YaiI/YqxD family protein] [protein\_id=WP\_002890230.1] [location=1344142..1344600] [gbkey=CDS]

MAIWVDADACPNVIKEILFRAAERTQTPLTLVANQPLRVPPSRFIRTLRVEQGFDVADNEIVRQCAAGDL

VITADIPLAAEVLAKGGAALNPRGERYSEATIRERLTMRDFMETLRASGVQTGGPDSLSQRDRQQFAAEL

EKWLLAVKRRQG

>lcl|NZ\_FO834906.1\_prot\_WP\_016531801.1\_1307 [locus\_tag=BN49\_RS07920] [protein=DUF2076 domain-containing protein] [protein\_id=WP\_016531801.1] [location=complement(1344597..1345292)] [gbkey=CDS]

MQSEEQRLIDGLFSRLKEAEAHSASRDASAEERIAQHVSAQPAAPYYMAQTILIQEAAIKQLNDRIQALE

SQVSQLQAAKPSSGGFLSGLFGGGGSSRGSDPIPGAEQYGRPQASAQPQYTPPPQQNYAPQAAARGGGFM

AGALQTAAGVAGGVVLGNMLTNMFSGSHPQEIVNIIEEKPQPDAASAQDTTAGDDPFRQGDDQFLADNTW

NDDFDAGFGDDDFGSDDDSWV

>lcl|NZ\_FO834906.1\_prot\_WP\_002890276.1\_1308 [gene=aroL] [locus\_tag=BN49\_RS07925] [protein=shikimate kinase AroL] [protein\_id=WP\_002890276.1] [location=1345621..1346154] [gbkey=CDS]

MTQPIFLIGPRGCGKTTVGHALARARHFQFSDTDHRLQAHEQRTVAEIVQAEGWARFRELETLSLKAVTL

PNTVIATGGGIVLAEGNRQFMRENGVVIYLQASVSALIDRLEAYPKAEQRPTLTGKPVREEVGEVLAQRE

ALYRDAAHHIVDATASPDRVVEQIMSMLCSATATPVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002890278.1\_1309 [locus\_tag=BN49\_RS07930] [protein=YaiA family protein] [protein\_id=WP\_002890278.1] [location=1346226..1346417] [gbkey=CDS]

MPNRPPYPREARVVAVEKGPQGQTVTWYQLRADYPEPDSLISEHPTEQEAVDAKRRYEDPDKS

>lcl|NZ\_FO834906.1\_prot\_WP\_004144619.1\_1310 [locus\_tag=BN49\_RS07935] [protein=AroM family protein] [protein\_id=WP\_004144619.1] [location=1346668..1347348] [gbkey=CDS]

MSSATMAILTIGVVPLAGVLPLLTEHIREEQIAHISLLGEMTPDEVMAEYAVGDGEKGLLTLLSNNQLVM

VSRQKIERDVRSAIAMLDRQHYDVILLLSSEQLTGFTTHHAILLEPQRIIPPLVASIVDGHQVGVIVPVE

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LLSNVLVSRLAAELLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002890284.1\_1311 [gene=ppnP] [locus\_tag=BN49\_RS07940] [protein=pyrimidine/purine nucleoside phosphorylase] [protein\_id=WP\_002890284.1] [location=1347426..1347710] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_002890285.1\_1312 [gene=rdgC] [locus\_tag=BN49\_RS07945] [protein=recombination-associated protein RdgC] [protein\_id=WP\_002890285.1] [location=complement(1347782..1348693)] [gbkey=CDS]

MLWFKNLMVYRLSRDIELRAEEMEKQLAELTFTPCGSQDMAKTGWVSPMGSHSDALTHTANGQIIICARK

EEKILPSPVIKQALEAKIQKLEADQGRKLKKTEKDSLKDEVLHSLLPRAFSRFSQTMMWIDTVNGLIMVD

CASAKKAEDTLALLRKTLGSLPVVPLTLENPIELTLTEWVRSGTVAQGFQLLDEAELKAMLEDGGVIRAK

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>lcl|NZ\_FO834906.1\_prot\_WP\_025861888.1\_1313 [gene=mak] [locus\_tag=BN49\_RS07950] [protein=fructokinase] [protein\_id=WP\_025861888.1] [location=1348785..1349699] [gbkey=CDS]

MRIGIDLGGTKTEVIALSDQGEQLFRHRLPTPREDYRQTIETIATLVAMAEQATGQQGTVGMGIPGSISP

YTGVVKNANSTWLNGQPFDKDLSLRLEREVRLANDANCLAVSEAVDGAAAGAQTVFAVIIGTGCGAGVAL

NGRAHIGGNGNAGEWGHNPLPWMNDDELRYRAEVPCYCGKQGCIETFISGTGFATDYQRLSGRGLTGSEI

MRLVGEGDEKAELALSRYEQRLAKSLAHVVNILDPDVIVLGGGMSNVERLYQTVPDLVKQWVFGGECETP

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042726.1\_1314 [gene=sbcC] [locus\_tag=BN49\_RS07955] [protein=exonuclease subunit SbcC] [protein\_id=WP\_046042726.1] [location=complement(1349773..1352910)] [gbkey=CDS]

MKILSLRLKNLNSLKGEWKIDFTAEPFASNGLFAITGATGAGKTTLLDAICLALYHETPRLNKVSQSQND

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VLLTEAQQQALQESLQVLTDEEKALLAQQQSQQQQLQWLTRRDELAQQQQQAATRQQQARQALADAAPAL

AKLELAQPAAQLRPLWERQQEQTAGLAQTRQRISEVNARLLASTALRARIRQGALRAQQQRQAELADLAQ

WLAAHERFRLWGQEIAGWRAQFSQLTRDKQQLTAQSTRLAALRQKLATLPASPLTLSADDVAAAIEQQTQ

SRPLRQRLLSLHEQHQLLRKRLRQNAESVQQAQAEQVKLNATLTLRREQYKDKNQHYLDLKALCQREETI

KDLESYRDRLEAGKPCPLCGACEHPAIEQYASLTLTDNQRRRDALEKEVAALKEEGLLILGQVKALTQQL

QRDTEAAGRLAEEEQALTKAWQETCASLHITRDIAQEINDWMQEQERYEQQLYQLSQRLMLQSQLNDQQA

LERQAEQQLAATRQGLESALQALALSLPAEGTEAAWLHARESEFAQWQAQQTRHDAIQQQIAALRPLLET

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AALLDDETAQRLTQLKQTLEQQLQQAAALCEQATRQHEAHLALRPQGVDADVPTLQTQLHALAQRLRDNT

TRQGEIRQQLRQDAESRQQQQALGQQIAEAAQLADDWGYLNSLIGSSTGDRFRKFAQGLTLDNLVWLANQ

QLNRLHGRYLLQRKASEALELEVVDTWQADAVRDTRTLSGGESFLVSLALALALSDLVSHKTRIDSLFLD

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042727.1\_1315 [gene=sbcD] [locus\_tag=BN49\_RS07960] [protein=exonuclease subunit SbcD] [protein\_id=WP\_046042727.1] [location=complement(1352907..1354112)] [gbkey=CDS]

MRLLHTSDWHLGQNFYSKSRAAEHDAFLTWLLDRAQEHEVDAIIVAGDIFDTGSPPSYARELYNRFVVQL

QQTGCRLVVLAGNHDSVAMLNESRDILAFLHTTVVANAGYAPIELPLRDGTPGAIFCPVPFLRPRELVTS

QAGHSGREKQQQLLHAISDYYQEQYQQACALRGDRPLPIIASGHLTTVGASKSDAVRDIYIGTLDAFPAQ

HFPPADYIALGHIHRAQMVGGCEHIRYSGSPLPLSFDETGKAKSVHLVSFSEGRLSAVETLEVPVTQPLA

VIKGDLATITAQLEQWRGVEQDPPVWLDIEITTEDYLHDIQRHIQALTEDLPVEVLLVRRSREQREKILL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002890343.1\_1316 [gene=phoB] [locus\_tag=BN49\_RS07965] [protein=phosphate response regulator transcription factor PhoB] [protein\_id=WP\_002890343.1] [location=1354295..1354984] [gbkey=CDS]

MARRILVVEDEAPIREMVCFVLEQNGFQPVEAEDYDSAVNQLNEPWPDLILLDWMLPGGSGLQFIKLLKR

EAMTRDIPVVMLTARGEEEDRVRGLETGADDYITKPFSPKELVARIKAVMRRISPMAVEEVIEMQGLSLD

PSSHRVMTGDSPLDMGPTEFKLLHFFMTHPERVYSREQLLNHVWGTNVYVEDRTVDVHIRRLRKALEHSG

HDRMVQTVRGTGYRFSARF

>lcl|NZ\_FO834906.1\_prot\_WP\_002890344.1\_1317 [gene=phoR] [locus\_tag=BN49\_RS07970] [protein=phosphate regulon sensor histidine kinase PhoR] [protein\_id=WP\_002890344.1] [location=1355006..1356301] [gbkey=CDS]

MLERLSWKRLALELFLACIPALILGAFVGHLPWFLLAAVTGLLIWHFWNLMRLSWWLWVDRSMTPPPGRG

SWEPLLYGLHQMQMRNKKRRRELGSLIKRFRSGAESLPDAVVLTTEEGAIFWCNGLAQQILNLRWPDDSG

QNILNLLRYPEFANYLKQRDFSKPLNLVLNNARHLEIRVMPYSDKQWLMVARDVTQMHQLEGARRNFFAN

VSHELRTPLTVLQGYLEMMQEQVLEGATREKALHTMREQTQRMEGLVKQLLTLSRIEAAPALAMNDRIDV

PMMLRVVEREAQTLSQEKQTLIFTVDEQLKVLGNEEQLRSAISNLVYNAVNHTPPGTEIRVSWQRTPQGA

LFSVEDNGPGIAPEHIPRLTERFYRVDKARSRQTGGSGLGLAIVKHAVNHHDSRLEIDSTVGKGTRFSFL

LPERLIAKNDA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144627.1\_1318 [gene=brnQ] [locus\_tag=BN49\_RS07975] [protein=branched-chain amino acid transporter carrier protein BrnQ] [protein\_id=WP\_004144627.1] [location=1356715..1358034] [gbkey=CDS]

MTHQLKSRDIIALGFMTFALFVGAGNIIFPPMVGLQAGEHVWTAAIGFLITAVGLPVLTVVALAKVGGGV

ESLSTPIGKVAGILLAVVCYLAVGPLFATPRTATVSFEVGIAPLTGDGPLPLLIYSVIYFALVILVSLYP

GKLLDTVGNFLAPLKIIALIVLAVAAIIWPAGPISDALEAYRTAPFSNGFVNGYLTMDTLGAMVFGIVIV

NAARSRGVSEARLLTRYTVWAGLMAGVGLTLLYLALFRLGSDSATLVDQSANGAAILHAYVQHTFGGAGS

FLLAALIFIACLVTAVGLTCACAEFFAQYLPFSYRTLVFVLGLFSMAVSNLGLSHLIQVSIPVLTAIYPP

CIALVVLSFTRSWWHNSSRVIAPAMFISLMFGIIDGIKSSAFAAILPDWTARLPLAEQGLAWLMPTAVMT

ILAVIWDRAAGRQVTSSAH

>lcl|NZ\_FO834906.1\_prot\_WP\_002890348.1\_1319 [gene=proY] [locus\_tag=BN49\_RS07980] [protein=proline-specific permease ProY] [protein\_id=WP\_002890348.1] [location=1358121..1359494] [gbkey=CDS]

MESSNKLKRGLSTRHIRFMALGSAIGTGLFYGSADAIKMAGPSVLLAYIIGGVAAYIIMRALGEMSVHNP

AASSFSRYAQENLGGLAGYITGWTYCFEILIVAIADVTAFGIYMGVWFPTVPHWIWVLSVVLIICAVNLM

SVKVFGELEFWFSFFKVATIIIMILAGFGIIIWGIGNGGQPTGIHNLWSNGGFFSNGWLGMVMSLQMVMF

AYGGIEIIGITAGEAKDPEKSIPRAINSVPMRILVFYVGTLFVIMSIYPWNQVGTDGSPFVLTFQHLGIT

FAASILNFVVLTASLSAINSDVFGVGRMLHGMAEQGSAPKVFAKTSRRGIPWVTVMVMTIALLFAVYLNY

IMPENVFLVIASLATFATVWVWIMILLSQIAFRRRLSPEEVKALKFKVPGGVVTTVIGLLFLAFIIALIG

YHPDTRISLYVGMAWIALLLLGWVFKTRRERRLAQAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004147293.1\_1320 [gene=malZ] [locus\_tag=BN49\_RS07985] [protein=maltodextrin glucosidase] [protein\_id=WP\_004147293.1] [location=1359646..1361463] [gbkey=CDS]

MLKAWHLPVAPFIKVQQDRLFITLWLSGESLPQRITLRAEEDNEELSLPMQRLRQAPQPGVVAWRGEISL

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ADQDAVYYHHAAGREIVRKAWDDPLTGEAGGSTFYGGDLDGISEKLPYLKQLGVTALYLNPVFAAPSVHK

YDTEDYRRVDPQFGGDAALLRLRHNTQRAGMRMILDGVFNHTGDSHPWFDRHQQGSGGAGHDPDSPWRDW

FTFSEEGQAHNWLGYASLPKLDYRSTSLVNEIYAGEDSIVRHWLKAPWSMDGWRLDVVHMLGEGGGARNN

LQHIAGITQAAKQAQPEAFVFGEHFGDARQWLQADAEDAAMNYRGFTFPIWGFLANTDISYDPQKIDAQT

CMAWMDNYRAGLSHQQQLRMFNQLDSHDTARFKSLLGKDVARLPLAVVWLFSWPGVPCIYYGDEVGVDGN

NDPFCRKPFPWDPALQDTQLLALYQRMAKLRKAHQALRYGGCQVIYAEDNVVVFVRVYKQQRVLVAINRG

EACEVVIEDSPLLNVAGWTLQEGAGAFQDGVLTLPAISANVWSGR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529703.1\_1321 [locus\_tag=BN49\_RS07990] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_016529703.1] [location=complement(1361460..1362338)] [gbkey=CDS]

MILDALDRHGSFATAAESLYKTPAALSYMIQKLESDLNIVLLDRSGHRAKFTDTGRLMLEKGRQLLSAAR

DLEKQAQQLSAGWERELAIALDASFPFSALLPLIAEFYAQNPQTRLNFSHHTLAGSWEELTHHGADIILG

AINEPPTSAEWSWQTLGALDNIFVVAPHHPLAQAKEPLANKQLSQHRAIVIRDSARYCHPLNSNLLDEQP

QIGVDDFASKVELLCAGLGCGFLPRHIARPWLVKGSLVEKSVACWREKDITYMAWRSGNDGLAQRWWREA

LLRGDLLSQLYH

>lcl|NZ\_FO834906.1\_prot\_WP\_002890357.1\_1322 [locus\_tag=BN49\_RS07995] [protein=hydrolase] [protein\_id=WP\_002890357.1] [location=1362629..1363270] [gbkey=CDS]

MSIRELLDPTNSALIFIDHQPQMSFGVANIDRQTLKNNTVALAKAGKIFNVPVIYTSVETKSFSGYIWPE

LLAVHPDVKPIERTSMNSWEDDAFVAAVKATGRKKLVISALWTEVCLTFPALMALEAGYEVYVVTDTSGG

TSVDAHERSIDRMVQAGAVPVTWQQVLLEYQRDWSRKATYDAVMDLVREHSGAYGMGVDYAYTMVHGAPE

RKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002890365.1\_1323 [locus\_tag=BN49\_RS08000] [protein=antibiotic biosynthesis monooxygenase] [protein\_id=WP\_002890365.1] [location=1363457..1364002] [gbkey=CDS]

MAQQKSVTLVISHLLDPQHSQRYEEWLGKIMPIAAEFPGHLGANVIRPAAGQNLWSVIIRFDTLEHLYAW

TQSETRRQLVAEIAPLLTEGDRTEVRTEPAFWFTPPTVNVRQPRRWKQFLITLLVIFPSTNLVPAVTGML

LPSLKGSLLLHLINDACVVALVVWFWMPIVTRLFAGWLKKN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529704.1\_1324 [locus\_tag=BN49\_RS08005] [protein=amidohydrolase] [protein\_id=WP\_016529704.1] [location=1364027..1365895] [gbkey=CDS]

MSQTATLILTHGQIHTLDRANPLAEAVAIADGKIVATGSHDRIMSFAAEGTQIVDLKGHTVVPGLNDSHL

HLIRGGLNYNLELRWEGVPSLADALRMLKDQADRTPSPQWVRVVGGWSEFQFAERRMPTLEELNEAAPDT

PVFVLHLYERALLNRAALKAVGYSKETPDPAGGEIVRDSHGNPTGMLIAKPNAMILYATLAKGPKLPLDL

QVNSTRQFMRELNRLGLTSAIDAGGGFQNYPEDYEIIEQLHAKDQMTVRIAYNLFTQRPKQELEDFERWT

DMLKPGQGTDFYRANGAGEMLVFSAADFEDFLQPRPDLPQGMEDELERVVRHLVEHRWPFRLHATYDESI

SRMLDVFEKVNRDIPFNGLHWFFDHAETITERNIERVKALGGGIAVQHRMAFQGEYFVDRYGKEAVKHTP

PVAKMLALDVPVGLGTDATRVASYNPWTALYWLVSGRTVGGMAMYDDANRLPRDVALELWTAGSAWFSSE

QGKKGRLAAGQLADLVVLSKDYFSVAEEEIKGIESVLTVVDGKVVYAAGHFSPLAPPPIPVLPEWSPVVK

VPGHYRSAPPATAKIGAMVQMHQCCGSCGVHGHQHDIARKSSIPVSDEQAFWGVLGCSCFAF

>lcl|NZ\_FO834906.1\_prot\_WP\_004218830.1\_1325 [gene=fba] [locus\_tag=BN49\_RS08010] [protein=class II fructose-1,6-bisphosphate aldolase] [protein\_id=WP\_004218830.1] [location=complement(1365954..1366808)] [gbkey=CDS]

MSMKDMLQHALRDGYAVGQFNINNLEWVGAVLSTAQQCRSPVILGVSGGTVKHMLGLKCIHDIVVNAMEY

LHIDVPVALHLDHGTSREACEAAIAAGFSSIMFDGSHLPFRENLAITRHLVTLAHSKGISVEAELGTIAG

SEDGIVNSEVIYADPQECYTLVTETQVDCLAAALGSTHGLYKGKARLGFTEMKAIAEQVKVPLVLHGGTG

IADEDMRRAIACGTAKINVNTENMYAWCQQVKAIFAADTGHDVNDPRKVIAQGLQPVREMIARRMALFGS

EQRY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529705.1\_1326 [locus\_tag=BN49\_RS08015] [protein=PfkB family carbohydrate kinase] [protein\_id=WP\_016529705.1] [location=complement(1366844..1367806)] [gbkey=CDS]

MAILSIGFACFDQFFFLNEWPQENTKNFCHDYIESGGGPAANAAWLLGLWGEEVYYIGHLQQDLYGQRII

DEFAEAGVDTSQVVFSDDMITPLASVLVNRLTGSRTIITRKMQTPPSLTYEQKLKLDDLAERLIASEEPV

TILIDGHEAEISEYLIKKLPNARVVMDGGSLRASNIKLAAWTDYFVVSEHFARDYMSYRSLSTEAEIKAA

LIELNKICRGEAFITLGEKGCAFLKSGMLQIVPSWLCNAVDTTGAGDVFHGAFTYGVHYSWHIDNIILFA

SLTAAISIEKKGVRESMPDLAVVHHSLNSYERNLTQYFEE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042731.1\_1327 [locus\_tag=BN49\_RS08020] [protein=PTS ascorbate transporter subunit IIC] [protein\_id=WP\_046042731.1] [location=complement(1367872..1369263)] [gbkey=CDS]

MQAILSFLTEIFSQPAFLMGLIAFIGLVALRSPGNKLLTGTLKPILGYLMLSAGAGVIVANLNPLGGIIE

AGFNIRGVIPNNEAIVSVAQKMLGVETMSILLLGFIFNLIIARCTKYKYIFLTGHHSFFLACLFSAVLQA

AEFQGWMLILIGGFLLGSWSAISPAIGQRYTRQVTEDGGIAMGHFGSLGYYLSAWIASRTGNPANSFADT

EISEKWGFLRDTTVTTGIVMFVIYFVCSAVAGSAYLSTITDQNMLIFSVLTGLQFAVGVAIVYNGVRLIL

GDLVPAFQGISQKLIPDSIPAVDCAVFFTFSPTAVVVGFISSFVGGLVGMLLLGGLGMALIIPGMVPHFF

CGGTSGVFADKLGGKRGCIIASFIGGIFLAFLPAMLLPALGNLGFENSTFADFDFAVWGIIIGNAFTQFG

QITIYLICLALLVALLAPFCFRHVQVVGNTLSYEELTAKQKNE

>lcl|NZ\_FO834906.1\_prot\_WP\_002890376.1\_1328 [locus\_tag=BN49\_RS08025] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_002890376.1] [location=complement(1369284..1369571)] [gbkey=CDS]

MLVIRTVCGNGIGSSLMAANNVKKICDELGIKADVASVDFANAVGEKADLYVTIKELANQFPAHCHVAII

RSYVHKAKIAEDITDALMKIAATHS

>lcl|NZ\_FO834906.1\_prot\_WP\_002890380.1\_1329 [locus\_tag=BN49\_RS08030] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_002890380.1] [location=complement(1369577..1370020)] [gbkey=CDS]

MEIIFDPSLIALKQNISRAEEAIELAGSLLARRQICSAEYVNEMLTVYEDFGAAIVIDDGIAMPHARPEK

GALQTGFSLVTTATPISFGHDEFDPVSVVIAIAGADADSHIKMIQLIASLIESDIVTFLQQENDVNSVLH

FIQKQME

>lcl|NZ\_FO834906.1\_prot\_WP\_004151344.1\_1330 [locus\_tag=BN49\_RS30900] [protein=hypothetical protein] [protein\_id=WP\_004151344.1] [location=1370076..1370243] [gbkey=CDS]

MKMMDEITSAVLNIDGDHIDGKVPAENDINNLYVFQSVMKALYFDAEICQRKSER

>lcl|NZ\_FO834906.1\_prot\_WP\_002890386.1\_1331 [locus\_tag=BN49\_RS08040] [protein=peroxiredoxin] [protein\_id=WP\_002890386.1] [location=complement(1370367..1370969)] [gbkey=CDS]

MVLVTRQAPDFTAAAVLGNGEIVEKFNFKQHTNGKPTVLFFWPMDFTFVCPSELIAFDKRYEEFQKRGVE

VVGVSFDSEFVHNAWRNTPVDQGGIGPVKYAMVADIKREIQKAYGIEHPDEGVALRGSFLIDANGIVRHQ

VVNDLPLGRNIDEMLRMVDALQFHEEHGEVCPAQWEKGKEGMAASPEGVAKYLTENVSSL

>lcl|NZ\_FO834906.1\_prot\_WP\_021312312.1\_1332 [gene=acpH] [locus\_tag=BN49\_RS08045] [protein=ACP phosphodiesterase] [protein\_id=WP\_021312312.1] [location=complement(1371097..1371678)] [gbkey=CDS]

MNFLAHLHLAHLADSSLPGNLMADFVRGNPQGDYPAEIIDGIFMHRRIDVMTDNLAEVKEAREWFRPQTR

RVAPITLDVMWDHFLSQHWAQLSPDLPLDEFVRYAERQIVPILPDSPPRFVNLNQYLWSERWLERYREMD

FIQRVLNGMASRRPRLEALRDSWQDLDTHYDRLETQFWRFYPQMMRQAENKQL

>lcl|NZ\_FO834906.1\_prot\_WP\_004218831.1\_1333 [locus\_tag=BN49\_RS30905] [protein=hypothetical protein] [protein\_id=WP\_004218831.1] [location=1371753..1371869] [gbkey=CDS]

MACCLAARGTFATGKAFGCRMAAFGMIWNIDYVIHPEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002890390.1\_1334 [gene=queA] [locus\_tag=BN49\_RS08055] [protein=tRNA preQ1(34) S-adenosylmethionine ribosyltransferase-isomerase QueA] [protein\_id=WP\_002890390.1] [location=1371934..1372998] [gbkey=CDS]

MRVTDFAFELPESLIAHYPMPERSSCRLLSLDGPTGALTHGTFTDILDKLNPGDLLVFNNTRVIPARLFG

RKASGGKIEVLVERMLDDKRILAHIRASKAPKPGAELLLGDDESIKATMLARHGALFEVEFNDERPVLEI

LNGIGHMPLPPYIDRPDEDADRELYQTVYGTRPGAVAAPTAGLHFDEPLLDKLRAKGVEMAFVTLHVGAG

TFQPVRVDSIEEHTMHSEYAEVPQEVVDAVLAAKARGNRVIAVGTTSVRSLESAAQAAKDALIAPFFDDT

QIFIYPGYQYQVIDALVTNFHLPESTLIMLVSAFAGYQHTMNAYKVAVEQKYRFFSYGDAMFITYNPQAI

SERP

>lcl|NZ\_FO834906.1\_prot\_WP\_002890395.1\_1335 [gene=tgt] [locus\_tag=BN49\_RS08060] [protein=tRNA guanosine(34) transglycosylase Tgt] [protein\_id=WP\_002890395.1] [location=1373107..1374234] [gbkey=CDS]

MKFELDTTDGRARRGRLVFERGVVETPAFMPVGTYGTVKGMTPEEVEATGAQIILGNTFHLWLRPGQEIM

KLHGDLHDFMQWKGPILTDSGGFQVFSLGDIRKITEQGVHFRNPINGDPIFLDPEKSMEIQYDLGSDIVM

IFDECTPYPADWDYAKRSMEMSLRWAKRSRDRFDSLGNKNALFGIIQGSVYEDLRDISVKGLVEIGFDGY

AVGGLAVGEPKEDMHRILEHVCPQIPADKPRYLMGVGKPEDLVEGVRRGIDMFDCVMPTRNARNGHLFVT

DGVVKIRNAKHKSDTAPLDAECDCYTCRNYSRAYLHHLDRCNEILGARLNTIHNLRYYQRLMAGLRKAIE

EGKLESFVTDFYQRQGRTVPPLNVD

>lcl|NZ\_FO834906.1\_prot\_WP\_002890398.1\_1336 [gene=yajC] [locus\_tag=BN49\_RS08065] [protein=preprotein translocase subunit YajC] [protein\_id=WP\_002890398.1] [location=1374257..1374589] [gbkey=CDS]

MSFFISDAVAATGAPAQGSPMSLILMLVVFGLIFYFMILRPQQKRTKEHKNLMNSIAKGDEVLTNGGLVG

RVTKVAETGYIAIALNDTTEVVIKRDFVAAVLPKGTMKAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002890400.1\_1337 [gene=secD] [locus\_tag=BN49\_RS08070] [protein=protein translocase subunit SecD] [protein\_id=WP\_002890400.1] [location=1374616..1376463] [gbkey=CDS]

MLNRYPLWKYVMLVVVIVVGLIYALPNLYGEDPAVQITGARGVAASEQTLIQVQKTLQEEKITAKSVALE

EGAILARFDTTDTQLRAREALLNVLGDKYVVALNLAPATPRWLAALYAEPMKLGLDLRGGVHFLMEVDMD

TALGKLQEQNIDSLRSELRDKGIPYATVRKEDNYGLSIVFRDSAARDQAISYLSPRHRDLVISSQGDNSL

KAVMTDERLKEAREYAVQQNINILRNRVNQLGVAEPLVQRQGADRIVVELPGIQDTARAKEILGATATLE

FRLVNTNVDQSAAASGRVPGDSEVKQTREGQPVVLYKRVILTGDHITDSTSSMDEYNQPQVNISLDSAGG

NIMSNFTKDNIGKPMATLFVEYKDSGKKDANGRAILAKEEEVINIANIQSRLGNSFRITGISNPNEARQL

SLLLRAGALIAPIQIVEERTIGPTLGMQNIKQGLEACLAGLVVSILFMILFYKKFGLIATSALIANLILI

VGIMSLIPGATLTMPGIAGIVLTLAVAVDANVLINERIKEELSNGRTVQQAIDEGYRGAFSSIFDANVTT

LIKVIILYAVGTGAIKGFAITTGIGIATSMFTAIVGTRAIVNLLYGGKRVKKLSI

>lcl|NZ\_FO834906.1\_prot\_WP\_002890403.1\_1338 [gene=secF] [locus\_tag=BN49\_RS08075] [protein=protein translocase subunit SecF] [protein\_id=WP\_002890403.1] [location=1376474..1377445] [gbkey=CDS]

MAQEYTVEQLNHGRKVWDFMRWDYWAFGISGFLLIVSIAIIGVRGFNWGLDFTGGTVIEITLEKPVDLDQ

MRDSLQKAGFEEPQVQNFGSSRDIMVRMPPVHDANGSQELGSKVVTVINESTSQNAAVKRIEFVGPSVGA

DLAQTGALALIAALVCILIYVGFRFEWRLAAGVVIALAHDVVITMGVLSLFHIEIDLTIVASLMSVIGYS

LNDSIVVSDRIRENFRKIRRGTPYEIFNVSLTQTLHRTLITSGTTLMVILMLFLFGGPILEGFSLTMLIG

VSIGTASSIYVASALALKLGMKREHLIQQKVEKEGADQPSILP

>lcl|NZ\_FO834906.1\_prot\_WP\_002890404.1\_1339 [locus\_tag=BN49\_RS08080] [protein=VOC family protein] [protein\_id=WP\_002890404.1] [location=1377582..1377947] [gbkey=CDS]

MNNVINWFEIPVADMDRAVAFYEPVMQVSLRRETMDCAELAVFPHQDPAPGGALAKFEGIAPSAQGAIIY

LHTDHLAATLERVASAGGACVFGPLTLPNDIGTIALFTDSEGNRVGLHQPA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529544.1\_1340 [locus\_tag=BN49\_RS08085] [protein=YafY family transcriptional regulator] [protein\_id=WP\_016529544.1] [location=1377971..1378666] [gbkey=CDS]

MTRRADRLFQIVQILRGRRLTTAALLAERLGVSERTVYRDIRDLSLSGVPVEGEAGSGYRLLAGYDLPPL

MLTTKESEALIAAIRLLKTWGGEALSQSLESAQEKMLAILPEARRRQAEQTRLFAPDFGAHRYAKTHFDV

IHQAVSGQQVLQLRYQDETGRVTERDVLPLGLFFWGERWLLVAWCELRNDYRNFRLDRCLEVRRTERRFS

ECADRSLSDFLRKVRCEVREK

>lcl|NZ\_FO834906.1\_prot\_WP\_002890412.1\_1341 [locus\_tag=BN49\_RS08090] [protein=nucleoside-specific channel-forming protein Tsx] [protein\_id=WP\_002890412.1] [location=complement(1378721..1379605)] [gbkey=CDS]

MKKTLLAAGAVVALSTTFAAGAAENDKPQYLSDWWHQSVNVVGSYHTRFGPQIRNDTYLEYEAFAKKDWF

DFYGYIDAPVFFGGNSTAKGIWNKGSPLFMEIEPRFSIDKLTNTDLSFGPFKEWYFANNYIYDMGRNDSQ

EQSTWYMGLGTDIDTGLPMSLSLNVYAKYQWQNYGASNENEWDGYRFKVKYFVPLTDLWGGSLSYIGFTN

FDWGSDLGDDNFYDLNGKHARTSNSIASSHILALNYAHWHYSIVARYFHNGGQWADDAKLNFGDGPFSVR

STGWGGYFVVGYNF

>lcl|NZ\_FO834906.1\_prot\_WP\_002890414.1\_1342 [locus\_tag=BN49\_RS08095] [protein=DUF3251 domain-containing protein] [protein\_id=WP\_002890414.1] [location=complement(1379904..1380443)] [gbkey=CDS]

MTRRYLKLAIAGCLFTLTACAQQSEIRQMHQSVSTLSQEMTQLNQQTIKITQQNALNAKSTRGVYLLPEA

KTPARLESQIGTLRMSVGSITPDGDGSRLTLRIQGESNDPLPAFTATVASGQITGTTHSYQEVNVQDQLI

SAPASTLAPSDVDIPLRLNVTPDKVGFIRVHDIQPAAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002890417.1\_1343 [gene=nrdR] [locus\_tag=BN49\_RS08100] [protein=transcriptional regulator NrdR] [protein\_id=WP\_002890417.1] [location=1380591..1381040] [gbkey=CDS]

MHCPFCFAVDTKVIDSRLVGEGSSVRRRRQCLVCNERFTTFEVAELVMPRVVKSNDVREPFNEDKLRSGM

LKALEKRPVSADDVEMAVNHIKTHLRGTGEREVASKMIGNLVMEQLKKLDKVAYIRFASVYRSFEDIKEF

GEEIARLQD

>lcl|NZ\_FO834906.1\_prot\_WP\_004144650.1\_1344 [gene=ribD] [locus\_tag=BN49\_RS08105] [protein=bifunctional diaminohydroxyphosphoribosylaminopyrimidine deaminase/5-amino-6-(5-phosphoribosylamino)uracil reductase RibD] [protein\_id=WP\_004144650.1] [location=1381044..1382147] [gbkey=CDS]

MQDEMYMARALKLAARGRFTTHPNPNVGCVIVKDGEIVGEGFHYRAGEPHAEVHALRMAGEKARGATAYV

TLEPCSHHGRTPPCCDALIAAGVSRVVAAMQDPNPQVAGRGLYRLQQAGIEVSHGLMMNEAEALNKGFLK

RMRTGFPWVQLKLGASLDGRTAMASGESQWITSPQARRDVQRLRAQSHAILTSSATVLADDPALTVRWQE

LSADTQALYPEENLRQPLRVVIDSQNRVTPEHRIVQQAGETLFARLRADERQWPESARTLLVPEHNGHLD

LVLLMMLLGKQQINSVWVEAGATLAGALLQAGLVDELIVYIAPKLLGNAARGLCALPGLEELSQAPHFKF

NEIRQVGPDVCLHLTTA

>lcl|NZ\_FO834906.1\_prot\_WP\_001021161.1\_1345 [gene=ribE] [locus\_tag=BN49\_RS08110] [protein=6,7-dimethyl-8-ribityllumazine synthase] [protein\_id=WP\_001021161.1] [location=1382235..1382705] [gbkey=CDS]

MNIIEANVATPDARVAITIARFNNFINDSLLEGAIDALKRIGQVKDENITVVWVPGAYELPLAAGALAKT

GKYDAVIALGTVIRGGTAHFEYVAGGASNGLAHVAQDSEIPVAFGVLTTESIEQAIERAGTKAGNKGAEA

ALTALEMINVLKAIKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002891356.1\_1346 [gene=nusB] [locus\_tag=BN49\_RS08115] [protein=transcription antitermination factor NusB] [protein\_id=WP\_002891356.1] [location=1382725..1383144] [gbkey=CDS]

MKPAARRRARECAVQALYSWQLSHNDIADVEYQFLAEQDVKDVDVLYFRELLSGVATNSAYLDGLMKPYL

SRQLEELGQVEKAVLRIALFELSKRDDVPYKVAINEAIELAKTFGAEDSHKFVNGVLDKAAPVIRPHKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004178737.1\_1347 [gene=thiL] [locus\_tag=BN49\_RS08120] [protein=thiamine-phosphate kinase] [protein\_id=WP\_004178737.1] [location=1383216..1384187] [gbkey=CDS]

MACGEFSLIARYFDRVKSARLDVETGIGDDCALLHIPEKKTLAISTDTLVAGNHFLPDIDPADLAYKALA

VNLSDLAAMGAEPAWLTLALTLPEVDEVWLEAFSDSLFVQLDYYDMQLIGGDTTRGPLSMTLGIHGFVPP

GRAMKRAGAKPGDWIYVTGTPGDSAAGLAVLQNRLTVDEPSDADYLLARHLRPMPRVLQGQALRDLATSA

IDLSDGLISDLGHILKASGCGARIDLDAMPYSDAMLRQVDSEQALRWALAGGEDYELCFTVPELNRGALD

VALGHLGARFTCIGQIAPESEGLQFIRDGKPVALDLKGYDHFA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177266.1\_1348 [gene=pgpA] [locus\_tag=BN49\_RS08125] [protein=phosphatidylglycerophosphatase A] [protein\_id=WP\_004177266.1] [location=1384180..1384683] [gbkey=CDS]

MRSRDEALSRLSMRNPWHLLATGFGSGLSPVVPGTMGSLAAIPFWYLMTFLPWQLYSLVVMMSICIGVYL

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MVDDIVAGVISAGVLYVIGHHWPIGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004147313.1\_1349 [locus\_tag=BN49\_RS08130] [protein=aldo/keto reductase] [protein\_id=WP\_004147313.1] [location=complement(1384729..1385703)] [gbkey=CDS]

MHYIPLGDTALRVSRLCLGCMTFGEPDRGRHAWTLPEESSRPLIQHAIEGGINFFDTANSYSDGSSEEIV

GRALRDFARRDEVVVATKVYHQVGDLAEGLSRAQILRSIDDSLRRLGMDYVDLLQIHRWDYTTPIEETLE

ALDEVVKAGKARYIGASSMHARQFAQALALQQQNGWARFVTMQDHYNLIYREEENEMLPLCQRNGVAVIP

WSPLARGRLTRPWGETTARLVSDEFGKSLYSASEENDAQIAGNLADVAEELDASRAQVALAWLLSKPGVA

APIIGPSRQEQLDDLLQAVDLTLSPEQIDKLEAPYQPHPVVGFK

>lcl|NZ\_FO834906.1\_prot\_WP\_004144655.1\_1350 [gene=dxs] [locus\_tag=BN49\_RS08135] [protein=1-deoxy-D-xylulose-5-phosphate synthase] [protein\_id=WP\_004144655.1] [location=complement(1385764..1387626)] [gbkey=CDS]

MSFDIAKYPTLALVDSTQELRLLPKESLPKLCDELRRYLLDSVSRSSGHFASGLGTVELTVALHYVYNTP

FDRLIWDVGHQAYPHKILTGRRDKIGTIRQKGGLHPFPWRGESEYDVLSVGHSSTSISAGIGVAIAAAKE

DKQRRAVCVIGDGAITAGMAFEAMNHAGDIKPDLLVVLNDNEMSISENVGALNNHLAQLLSGKLYSTLRE

GGKKVFSGVPPIKELLKRTEEHIKGMVVPGTLFEELGFNYIGPVDGHDVLGLVSTLKNMRDLKGPQFLHI

MTKKGRGYEPAEKDPITFHAVPKFDHTSGVLPKSSGGLPSYSKIFGDWLCETAAKDNKLMAITPAMREGS

GMVEFSKKFPDRYFDVAIAEQHAVTFAAGLAIGDYKPVVAIYSTFLQRAYDQVIHDVAIQKLPVLFAIDR

AGIVGADGQTHQGAFDLSFLRCIPDMVVMTPSDENECRQMLYTGYHYSDGPCAVRYPRGSGTGATLEPLA

SLPIGKGVVKRQGEKIAILNFGTLLPEAAAVADKLNATLVDMRFVKPLDTALILQLAGEHDALVTLEENA

IMGGAGSGVNEVLMAHRRAVPVLNIGLPDYFIPQGTQEEIRADLGLDAAGIEAKIRDWLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144656.1\_1351 [gene=ispA] [locus\_tag=BN49\_RS08140] [protein=(2E,6E)-farnesyl diphosphate synthase] [protein\_id=WP\_004144656.1] [location=complement(1387645..1388544)] [gbkey=CDS]

MDFPQQLQACVEQANEALRRFIAPQPFQNTPLVEAMHYGALLGGKRLRPFLVYATGEMFGVCRTTLDAPA

AAVECIHAYSLMHDDLPAMDDDDLRRGLPTCHIKFGEANAILAGDALQTLAFSILSDAPMVDVPDRDRLA

MVSELAQASGVAGMCGGQALDLQAEGQQVDLQALERIHRHKTGALIRAAVRMGALSAGERGRAALPALDR

YAENIGLAFQVQDDILDVVGDTATLGKRQGADQQLGKSTYPALLGLEQARKKAHDLIADARRSLDELAAQ

SLDTSALEALANYIIQRDK

>lcl|NZ\_FO834906.1\_prot\_WP\_002891398.1\_1352 [gene=xseB] [locus\_tag=BN49\_RS08145] [protein=exodeoxyribonuclease VII small subunit] [protein\_id=WP\_002891398.1] [location=complement(1388545..1388787)] [gbkey=CDS]

MPKKNEAPASFETALGELEQIVNRLESGDLPLEEALSEFERGVQLARQGQSQLQKAEQRVQILLADSEDS

PTTPFTPDAE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042740.1\_1353 [gene=thiI] [locus\_tag=BN49\_RS08150] [protein=tRNA 4-thiouridine(8) synthase ThiI] [protein\_id=WP\_046042740.1] [location=1388969..1390417] [gbkey=CDS]

MKFIIKLFPEITIKSQSVRLRFIKILTGNIRNVLKNYDETLAVVRHWDHIEVRAKDENQRPAIRDALTRI

PGIHHILEVEDVPFTSLHDIFEQTLPLWREALEGKTFCVRVKRRGKHEFTSIEVERYVGGGLNQHIETAR

VKLTDPDVTVNLEIENDRLLLVKGRYEGIGGFPIGTQEDVLSLISGGFDSGVSSYMLMRRGCRVHYCFFN

LGGAAHEIGVRQVAHYLWNRFGSSHRVRFVAINFEPVVGEILEKVDDGQMGVVLKRMMVRAASKVAERYG

VQALVTGEALGQVSSQTLTNLRLIDNVSDTLILRPLISHDKEHIIDLAREIGTEDFARTMPEYCGVISKS

PTVKAVKAKIEAEEEHFDFSILDKVVEEASNIDIREIAQQTEETVVEVETVTGFGANDAILDIRSIDEQE

DKPLKVEGGEVVSLPFYKLSTKFGDLDQSKTWLLWCERGVMSRLQALYLREQGFSNVKVYRP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531839.1\_1354 [locus\_tag=BN49\_RS08155] [protein=SRPBCC family protein] [protein\_id=WP\_016531839.1] [location=complement(1390484..1390960)] [gbkey=CDS]

MSRSATDSRDLVISRLLSAPAPALWRAWADPALLRTWWCPKPWQTEILAFDFRAGGAFHTVMHGPDGERS

DNPGCFLEVIPQQKSVMTSMLTADYRPAVSPFAMTAIITFADEQVGCRYTATVLHADDETREQHEQMGFF

EGWNIVIDQLNDLALTLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002891460.1\_1355 [gene=yajL] [locus\_tag=BN49\_RS08160] [protein=protein deglycase YajL] [protein\_id=WP\_002891460.1] [location=complement(1391011..1391604)] [gbkey=CDS]

MSASALICLAPGSEETEAVTTIDLLVRGGVKVTTASVASDGSLTIVCSRGVKLLADAPLVEVADGDFDII

VLPGGIKGAECFRDSTLLVETVRQFHLSGRIVAAICAAPATVLVPHNLFPIGNMTGFPALKEHIPAEQWQ

DKRVVWDPRVNLLTSQGPGTSIDFALKMIDLLVGREKAYEVASQLVMAAGIYNYYEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004178742.1\_1356 [gene=panE] [locus\_tag=BN49\_RS08165] [protein=2-dehydropantoate 2-reductase] [protein\_id=WP\_004178742.1] [location=complement(1391567..1392478)] [gbkey=CDS]

MKVTVLGCGALGQLWLTALYKQGHEVQGWLRVPQPFCSVNVIETDGSVFNESLTANDPDFLASSELLIVT

LKAWQVSNAVKHLAGILSDTTPIVLIHNGMGTVEELRGVKQPLLLASTTQAARRDGNVIIHVAQGTTHIG

PAKSYEGDYSYLAEVLQSVLPDVAWHNNIHSAIWRKLAVNCVINPLTALKGCKNGDLRDYTQEVAAICRE

VAAVMEREGIHTSAENLLFYVEQVIESTAENISSMLQDVRAQRHTEIDYITGFLLNRARAHGVAVPENAR

LFELIKRKENEYERVGTDLPRPW

>lcl|NZ\_FO834906.1\_prot\_WP\_016531841.1\_1357 [locus\_tag=BN49\_RS08170] [protein=YajQ family cyclic di-GMP-binding protein] [protein\_id=WP\_016531841.1] [location=1392670..1393161] [gbkey=CDS]

MPSFDIVSEVDLQEARNAVDNASREVESRFDFRGVEATFELNDANKTIKVLSESDFQVNQLLDILRAKLL

KRGIEGTSLDVPEDIVHSGKTWFVEAKLKQGIESAVQKKIVRLIKDSKLKVQAQIQGEEIRVTGKSRDDL

QSVMALVRGGDLGQPFQFKNFRD

>lcl|NZ\_FO834906.1\_prot\_WP\_016531842.1\_1358 [locus\_tag=BN49\_RS08175] [protein=MFS transporter] [protein\_id=WP\_016531842.1] [location=complement(1393205..1394557)] [gbkey=CDS]

MNDNKMTPGELRATWGLGTVFSLRMLGMFMVLPVLTTYGMALQGASEALIGLAIGIYGLAQAVFQIPFGL

LSDRIGRKPLIVGGLLIFVLGSVIAALTDSIWGIILGRALQGSGAIAAAVMALLSDLTREQNRTKAMAFI

GVTFAIAMVLGPIVTHQLGLHALFWMIAILATVGILLTLWVVPNSHNHVLNRESGMVKGCFSKVLAEPRL

LKLNFGIMCLHIMLMSTFVALPGQLEAAGFPAAEHWKIYLVTMVISFISVVPFIIYAEVKRKMKRVFLLC

VAILLIAEIVLWGAGGYFWELVAGVQLFFLAFNLLEALLPSLISKESPAGYKGTAMGVYSTSQFLGVAIG

GALGGWVDGFFDSQTVFLLGALLAMLWLLVASTMSEPPYVSSLRVEVPDGVVVDSALQARLLSASGVHQA

LVVPEERSVYIKIDSKVTNRFEIEQLIKGV

>lcl|NZ\_FO834906.1\_prot\_WP\_004191717.1\_1359 [locus\_tag=BN49\_RS08180] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_004191717.1] [location=complement(1394717..1395895)] [gbkey=CDS]

MLNGLKPLSRSLRWGMVGGGGTSQIGYSHRCAALRDNVYTLLAGALDVDAERGRAFGEQLGIAPERCYAD

YQTLFREEAQRPDGIEVVSVTTPNNTHFAITKAALEAGLHVICEKPLCFTAEEARELVDLSKKQNKIVGV

TYGYAGYQMIQQARQMIADGLLGEIRIVNMQFAHGFHNQAVELQAESTRWRVTPKFAGPSYVLGDLATHP

LFVAETMAPQLNIKRLMCSRQSFVPSRAPLEDNAFVLMEYDNGAVGSMWTSAVNSGAMHSQKVRIVGEKA

SIEWWDEHPNQLSYEVQGEPARILERGMPYLSPNALADDRIGGGHPEGLFEAWANLYRRYAQAIDATDRD

DRAFLQDFWYPDVEAGLHGVYWVEQCVKSADAGSQWVDFTLP

>lcl|NZ\_FO834906.1\_prot\_WP\_004177260.1\_1360 [locus\_tag=BN49\_RS08185] [protein=aromatic acid/H+ symport family MFS transporter] [protein\_id=WP\_004177260.1] [location=complement(1396226..1397590)] [gbkey=CDS]

MTQTQRLDVRELINRNPLSRFQKLIIFLGFCVIALDGFDIAIMGFIAPTLKLEWGVSNHQLGLVISAALI

GLALGAIFSGPLADWLGRKKIIINSVFFFGFWTIATAFSHNVEQMMFFRFMTGLGLGAAMPNIGTLVSEY

APERQRSFIITVIFCGFTFGAAAGGFSASWLIPQFGWHSLMALGGILPLLFAPLLIWLLPESVRFLVIKQ

APAARIRAILNRLYPGQISDNVTFILPAQPAAGNAMRIVLSRQYGFGSLMLWLVYFMGLFLVYILGSWLP

TLVKAVGMTVSQAAIMTAIYQAGGTLGSLFAGWLMDRINPHRALGIIYAVGGLFTMAMGYAAGSFALLCM

LAFISGACLNGANTGMNALSARYYPTQARATGSSWMHGVGRIGAILSAFAGAEMMALNLPFESVFLILGI

PAALTVAGLAAKGIFAAGHPPVASTSPASVRGAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002891476.1\_1361 [locus\_tag=BN49\_RS08190] [protein=sugar phosphate isomerase/epimerase] [protein\_id=WP\_002891476.1] [location=complement(1397601..1398419)] [gbkey=CDS]

MNKRTLSLAALTLLDVPPPEQVRIAARTGFTHVGLRLLPATPTDPDYDMLGDTPAVRATLAALMETGIRV

SDVEIVRLTPGFTLDDRLQRFMETAARLGAGQVLVAGNDDNLQRSADNLAILAAAGRPFGLTMNLEPMPW

TQLRNIAAAQALIAASGREDIGILVDALHFWRAGESLAALSSLPAHHLNYMQLCDGAAQRPESEQELIRQ

ARSARNVPGEGGLDLHGLMSALPATLPVSLEVPLDGEQGALPPLQRAQLLFDAAQPYLRACA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529189.1\_1362 [locus\_tag=BN49\_RS08195] [protein=FAD-dependent oxidoreductase] [protein\_id=WP\_016529189.1] [location=complement(1398477..1400174)] [gbkey=CDS]

MSGPVKVDVLVVGSGAAGLSAAVTAAMHGASVMVAEKASVLGGTSAWSGGWLWIPRNPLARAEGIDEAAD

APLTYLQHEMGGEAADIRLQTFLRYGPEMVEFFHQRTAVQFLSGSAMPDFHPSPGAANGGRSVTAQPYDG

RLLGDWLHRLRPPLETISLGGMGIAGGADMAHFFNATRSPRSALYAARRLLRHGWQRLRAGRGQHLVNGN

ALVARLLRSALDAGVRFQLNAPVVRLLQGPPGVSGAVLRSDGGEIHVEAGAVVLACGGFPHDRQRLAQVV

PHAAEGYGHFSAAPPDNQGEGIRLGESVGGQFDTSLRHPLAWAPVSRVTLASGQQLMFPHLVERAKPGVI

AVLPNGKRFVNEADSYHDFIAALLAATPAGDTPQAWLLADRRTLRRYGLGHARPFPFTPTAWLRTGYLQR

GNTLAELAKQCAIDANALAETVERFNHFASTGEDVDFHRGASAYNRAQGDHQVTLGPLREGPFYAVRILP

GSLGTFSGLQTDEHARVLDEQQQPIPGLYAIGNDMSSVMRGYYPSGGITLGPAMTFGYLVGKGLTKKTNI

NNNIT

>lcl|NZ\_FO834906.1\_prot\_WP\_002891541.1\_1363 [locus\_tag=BN49\_RS08200] [protein=NIPSNAP family protein] [protein\_id=WP\_002891541.1] [location=complement(1400185..1400505)] [gbkey=CDS]

MIYEKRTYTINPLKMADWLALYQSDALAVQTDHLGQLIGFFFTEIGVVNQVVHIWAYESLDDRLVRRARM

AQDERWQTFSRKNRELAAVERLESVLMRPTAFSPLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529188.1\_1364 [locus\_tag=BN49\_RS08205] [protein=FAD-dependent oxidoreductase] [protein\_id=WP\_016529188.1] [location=complement(1400519..1402180)] [gbkey=CDS]

MKSWDVIVIGSGAAGFAAAVTACCKGLSVLMLEKAGQFGGTSAISGGAVWLHDTDQARAEGKSGSAEAMK

TYLRTIIGEGQYREDLAEAFVSAGREALAFLEREGAVKYSLRPLSPDYYPDEPGAVDVGRALEVVEYDGR

ELGDAFRDLRSPPPGMLLFGGMMVNRVDIQHFLDMRRSLRSLAHCTRLLLRYARDRVKYPRGTRLAMGNA

LIARMATTALRKGMNLRLNVNVLALCEAQGAVHGVEIEYQGQRETLHARRGVVLAAGALAARYRPHTREH

FTMSPPANDGAALHLAAALNAREGADRPSNFFWAPVSVLTRADGSEERFPHLVTDRAKPGVIAVNQRAVR

FVNESSSYHHFASAMQDAAENAPCFLLCDAQAMKRYGLGLARPAPVNNDALVAAGYLHKADTLAALAQQL

GLDAQTLSKTVARYNRDAVQGVDREFAKGGNSYNRAMGDPGHQPDACNAPLLSAPFYAIKLYTGDLGTSR

GLVTTADAQVVNTEGHPIPGLYAVGNDMDSLMAGTYPGPGITLGPGLTFGYLAACHLAQHSTH

>lcl|NZ\_FO834906.1\_prot\_WP\_004178747.1\_1365 [locus\_tag=BN49\_RS08210] [protein=shikimate 5-dehydrogenase] [protein\_id=WP\_004178747.1] [location=complement(1402177..1402998)] [gbkey=CDS]

MVSGTTQVVAVIGHPIAQVKSPDNFNRYFAEQHMDSVMIPVDIVPDAVAAYLNALRGWQNMTGVLVTVPH

KQRAAALVDDLTPRARRLNAVNVIRKLADGRLQGDMLDGVGFQLAAEAQGFQPAGKQALLSGCGGVGSAI

AWGLCEAGIRRLALHDQTPATRQRLHDLLAEAFPAVQLSALPDTLYGLDLLVNGSPAGMAGFDELPLPQA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530250.1\_1366 [locus\_tag=BN49\_RS08215] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016530250.1] [location=1403151..1403909] [gbkey=CDS]

MQNTIHPRDLIVGLQKGLALIQLFSKTCPKLTVAQTAKMSGLTQSAARRFLLTLLHERYLQTDGRYYWLT

PKTLRLGQAYVDSAQFPRMVRPIVEYIASRTEEHASVGGVDEDELVYIARSRHTPFNSTSVRLGERVPIF

CTAGGRLWLASLPEAECETVLQRITREQRTPYTVTDIASLMEKIAQVRRQGYATIEQEFEIGMLVLAVPL

TDREGTWWGALSLTSHQSRTSLEALCRDHLDLLYSAQAMLVG

>lcl|NZ\_FO834906.1\_prot\_WP\_004178748.1\_1367 [locus\_tag=BN49\_RS08220] [protein=hypothetical protein] [protein\_id=WP\_004178748.1] [location=complement(1403949..1404281)] [gbkey=CDS]

MKELTLNEMEYISGGFNLFGAASGFASFVANSGVGFTSFVLTSGTAFASFVGDSAMAFGSFLTGQSNWET

FVTAGKENWGSFVNTAGNSWNTFVNNAASDWNTFLTKASA

>lcl|NZ\_FO834906.1\_prot\_WP\_002891629.1\_1368 [gene=cyoE] [locus\_tag=BN49\_RS08225] [protein=heme o synthase] [protein\_id=WP\_002891629.1] [location=complement(1404531..1405418)] [gbkey=CDS]

MFKQYLQVTKPGIIFGNLISVIGGFLLASKGHIDYPLFVWTLLGVSLVVASGCVFNNYIDRDIDRKMERT

KNRVLVKGLISPEASLVYATLLGIAGFMLLWFGANPLACWLGVMGFVVYVGVYSLYMKRHSVYGTLIGSL

SGAAPPVIGYCAVTGDFDSGAAILLAIFSLWQMPHSYAIAIFRFKDYQAANIPVLPVVKGISVAKNHITL

YIVAFAVATLMLSLGGYAGYKYLVVAAAVSVWWLGMALRGYKVADDKVWARKLFVFSIVAITALSVMMSV

DFMVPDSHSLLAYVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002891634.1\_1369 [locus\_tag=BN49\_RS08230] [protein=cytochrome o ubiquinol oxidase subunit IV] [protein\_id=WP\_002891634.1] [location=complement(1405430..1405759)] [gbkey=CDS]

MSHSTDHSGASHGSVKSYMTGFILSIILTVIPFAMVMSGSASHAVILGTILVTAVVQIVVHLVYFLHMNS

KSDEGWNLTAFIFTVIIIAIVVVGSIWIMWNLNYNMMMH

>lcl|NZ\_FO834906.1\_prot\_WP\_002891635.1\_1370 [locus\_tag=BN49\_RS08235] [protein=cytochrome o ubiquinol oxidase subunit III] [protein\_id=WP\_002891635.1] [location=complement(1405759..1406370)] [gbkey=CDS]

MATDTLAHTAHAHEHGHHDTGPMKVFGFWIYLMSDCIIFATLFATYAVLVNGTAGGPTGKDIFELPFVLV

ETALLLFSSITYGMAAIAMYKNNKSQVVSWLALTWLFGAGFIGMEIYEFHHLIMEGFGPDRSGFLSAFFA

LVGTHGLHVTSGLIWMAVLMFQVSRRGLTSTNRTRILCLSLFWHFLDVVWICVFSVVYLMGAM

>lcl|NZ\_FO834906.1\_prot\_WP\_002891638.1\_1371 [gene=cyoB] [locus\_tag=BN49\_RS08240] [protein=cytochrome o ubiquinol oxidase subunit I] [protein\_id=WP\_002891638.1] [location=complement(1406360..1408351)] [gbkey=CDS]

MFGKLTLDAVPYHEPIIVVTVAAIIIGGLALLAAITYFGKWSYLWNEWLTSVDHKRLGIMYVIVAIVMLL

RGFADAIMMRSQQVLASAGEAGFLPPHHYDQIFTAHGVIMIFFVAMPFVIGLMNLVVPLQLGARDVAFPF

LNNLSFWFTVVGVILVNLSLGVGEFAQTGWLAYPPLSGIEYSPGVGVDYWIWALQLSGIGTTLTGINFFV

TIIKMRAPGMTMFKMPVFSWASLCANILIIASFPILTVTIALLTLDRYLGTHFFTNDMGGNMMMYINLIW

AWGHPEVYILVLPVFGVFSEIAATFSRKRLFGYTSLVWATVCITVLSFIVWLHHFFTMGAGANVNAFFGI

TTMIIAIPTGVKIFNWLFTMYQGRIVFNSAMMWTIGFIVTFSVGGMTGVLLAVPGADFVLHNSLFLIAHF

HNVIIGGVVFGCFAGLTYWWPKAFGFTLNETWGKRAFWFWIIGFFVAFMPLYVLGFMGMTRRLSQQIDPQ

FHPMLVIAACGAALIACGILCQLIQFYVSIRDRDQNRDLTGDPWGGRTLEWATSSPPPFYNFAIVPQVHE

RDAFWEMKEKGEAYKQPAHYEEIHMPKNSGAGIVIAAFATVFGFAMIWHIWWMAIASFIGIVATWIIKSF

DEDVDYYVPVAEVEKLEKQHFDEINKAGLKNGN

>lcl|NZ\_FO834906.1\_prot\_WP\_002891641.1\_1372 [gene=cyoA] [locus\_tag=BN49\_RS08245] [protein=cytochrome o ubiquinol oxidase subunit II] [protein\_id=WP\_002891641.1] [location=complement(1408371..1409315)] [gbkey=CDS]

MRLRKYNKSLGWMSLIAGTVLLSGCDSALLDPKGQIGLEQRSLILTAFGLMMIVVIPAVLMAVGFAWKYR

ASNKDAKYSPNWSHSNKVEAVVWTVPILIILFLAVLTWKTTHALEPSKPLVHDEKPITIEVVSMDWKWFF

IYPEQGIATVNEIAFPANVPVHFKVTSNSVMNSFFIPRLGSQIYAMAGMQTQLHLIADEAGTYDGISASY

SGPGFSGMKFKAIATPDRATFDQWVAKAKQSPNSMDSMAAFEKVAVPSEYNKVEYFSNVKPDLFKDVVNK

FMSHESMNMSKPEGEHAAHDGMEGMDMSHAETAH

>lcl|NZ\_FO834906.1\_prot\_WP\_004178749.1\_1373 [gene=ampG] [locus\_tag=BN49\_RS08250] [protein=muropeptide MFS transporter AmpG] [protein\_id=WP\_004178749.1] [location=complement(1409795..1411270)] [gbkey=CDS]

MSSHYLRIFQQPKSAILLILGFASGLPLALTSGTLQAWMTVENIDLKTIGFFSLVGQAYVFKFLWSPLMD

RYTPPFLGRRRGWLLTTQVLLLLAIAAMGFLEPVTQLRWMAALAVVIAFCSASQDIVFDAWKTDVLPAEE

RGAGAAISVLGYRLGMLVSGGLALWLADRYLGWQGMYWLMAALLVPCIIATLLAPEPSDVIPVPRSLEQA

VAEPLRDFFGRNNAWLILLLIVLYKLGDAFAMSLTTTFLIRGVGFDAGEVGMVNKTLGLFATILGALYGG

VLMQRLTLFRALLIFGLLQGVSNAGYWLLSITDKHLYSMATAVFFENLCGGMGTAAFVALLMTLCNKSFS

ATQFALLSALSAVGRVYVGPIAGWFVEAHGWSTFYLFSVVAAVPGIALLLLCRQTLEHTQRTASFMPRSE

FPQAYALALGILTLGCLLLAVWLALLILNALDYTSFSFLSGLLEVAALTAVGGILFGGLLDYLALRKTRL

I

>lcl|NZ\_FO834906.1\_prot\_WP\_002891647.1\_1374 [locus\_tag=BN49\_RS08255] [protein=lipoprotein] [protein\_id=WP\_002891647.1] [location=complement(1411314..1411892)] [gbkey=CDS]

MLKKILFPLVAMFMLAGCATPPTTIEVSPKITLPQQDPSLMGVTVSINGADQRPDQALAKVTRDNQLVTL

TASRDLRFLLQEVLEKQMTSRGYMIGPNGAVDLQIIVNKLYADVSQGNVRYNIATKADIAIIATAANGTK

MTKNYRASYSVEGAFQASNKNIADAVNSVLTDTIADMAQDTSIHDFIKQNAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002891649.1\_1375 [gene=bolA] [locus\_tag=BN49\_RS08260] [protein=transcriptional regulator BolA] [protein\_id=WP\_002891649.1] [location=1412195..1412512] [gbkey=CDS]

MMIREQIEAKLRAAFDPMYLEVVDESYRHNVPAGSESHFKVVLVSDRFTGERFLNRHRMIYGTLTEELSN

TVHALALHTYTIKEWEALQDTVFASPPCRGAGSIA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530248.1\_1376 [gene=tig] [locus\_tag=BN49\_RS08265] [protein=trigger factor] [protein\_id=WP\_016530248.1] [location=1412858..1414156] [gbkey=CDS]

MQVSVETTQGLGRRVTITIAADSIENAVKSELVNVAKKVRIDGFRKGKVPMNIVAQRYGASVRQDVLGDL

MSRHFVDAIIKEKINPDGAPNYVPGEYKLGEDFTYAVEFEVYPEVELQGLDAIEVEKPVVEVTDADVDTM

LETLRKQQATWKEKEGAVDAEDRVTIDFTGSVDGEEFEGGKASDFVLAMGQGRMIPGFEDGIKGHKAGEE

FTIDVTFPEEYHAENLKGKAAKFVINLKKVEERELPELTEEFIKRFGVEDGSVAGLRAEVRKNMERELKG

AVRNRVKSQAIEGLVKANEIDVPAALIDSEIDVLRRQAAQRFGGNEKQALELPRELFEEQAKRRVVVGLL

LGEVIRTNELKADEERVKALIEEMASAYEDPSEVVEFYSKNKELMDNMRNVALEEQAVEAVLAKAKVSEK

ATSFNELMNQQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002891804.1\_1377 [gene=clpP] [locus\_tag=BN49\_RS08270] [protein=ATP-dependent Clp endopeptidase proteolytic subunit ClpP] [protein\_id=WP\_002891804.1] [location=1414465..1415088] [gbkey=CDS]

MSYSGERDNFAPHMALVPMVIEQTSRGERSFDIYSRLLKERVIFLTGQVEDHMANLIVAQMLFLEAENPE

KDIYLYINSPGGVITAGMSIYDTMQFIKPDVSTICMGQAASMGAFLLTAGAKGKRFCLPNSRVMIHQPLG

GYQGQATDIEIHAREILKVKGRMNELMAHHTGQSLEQIERDTERDRFLSAAEAVEYGLVDSILTHRN

>lcl|NZ\_FO834906.1\_prot\_WP\_002891807.1\_1378 [gene=clpX] [locus\_tag=BN49\_RS08275] [protein=ATP-dependent protease ATP-binding subunit ClpX] [protein\_id=WP\_002891807.1] [location=1415339..1416613] [gbkey=CDS]

MTDKRKDGSGKLLYCSFCGKSQHEVRKLIAGPSVYICDECVDLCNDIIREEIKEVAPHRERSALPTPHEI

RHHLDDYVIGQEQAKKVLAVAVYNHYKRLRNGDTSNGVELGKSNILLIGPTGSGKTLLAETLARLLDVPF

TMADATTLTEAGYVGEDVENIIQKLLQKCDYDVQKAQRGIVYIDEIDKISRKSDNPSITRDVSGEGVQQA

LLKLIEGTVAAVPPQGGRKHPQQEFLQVDTSKILFICGGAFAGLDKVISHRVETGSGIGFGATVKAKSDK

ASEGELLAQVEPEDLIKFGLIPEFIGRLPVVATLNELSEEALIQILKEPKNALTKQYQALFSLEGAELEF

RDEALDAIAKKAMARKTGARGLRSIVEAALLDTMYDLPSMEDVEKVVIDESVIAGQSKPLLIYGKPEAQQ

ASGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151336.1\_1379 [gene=lon] [locus\_tag=BN49\_RS08280] [protein=endopeptidase La] [protein\_id=WP\_004151336.1] [location=1416797..1419151] [gbkey=CDS]

MNPERSERIEIPVLPLRDVVVYPHMVIPLFVGREKSIRCLEAAMDHDKKIMLVAQKEASTDEPGVNDLFT

VGTVASILQMLKLPDGTVKVLVEGLQRARISALSDNGEHFSAKAEYLDSPAIDEREQEVLVRTAISQFEG

YIKLNKKIPPEVLTSLNSIDDPARLADTIAAHMPLKLADKQSVLEMSDVNERLEYLMAMMESEIDLLQVE

KRIRNRVKKQMEKSQREYYLNEQMKAIQKELGEMDDAPDENEALKRKIDAAKMPKEAKEKTEAELQKLKM

MSPMSAEATVVRGYIDWMVQVPWNARSKVKKDLRQAQEILDTDHYGLERVKDRILEYLAVQSRVNKIKGP

ILCLVGPPGVGKTSLGQSIAKATGRKYVRMALGGVRDEAEIRGHRRTYIGSMPGKLIQKMAKVGVKNPLF

LLDEIDKMSSDMRGDPASALLEVLDPEQNVAFNDHYLEVDYDLSDVMFVATSNSMNIPAPLLDRMEVIRL

SGYTEDEKLNIAKRHLLPKQIERNALKKGELTVDDSAIIGIIRYYTREAGVRSLEREISKLCRKAVKQLL

LDKSLKHIEINGENLHDYLGVQRFDYGRADSENRVGQVTGLAWTEVGGDLLTIETACVPGKGKLTYTGSL

GEVMQESIQAALTVVRSRADKLGINADFYEKRDIHVHVPEGATPKDGPSAGIAMCTALVSCLTGNPVRAD

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LQNEPFGMQVVTAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002444653.1\_1380 [gene=hupB] [locus\_tag=BN49\_RS08285] [protein=DNA-binding protein HU-beta] [protein\_id=WP\_002444653.1] [location=1419361..1419633] [gbkey=CDS]

MNKSQLIDKIAAGADISKAAAGRALDALIASVTESLQAGDDVALVGFGTFAVKERAARTGRNPQTGKEIT

IAAAKVPGFRAGKALKDAVN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530152.1\_1381 [gene=ppiD] [locus\_tag=BN49\_RS08290] [protein=peptidylprolyl isomerase] [protein\_id=WP\_016530152.1] [location=1419848..1421722] [gbkey=CDS]

MMDNLRTAANSVVLKIIFGIIIVSFILTGVSGYLIGGGKNYAAKVNGQEIGRGQFENAVASERNRMQQQL

GDQFSELAANENYMKTMRQQVLNRLIDESLLDQYARELGLSISDEQVKQAIFQTQAFQTNGKFDNQRFSG

IVAQMGMTTDQYAQALRNQLTTQQLINAIAGTDFMLPGESDQLAALVSQQRVVREATINVNALAAKQTAS

DEEINAFWQQNQARFMAPEQFRVSYIKMDAASMQESASDDEIQSWYDQHKEQFTQPQRNRYSVIQTKTEA

DAKAVLAELQKGADFATLAKEKSTDIISARNGGDMGWMEDASTVPELKDAGLKEKGQLSGVIKSSVGFLV

ARLDDVQPAQVKPLADVRNDIAAKVKQEKALDAYYALQQKVSDAASNDNESLASAAQVAGLKVVETGWFG

RDNLPEELNFKPVADAIFNGGLVGENGAPGSNSDIITVDGDRAFVLRISEHKAEAVKPLAEVKAQVSDIV

KHNKAEQQAKLEADKLLAALKDGKGDEAMKAAGLSFGAPQTLSRTGQDPLSQLAFTLPLPQQGKPVYGVG

SNMQGDVVLVALDEVKAGSMPEEQKKAMVQGITQNNAQIAFEALMSNLRKAAKIKLGDSIDQQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004191677.1\_1382 [locus\_tag=BN49\_RS08295] [protein=helix-hairpin-helix domain-containing protein] [protein\_id=WP\_004191677.1] [location=1421871..1422239] [gbkey=CDS]

MKYGIKALMAAGVLVFAVGVQGALAAPASGKAAVNKENVQASSSAKAEAVPGEADNGATKVSINRASAEQ

LAQALNGVGLKKAQAIVSYREEYGPFKTLDDLKQVPGMGSALVERNLAHLTL

>lcl|NZ\_FO834906.1\_prot\_WP\_002891860.1\_1383 [locus\_tag=BN49\_RS08300] [protein=YbgC/FadM family acyl-CoA thioesterase] [protein\_id=WP\_002891860.1] [location=1422351..1422752] [gbkey=CDS]

MQTQIKVRGYHLDVYQHVNNARYLEFLEEARWDGLENSPAFQWMMEKNIAFVVVNININYRRPAVLGDVL

TVSSKLEQLNGKSGTLSQVVTLNPNGEVVADALITFVCIDLKTQKALPLEGELRAKLDQMNLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002891863.1\_1384 [gene=queC] [locus\_tag=BN49\_RS08305] [protein=7-cyano-7-deazaguanine synthase QueC] [protein\_id=WP\_002891863.1] [location=complement(1422864..1423565)] [gbkey=CDS]

MKRAVVVFSGGQDSTTCLVQALQQYDEVHCVTFDYGQRHRAEIDVARELALKLGAVAHKVLDVTLLNELA

VSSLTRDNIPVPDYQPDAEGIPNTFVPGRNILFLTLTAIYAYQVKAEAIITGVCETDFSGYPDCRDEFVK

ALHHAVSLGMAKDIRFETPLMWLNKAETWALADYWGQLDLVRRETLTCYNGIKGDGCGQCAACNLRANGL

NQYLADKVGVMAVMQQKTGLAQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177251.1\_1385 [locus\_tag=BN49\_RS08310] [protein=SgrR family transcriptional regulator] [protein\_id=WP\_004177251.1] [location=complement(1423632..1425332)] [gbkey=CDS]

MRLLHRLNQYQRLWQPSAGAPQQVTVGELAERCFCSERHVRTLLRQAQEAGWLSWQASSGRGKRGQLSFH

KTPESLRNEMMEQALNNGQQQTALELAQLAPVELKALLHPFLGGQWQNNTPTLRIPYYRPLEPLRPGFLP

GRAEQHLAGQIYAGLTRFDEGDNMPIGDLAHHWQVSPDGLRWHFYIRSTLCWHNGDTVETAQLRQRLLLL

LELPALRTLFASISRIDVTHAQCLTITLHRPDYWLPFRLASYCSVLAHPDDPAIGCGPFRLKRFSPELVR

LENHPRYHLQHPLIQAVEYWITPQLFDRDLGTSCRHPVQITIGDREELHNLRQVSNRISLGFCYLTLRHS

PRLSKAQAQRLVSIIHHSSLLDTLPLEEDLITPSHEVLPGWSIPQGPANNAVPLPARLTLLYHLPVELHA

MAEQLRQRLALLGCELTLLFHDAKNWEGCQHLGQADLMMGDRLIGEAPEYALEQWLRCDMLWPNLLTGAQ

YAHLQATLDAVQSQPDARSRNDALRNVFNSLMEDAIMTPLFKYNYRISAPPGVNGLRLNARGWFDFASAW

LPASST

>lcl|NZ\_FO834906.1\_prot\_WP\_004151335.1\_1386 [gene=cof] [locus\_tag=BN49\_RS08315] [protein=HMP-PP phosphatase] [protein\_id=WP\_004151335.1] [location=1425460..1426278] [gbkey=CDS]

MAKLAAFDMDGTLLMPDHRLGEKTLSALKRLRERDITLTFATGRHVLEMHHVIGEFSLDAFLITGNGTRI

HSLEGEELYRQDLAPEAAEAVLHGKWDTQASMHVFNDGGWFTGQARPELLQAHVFSGFHYQLCDLKRMSA

QHVTKICFCGDHDDLRRLRIQLNETLGDRAFLCFSAMDCLEVLPVGCNKGAALAVLSQHLGFTLQECMAF

GDAMNDREMLGSVGRGFIMGNAMPQLKAELPHLPVIGDCRNQAVSHFLTHWLDNPDLPYSPE

>lcl|NZ\_FO834906.1\_prot\_WP\_009307943.1\_1387 [locus\_tag=BN49\_RS08320] [protein=PLP-dependent cysteine synthase family protein] [protein\_id=WP\_009307943.1] [location=complement(1426323..1427375)] [gbkey=CDS]

MNSAWVKHAISEINADYQRSADTHLIRLPLPAFPGIHLYLKDESTHPTGSLKHRLARSLFLYGLCNGWIK

EGTPIIESSSGSTAVSEAYFARLLGLPFIAVMPSCTARRKIEQIEFYGGRCHFVQSAGEIYAASETLARE

LNGHYMDQFTFAERATDWRGNNNIADSIFRQMSHEPHPQPSWIVMSAGTGGTSATIGRYIRSQGYETQLM

VVDPQNSVFLDYWQTRDASLRSPVGSKIEGIGRPRVEPSFIPDVVDEMLRVPDAASVATALWLETQLGRK

VGASTGTNMWGVLQLAARMREEGRTGSIVTLLCDSGERYLESYYNPQWVADNIGDIAPWQAEIAGLVERR

>lcl|NZ\_FO834906.1\_prot\_WP\_002891873.1\_1388 [locus\_tag=BN49\_RS08325] [protein=Lrp/AsnC family transcriptional regulator] [protein\_id=WP\_002891873.1] [location=1427491..1427949] [gbkey=CDS]

MLDKIDRKLLALLQEDCTLSLQALADAVNLTTTPCWKRLKRLEDEGILRGRVALLDAEKVGLGLTAFVLI

KTQHHSSDWYCQFVSEVTQMAEVLGFWRMAGEYDYLLRVQVADMKRYDDFYKRLVNSVPGLSDVTSSFAM

EQIKYTTALPVE

>lcl|NZ\_FO834906.1\_prot\_WP\_004213754.1\_1389 [locus\_tag=BN49\_RS08330] [protein=SmdA family multidrug ABC transporter permease/ATP-binding protein] [protein\_id=WP\_004213754.1] [location=1427993..1429765] [gbkey=CDS]

MRLFAQLSWYFRREWRRYLGAIALLVIIAVLQLIPPKVVGIVVDGVTQQHYTAEKVWMWIGALVLIAVMV

YLLRYVWRVLLFGASYQLAVELREDFYRQLSRQHPAFYLRHRTGDLIARATNDVDRVVFAAGEGVLTLVD

SLVMGCAVLIVMSTQISWQLTLLALLPMPLMALAIKRNGDALHERFRVAQAAFSSLNDRTQESLTSIRMI

KAFGLEDRQSAQFAADAADTGAKNMRVARIDARFDPTIYIAIGAANLLAIGGGSWMVIHGSLTLGQLTSF

VMYLGLMIWPMLALAWMFNIVERGSAAYGRIRTMLEEAPAVDDGTEAVPAGRGLLQVAIRDFIYPQASKP

SLEQVNFTLQPGQMLGICGPTGAGKSTILALLQRHFDVTHGEIRFHDLPLPILQLDSWRARLAVVNQTPF

LFSDTVANNIALGKPDATQAQIERVAQLASVHDDILRLPQGYETEVGERGVMLSGGQKQRISIARALLLE

AEILILDDALSAVDGRTEHQILHNLRQWGEGRTVIISAHRLSALTEASEILVLQHGHIAQRGRHEALAVQ

PGWYRDMYRYQQLEAALDEVPQTQEEALDA

>lcl|NZ\_FO834906.1\_prot\_WP\_004178754.1\_1390 [locus\_tag=BN49\_RS08335] [protein=SmdB family multidrug efflux ABC transporter permease/ATP-binding protein] [protein\_id=WP\_004178754.1] [location=1429758..1431536] [gbkey=CDS]

MRSFTELWPTLKRLLAYGSPWRKPLAIAVAMMWIAAAAEVSGPLLISYFIDNMVAKHTLPLKLVAGLAVA

YIGLQLLAALLHYNQSLLFNRAAVGVVQQLRSDVMDAALHQPLSEFDTQPVGQLISRVTNDTEVIRDLYV

TVVATVLRSAALIGAMLVAMFSLDWRMALVAIAIFPAVLIVMIIYQRYSTPIVRRVRAWLADINDGFNEV

INGMGVIQQFRQQARFGERMREASYAHYLARMQTLRLDGFLLRPLLSLFSSLVLCGLLMLFGFSAVGTIE

VGVLYAFISYLGRLNEPLIELTTQQSMLQQAVVAGERVFELMDRPRQAWGADDAPLSSGRVEIDHLSFAY

RGDRLVLQDITLDIPSRSFVALVGHTGSGKSTLASLMMGYYPLTHGEIRIDGRPLASLSHSALRRGIAMV

QQDPVVLADTFYANVALGRDISEAQVWEALEAVQLAAVARSMSDGLYTQLGEQGNNLSVGQKQLLALARV

LVDTPQVLILDEATANIDSGTEQAIQQALAKVRQHTTLVVIAHRLSTIVEADTILVLHRGQAVERGTHQQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_002891893.1\_1391 [gene=glnK] [locus\_tag=BN49\_RS08340] [protein=P-II family nitrogen regulator] [protein\_id=WP\_002891893.1] [location=1431780..1432118] [gbkey=CDS]

MKLVTVVIKPFKLEDVREALSSIGIQGLTVTEVKGFGRQKGHAELYRGAEYSVNFLPKVKIDVAIADDQL

DEVIDVISKAAYTGKIGDGKIFVAELQRVIRIRTGEADEAAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004152876.1\_1392 [gene=amtB] [locus\_tag=BN49\_RS08345] [protein=ammonium transporter AmtB] [protein\_id=WP\_004152876.1] [location=1432152..1433438] [gbkey=CDS]

MKMATMKSGLGALALLPGLAMAAPAVADKADNAFMMICTALVLFMTIPGIALFYGGLIRGKNVLSMLTQV

IVTFGLVCVLWVIYGYTLAFGTGGSFFGSFDWVMLKNIELKALMGTFYQYIHVAFQGSFACITVGLIVGA

LAERIRFSAVLIFVVVWMTLSYVPIAHMVWGGGLLATHGALDFAGGTVVHINAAVAGLVGAYMMGKRVGF

GKEAFKPHNLPMVFTGTAILYVGWFGFNAGSASAANEIAALAFVNTVVATAAAILAWTFGEWALRGKPSL

LGACSGAIAGLVGVTPACGYIGVGGALIVGIASGLAGIWGVTALKRWLRVDDPCDVFGVHGVCGIVGCIL

TGIFAATSLGGVGYAEGVTMGHQLLVQLESIAITVVWSGVVAFIGYKVADMTVGLRVPEEQEREGLDVNS

HGENAYNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002891899.1\_1393 [gene=tesB] [locus\_tag=BN49\_RS08350] [protein=acyl-CoA thioesterase II] [protein\_id=WP\_002891899.1] [location=complement(1433493..1434356)] [gbkey=CDS]

MSQALSNLLALLDLEKIEEGLFRGQSEDLGLRQVFGGQVVGQALYAAKETVPVERLVHSFHSYFLRPGDS

QKPIVYDVEVLRDGNSFSARRVAAIQNGKPIFYMTASFQAPENGYEHQKAMPAAPSPDGLPSETDIARKL

AHLLPPQVKDKFLCDKPLEIRPVEFHNPMKGHIAEPVRQVWLRANGAVPDDLRIHQYLLGYASDFNFLPV

ALQPHGVGFLEPGMQVATIDHSMWFHRPFNINEWLLYSVESTSASSARGFVRGEFYTQDGTLVASTVQEG

VMRNRNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002891903.1\_1394 [locus\_tag=BN49\_RS08355] [protein=YbaY family lipoprotein] [protein\_id=WP\_002891903.1] [location=1434573..1435064] [gbkey=CDS]

MKFAYMFSALAVAATLTACANHHSNNSSTQAAAPDPYGIATLSVAQQQPSVTGTINIRQRIALPPDAVLT

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NQGGTHADLTLVPVQQTAVPVAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004213753.1\_1395 [locus\_tag=BN49\_RS08360] [protein=MGMT family protein] [protein\_id=WP\_004213753.1] [location=complement(1435102..1435413)] [gbkey=CDS]

MAPHDTFPQRVWHIVASIPEGYVTTYGEVARLAGSPRAARQVGGVLKRLPEGSTLPWHRVVNRHGDISLT

GPDLQRQRQALLAEGVQVSGNGHIDLQHYRWVY

>lcl|NZ\_FO834906.1\_prot\_WP\_004178755.1\_1396 [locus\_tag=BN49\_RS08365] [protein=dTDP-glucose pyrophosphorylase] [protein\_id=WP\_004178755.1] [location=complement(1435481..1435888)] [gbkey=CDS]

MTDSSPQTITLPLPAIEGMTIAFQGVNYLRPEKMLDFATISPAPVRAVTPLALLYSTVGVLRQVELRKLP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002891977.1\_1397 [locus\_tag=BN49\_RS08370] [protein=hypothetical protein] [protein\_id=WP\_002891977.1] [location=1436535..1436792] [gbkey=CDS]

MTTVVLNVKIDAELKEKLRHYAEVNNENLGTATEKLLQLAFQLEESAGEAGVTEEDIDSQHTEEEATPLT

PKEIKALRKLLKKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004142688.1\_1398 [locus\_tag=BN49\_RS08375] [protein=hypothetical protein] [protein\_id=WP\_004142688.1] [location=1436789..1437004] [gbkey=CDS]

MKQQFSTASNYSEACDMLRSGYVKHVRLNWNIGSDEFFRIASDWCDTGAKIKKDEDGFIISLKGFPIPRQ

H

>lcl|NZ\_FO834906.1\_prot\_WP\_004142690.1\_1399 [locus\_tag=BN49\_RS08380] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_004142690.1] [location=complement(1437139..1438566)] [gbkey=CDS]

MSARRFGTQSLVRLLGNWQETSSRTPLWRQLAEALRLLILDGRLTLQTRLPGERELAAALNVSRTTIASA

LGQLREEGFLYSRQGSGSRIVLPERPADLPLPAGISSTLNLSTAALSAGPEVHQAFQHAMTLLPPYLAQT

GYDQQGLPVLREAIARRYSERGLPTRPDEVMVVNGALSAFALILRLFTGPGDRVVIDAPTYPMAISAIQG

ASCRPVGVALPQQGWDCDGLAATIAQTAPRLAWLMPDFHNPTGRCMDAPTRQRVADIAARTRTTLVIDET

MADLWYNAPPPPPLASFNPDAAVLTIGSAGKSFWGGLRIGWIRASARTIASLIQARDSLDLGTPLLEQLA

CSWLLENAATLLPPRRDMLKARRDMCETLMAEYFPRWRFSPPEGGLSFWVELPDMLATLFSARAESQGIH

IGTGTRFGLEGAFDRYLRLPFTLPDEALRRAFSTLQPLWQSLAEQKENTRLRKII

>lcl|NZ\_FO834906.1\_prot\_WP\_004893843.1\_1400 [locus\_tag=BN49\_RS08385] [protein=membrane protein] [protein\_id=WP\_004893843.1] [location=1438655..1439269] [gbkey=CDS]

MLRRLLQLYIGLVLYGVSTALFVHANLGADPWDVFHLGVAKQLGISFGTVIILTGAAVLLLWIPIRQMPG

LGTVSNVIVLGLAADATLAVLPPLESLVARSALLAGAIVLNAIATGMYIGAGFGPGPRDGLMTGLHARTG

WSLRGIRTAIELSVLLIGWLLGGKFGVGTVIYALSIGPLIQLCLPWFSQPVSRNAVSPPREIVS

>lcl|NZ\_FO834906.1\_prot\_WP\_227504843.1\_1401 [locus\_tag=BN49\_RS08390] [protein=nickel/cobalt efflux protein RcnA] [protein\_id=WP\_227504843.1] [location=complement(1439314..1440051)] [gbkey=CDS]

MFIPSAILLGALHGLEPGHSKTMMAAFIVAVRGTLKQAVLLGLAATVSHTAVVWLIAMAGLWFGRGWNAQ

TSEPWFQLISGIAIVLIACWMLWRTWRESQPHMHHDHHHASSSAAPLVAEEWQDAHQRAHAQEINRRFDG

RQVTTGQIVLFGLTGGLIPCPASITVLLICLQLKKFSLGATLVLGFSVGLALTLVASGAIAALSLKHATR

RWPWLNDLSRKAPWFSGLLIIVVGIYMMLHGLSGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002891985.1\_1402 [locus\_tag=BN49\_RS08395] [protein=metal/formaldehyde-sensitive transcriptional repressor] [protein\_id=WP\_002891985.1] [location=1440258..1440530] [gbkey=CDS]

MSHTVRHKKMLLTRLKKIQGQSTALEKMLNREHECAEILQQLAAIRGAVNGMMLQVIQGHLTDHVVKEPD

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042752.1\_1403 [locus\_tag=BN49\_RS08400] [protein=EAL domain-containing protein] [protein\_id=WP\_046042752.1] [location=complement(1440565..1442124)] [gbkey=CDS]

MRTRHLMALFTGVLILAIILPISLSIWQAARQAKMQFYRELDDYSNRIVVRTLQVADQAREALREADAHT

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DHQMTAMGSRQHMVMIDPVSFIDVVPASEEKIHTMLFGLDHQKMVISSQPLPAKVWQRIKDPYVDMLTLD

NTVYRIQRIPELGSGIVTWSSTLPLQQRIRQQLFFWLPAGIFTSLLATWLLLRLLRHLRSPRNSMLDALN

SEAIQVYYQPIISLQEGKIAGAEALARWQQPDGTFLSPDIFIPLAEQTGLITQLTEDIVRKIFADLGPWL

RQRPEVHISINLSVDDLRSPTLPTLLHNQLQHWGIAAEQIILEITERGFVDPETAMPVIAHYRQAGHRIS

IDDFGTGYSSLSYLQKLDVDTLKIDKSFVDTLEYRPLTPHIIEMAKALNLATVAEGVETESQRDWLRQHG

VQYAQGWLYSKALPKEQFILWAEHNLHAH

>lcl|NZ\_FO834906.1\_prot\_WP\_009307951.1\_1404 [gene=ugpC] [locus\_tag=BN49\_RS08405] [protein=sn-glycerol-3-phosphate ABC transporter ATP-binding protein UgpC] [protein\_id=WP\_009307951.1] [location=complement(1442358..1443467)] [gbkey=CDS]

MSNIRLRNVTKRFGSTVTLHQVNLDIEDGEFAVFVGPSGCGKSTLLRMIAGLEEVSEGEVLIGDEVMNDV

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RVAIGRAIVRNPRVFMFDEPLSNLDAELRVDMRLHIARLHQELKTTMVYVTHDQVEAMTLADKIVVMNYG

KVEQMGSPMALYYNPVNKFVAGFIGSPKMNFLPAIVSDWQPERLTVTLAQDHQLALNIATQPLKPGAAVT

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VFDENDLRISADIPAPDAH

>lcl|NZ\_FO834906.1\_prot\_WP\_002891991.1\_1405 [locus\_tag=BN49\_RS08415] [protein=maltodextrin ABC transporter substrate-binding protein] [protein\_id=WP\_002891991.1] [location=1443824..1445056] [gbkey=CDS]

MKKNTLAALILTTLAAGQLASLQAHAAGQLNVWEDIKKSAGIKTAVSDFEKQYNVKVNLQEMPYAQQLEK

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YNKDLIDKPLDSLQAWLDYSKTQREQNKYGLLAKFDQIYYSWGAIGPMGGYIFAKNDSGGFNPQQVGLNT

PGAVEAVTFLKKFYAEKVFPAGILGDNGLNAIDSLFTEKKAAAVINGPWAFQPYEAAGINYGVAPLPTLP

DGKPMSSFLGVKGYVVSTWSKDKALAQQFIEFINQPQYVKARYVATGEIPPLKAMIDDPVIKNDQKASAV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177243.1\_1406 [locus\_tag=BN49\_RS08420] [protein=sugar ABC transporter permease] [protein\_id=WP\_004177243.1] [location=1445119..1446426] [gbkey=CDS]

MSIHSSENFSDARGPGRHAWCGLLLAIVPGFGQFYHRQWLKGLVFLVLLSSFLGIFYDFLREGLWGLYTL

GEEVPRDNSIFLLAEGIISVLIVAFGVLIYFLSLRDAWLNGKKRDEGIALNSVRKQYQMLLSDGFPYLMI

TPGFILLVFVVIFPILFGFAIAFTNYNLYHTPPAKLVDWVGLKNFINIFTLSIWRSTFLDVLQWTVVWTL

LATTLQCTVGVLLAILVNQKDLRFKPLIRTIFILPWAVPGFVTILVFAGMFNDSFGVINNAILSFFGISP

KAWLTDPFWTKTALIMMQTWLGFPFVFAMTTGVLQAIPDDLYEAATMDGASAFTRLRTITLPLVLYAIAP

IIITQYTFNFNNFNIIYLFNNGGPAVAGSNAGGTDILVSWIYKLTMSSSQYAIAATITILLSIFVVGLAL

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>lcl|NZ\_FO834906.1\_prot\_1407 [locus\_tag=BN49\_RS08425] [protein=sugar ABC transporter permease] [pseudo=true] [location=1446437..1447288] [gbkey=CDS]

MAQSPSIKREKWIRLSLTWLVVILVSVVIIYPLVWTVGASLNAGNSLLSTSIIPENLSFQHYADLFNGNV

NYLT\*YWNSMKISFLTMVLTLISVSFTAYAFSRFRFKGRQNGLMLFLLLQMIPQFSALIAIFVLSQLLGL

INSHLALVLIYVGGMIPMNTWLMKGYLDAIPKDLDESARMDGASSFRIFIEIIMPLSRPILAVVALFSFT

GPLGDFILSSTILRTPDKYTLPIGLYNLVAQKMGASYTTYAAGAVLIAVPVAILYLALQKYFVSGLTSGS

TKG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042757.1\_1408 [locus\_tag=BN49\_RS08430] [protein=arabinogalactan endo-beta-1,4-galactanase] [protein\_id=WP\_046042757.1] [location=1447293..1448495] [gbkey=CDS]

MKRFTPAWLAVCLACSFSTSSLAADALATRAFQGMPADFIKGADISTLLDAEKHGATFYDQNNQRKDPIA

ILKENGVNYVRLRLWVDPQSASGEDYGGGNNDLATTLALAKRAKAQGMKLLLDFHYSDFWTDPGKQFKPK

ALEKLDYPQLKTAIHDYTRDTIARFKQAGVLPDMVQIGNEINGGILWPEGKSWGQGGGEFDRLAGLLNAA

IAGLKENLRQGEQVKIMLHLAEGTKNDTFRWWFDEIDKRHVPYDVIGLSMYTYWNGPISALKANMDDISK

RYNKDVIVVEAAYAYTLANCDNAENSFQAKEEKDGGYPASVQGQYNYIHDLMQAVVDVPDQRGKGIFYWE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004147366.1\_1409 [locus\_tag=BN49\_RS08435] [protein=beta-galactosidase] [protein\_id=WP\_004147366.1] [location=1448527..1450584] [gbkey=CDS]

MNKFAPLHPKVSTLLHGADYNPEQWENDPDIIDKDIAMMQQAKCNVMSVGIFSWAKLEPREGVFNFAWLD

IILDKLYAAGIHVFLATPSGARPAWMSQRYPQVLRVGRDRVPALHGGRHNHCMSSPVYREKTLQINTLLA

ERYSSHPAVLGWHISNEYGGECHCDLCQNRFRDWLKARYQTLENLNQAWWSTFWSHTYTDWSQIESPAPQ

GEMSIHGLNLDWHRFNTAQVTDFCRHEIAPLKAANASLPVTTNFMEYFYDYDYWQLAEALDFISWDSYPM

WHRDKDETALACYTAMYHDMMRSLKGGKPFVLMESTPGATNWQPTSKLKKPGMHILSSLQAVAHGADSVQ

YFQWRKSRGSVEKFHGAVVDHVGHIDTRIGREVCQLGEILSKLPEVRGCRTEAKVAIIFDQQNRWALDDA

QGPRNLGMEYEKTVNEHYRPFWEQGIAVDVIDADVDLTPYQLVIAPMLYMVRDGFAGRAEAFVANGGHLV

TTYWTGIVNESDLCYLGGFPGPLRNLLGIWAEEIDCLNDGEFNLVQGLAGNQCGLQGPYQVRHLCELIHI

ESAQALATYRDDFYAGRPAVTVNAFGKGKAWHVASRNDLAFQRDFFTALSKELALPRAIATELPPGVVAT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002892003.1\_1410 [locus\_tag=BN49\_RS08440] [protein=glucose PTS transporter subunit EIIB] [protein\_id=WP\_002892003.1] [location=1450648..1450962] [gbkey=CDS]

MVSLKSFLHYFSPARPAQPLSEAEKQQIEALIQAFGGEANITQVDACITRLRVSVRHLAAVDSEALQQQG

ALGVIILGQQVHAIFGKQSDALRQLLDEHFAARK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177240.1\_1411 [locus\_tag=BN49\_RS08445] [protein=maltoporin] [protein\_id=WP\_004177240.1] [location=complement(1451099..1452370)] [gbkey=CDS]

MNTTLRALSVALAAALIAPSAFAATAAIPTIDFHGYMRAGVGVSGDGSEAEWQKNKLGRLGNESDTYGEL

ELGSEVYKKDDVSFYLDSMVSMVSDGSNDNETTLNDDAQFGLRQLNLQIKGLIPGDPNAVIWGGKRYYQR

HDLHIIDTKYWNISGSGAGVENYTLGPGAVSLAWIRGDANDVDYRVDGDSNVNINYIDLRYAGWKPWAGS

WTEFGIDYAMPNTTKKQDSYGGLYDADNGVMLTGEISQDMLGGYNKTVLQYANKGLAQNMVSQGGGWYDM

WNYVNDATGYRVINTGLIPITEKFSINHVLTWGSADDITDYTDKTRMLSLVARGQYQFTDYVRLIGEVGG

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AWW

>lcl|NZ\_FO834906.1\_prot\_WP\_002892007.1\_1412 [locus\_tag=BN49\_RS08450] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_002892007.1] [location=1452641..1453711] [gbkey=CDS]

MKSKSATLEDVARHAGVSYQTVSRVLNKSANVSEATRRKVEKSIEALRYVPNRLAQQLVGKESQTVGLVT

ISLAWHAPSQVAAAVKRYANLEGYQVLISMIDESVNQSIQDSINELKSQRVDKVIINVPLETEQAQKIAA

DNDDIVCLFLDVDPYSSVFNVSFNPADGTRASVKYLYEMGHREIALLAGPDSSVSAKLRLKSWLETLDGY

GLKPVTVLHGNWDAQSGYAGALQMLRETPNFSAVLVGNDQMALGVLSAFHQHQVAVPGEKSVIGYDDTYE

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AHRLAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002892011.1\_1413 [locus\_tag=BN49\_RS08455] [protein=type B 50S ribosomal protein L31] [protein\_id=WP\_002892011.1] [location=1453827..1454090] [gbkey=CDS]

MKAHIHPPYRTVVFHDTSANEYFKVGSTIRTDRVIELDGETFPYVTIDVSSKSHPYYTGKQKTFANEGSA

ARFRQRFGGFIDAKRKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002892018.1\_1414 [gene=ykgO] [locus\_tag=BN49\_RS08460] [protein=type B 50S ribosomal protein L36] [protein\_id=WP\_002892018.1] [location=1454090..1454230] [gbkey=CDS]

MQVVNSLRSAKQRHPDCQLVKRKGRLYVICKSNPRFKAVQGRKKRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002892021.1\_1415 [locus\_tag=BN49\_RS08465] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002892021.1] [location=complement(1454227..1454925)] [gbkey=CDS]

MCEYNQFGQALGVALPDWQPRPWPTRQVLQGSRCRLEPLTLAHASDLFAAHQLAPDARSWTWLLREPESN

LAEFSAWVEQVATLADPIHFAVVDQQRGKAVGSLALMRIDIAHGVVEVGHVHFSPLLSRTAMATEAHWLL

MQYVFDTLGYRRYEWKCNSLNIPSARAARRLGFQYEGRFRQALVSKGHNRDTDWFSVIDGEWPELDNAMR

QWLAADNFTADGQQRRSLESFR

>lcl|NZ\_FO834906.1\_prot\_WP\_002892023.1\_1416 [locus\_tag=BN49\_RS08470] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_002892023.1] [location=1455026..1456477] [gbkey=CDS]

MNIPDEGFFTLLTQGMRNRTVETLQRALYHTLRDAILQGTLTARCRLPGSRVMAERLHLSRNTVNAALEQ

LALEGYLTRSRQGTQVAPLASCRQEAGQMPPVVLPERLQRLPAAMRRDSPTLAFTPGMPAVNYFPLPLWR

RLMDNVLREDGSALLGYGEAAGDPLLREAIARHLALSRGIRCDIRQIVITEGALEGVNLCASLLTNPGDS

VWLEEPGYLGARSGFQRAGLRVRGMAVDDEGMCIANGVAEPPRLIFTSPSHQYPCGSIMSAGRRLALVEY

ARRHGAWIVEDDYDSEFRHSGEPIPAMLGMVPDAPVVYLGTFSKTLFPALRIGFMVMPPALADAAQDAIG

ALLRGGHRAEQRALASFIEKGHYARHLAAMRRLYRKRQQQLREALAQEITVPCDVLGGGGGMHLTVAMEG

VNDRTLAQQARQFQLAPAALSHFYLDPQRARSGLVLGYGNTSASRYLPALRTLNRLIAQHRRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002892026.1\_1417 [locus\_tag=BN49\_RS08475] [protein=YlaC family protein] [protein\_id=WP\_002892026.1] [location=complement(1456452..1456922)] [gbkey=CDS]

MTEIQRLLIHTIDELNVQEKRDNRPRFSISFIRNHPGLFVAMYAAFLATLVVMLRSETLVDSVWLLVVLF

ILFNAFFFFDVYPRYRYEDIDVLDFRVCYNGEWYNTRFVPRQLIDRILQSPDVDSEQKAQLKKMVATKGE

LSFYDVFTLTRAGAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004147370.1\_1418 [locus\_tag=BN49\_RS30910] [protein=hypothetical protein] [protein\_id=WP\_004147370.1] [location=1456943..1457083] [gbkey=CDS]

MSLPRPADQARQAQPEGYFMLQYSAEKVTDQLQKSITVTDLSAEGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002892030.1\_1419 [gene=maa] [locus\_tag=BN49\_RS08485] [protein=maltose O-acetyltransferase] [protein\_id=WP\_002892030.1] [location=complement(1457055..1457621)] [gbkey=CDS]

MSEEKRKMIAGELYLSGDPTLRADRLRARQLLHRYNHSAPDDQEQRQHILAELFARAGDAYIEPSFRCDY

GYNIFLGAGFYANFDCVMLDVCPIHIGDNCMLAPGVHIYTATHPLDADARNSGQEYGKPVTIGHNVWIGG

RAVINPGVTIGDNAVIASGAVVTKDVPACTVVGGNPAQIIKRLPPTNP

>lcl|NZ\_FO834906.1\_prot\_WP\_002892050.1\_1420 [gene=hha] [locus\_tag=BN49\_RS08490] [protein=hemolysin expression modulator Hha] [protein\_id=WP\_002892050.1] [location=complement(1457780..1457998)] [gbkey=CDS]

MSDKPLTKTDYLMRLRRCQTIDTLERVIEKNKYELSDNELAVFYSAADHRLAELTMNKLYDKIPTSVWKF

IR

>lcl|NZ\_FO834906.1\_prot\_WP\_002892066.1\_1421 [gene=tomB] [locus\_tag=BN49\_RS08495] [protein=Hha toxicity modulator TomB] [protein\_id=WP\_002892066.1] [location=complement(1458025..1458399)] [gbkey=CDS]

MDEYSPKRHDIAQLRFLCETLYHDCLANLEESNHGWVNDPTSAVNLQLNELIEHIATFALNYKIKYAEDN

KLIAQVDEYLDDTFTLFSNYGINSTDLQKWKKSGNRLFRCFVNASRENPASLSC

>lcl|NZ\_FO834906.1\_prot\_WP\_002892069.1\_1422 [gene=acrB] [locus\_tag=BN49\_RS08500] [protein=multidrug efflux RND transporter permease subunit AcrB] [protein\_id=WP\_002892069.1] [location=complement(1458885..1462031)] [gbkey=CDS]

MPNFFIDRPIFAWVIAIIIMLAGGLSILKLPVAQYPTIAPPAISITAMYPGADAETVQNTVTQVIEQNMN

GIDHLMYMSSNGDSTGTATITLTFESGTDPDIAQVQVQNKLALATPLLPQEVQQQGISVEKASSSFLMVV

GVINTNGTMNQDDISDYVAANMKDPISRTSGVGDVQLFGSQYAMRIWMDPNKLNNFQLTPVDVISALKAQ

NAQVAAGQLGGTPPVKGQQLNASIIAQTRLTNTEEFGNILLKVNQDGSQVRLRDVAKIELGGESYDVVAK

FNGQPASGLGIKLATGANALDTANAIRAELAKMEPFFPSGMKIVYPYDTTPFVKISIHEVVKTLVEAIIL

VFLVMYLFLQNFRATLIPTIAVPVVLLGTFAVLAAFGFSINTLTMFGMVLAIGLLVDDAIVVVENVERVM

AEEGLPPKEATRKSMGQIQGALVGIAMVLSAVFIPMAFFGGSTGAIYRQFSITIVSAMALSVLVALILTP

ALCATMLKPIQKGSHGATTGFFGWFNRMFDKSTHHYTDSVGNILRSTGRYLVLYLIIVVGMAWLFVRLPS

SFLPDEDQGVFLSMAQLPAGATQERTQKVLDEMTNYYLTKEKDNVESVFAVNGFGFAGRGQNTGIAFVSL

KDWSQRPGEENKVEAITARAMGYFSQIKDAMVFAFNLPAIVELGTATGFDFELIDQGGLGHEKLTQARNQ

LFGMVAQHPDVLTGVRPNGLEDTPQFKIDIDQEKAQALGVSISDINTTLGAAWGGSYVNDFIDRGRVKKV

YIMSEAKYRMLPEDIGKWYVRGSDGQMVPFSAFSTSRWEYGSPRLERYNGLPSLEILGQAAPGKSTGEAM

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ALLAATFRGLTNDVYFQVGLLTTIGLSAKNAILIVEFAKDLMEKEGKGLIEATLEAVRMRLRPILMTSLA

FILGVMPLVISSGAGSGAQNAVGTGVMGGMVTATILAIFFVPVFFVVVRRRFSKKSEDIEHSHQVEHH

>lcl|NZ\_FO834906.1\_prot\_WP\_004177236.1\_1423 [gene=acrA] [locus\_tag=BN49\_RS08505] [protein=multidrug efflux RND transporter periplasmic adaptor subunit AcrA] [protein\_id=WP\_004177236.1] [location=complement(1462054..1463247)] [gbkey=CDS]

MNKNRGLTPLAVVLMLSGSLALTGCDDKPAQQGAQHMPEVGIVTLKSAPLQITTELPGRTSAYRIAEVRP

QVSGIILKRNFVEGSDIQAGVSLYQIDPATYQASYDSAKGDLAKAQAAANMDQLTVKRYQKLLGTKYISQ

QDYDTAVATAQQSNAAVVAAKAAVETARINLAYTKVTSPISGRIGKSAVTEGALVQNGQTTALATVQQLD

PIYVDVTQSSNDFLRLKQELADGRLKQENGKAKVELVTNDGLKYPQSGTLEFSDVTVDQTTGSITLRAIF

PNPDHTLLPGMFVRARLEEGINPDALLVPQQGVTRTPRGDASVMVVGEGDKVEVRQVTASQAIGDKWLVT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002892080.1\_1424 [gene=acrR] [locus\_tag=BN49\_RS08510] [protein=multidrug efflux transporter transcriptional repressor AcrR] [protein\_id=WP\_002892080.1] [location=1463390..1464040] [gbkey=CDS]

MARKTKQQARETRQLILDVALRLFSQQGVSSTSLATIAKAAGVTRGAIYWHFKNKSDLFNEIWELSDASI

SDLEIEYRAKFPNDPLSVIREILVYVLEATVTEERRRLMMEIIYHKCEFVGEMTVVQQAQRQLSLASYER

IEQTLKECIAAKLLPANLLTRRAAVLMRSYLSGLMENWLFAPDSFDLHAEARDYVAILLEMYQFCPTLRG

PESLSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177234.1\_1425 [gene=mscK] [locus\_tag=BN49\_RS08515] [protein=mechanosensitive channel MscK] [protein\_id=WP\_004177234.1] [location=1464170..1467517] [gbkey=CDS]

MLHTISRQRATFIFIITLLCFIGLFSPVQGRAADLPDRAEVQSQLNTLNKQKELTPQDKLVQQDLTQTLE

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AQNDLATYNSQLVSLQTQPERVQNAMFNASQQLQQIRNRLNGTSVGDETLRPTQQVLLQAQQALLNAQIE

QQRKSLEGNTILQDTLQKQRDYVTAWSNRLEHQLQLLQEAVNSKRLTLTEKTAQEAVTPDETARIQANPL

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PSADELQDMTNRIADLRLEQFEVNQQRDALFQSDAFVAKLEEGHSSEVNDEVHAALLEVIDMRRELLDQF

NKQLGNQLMMAINLQINQQQLMSVSSSLKEILTQQIFWVNSNKPMDWEWIKAFPEALKGQFKAMKITVNW

EKAWPAVFVAFLAGLPLLLIAGLIRWRLQWLKDYQAKLASQVGQLRNDTQLHTPKAILIDLIRALPVVLL

ILAIGLILLTMQLNISGLLWAYSKKLAMFWLVFGLCWKVLEKNGVAVNHFNMPAQLTSHWRRQIVRVSLA

LLPLNFWSVISELSPLNLMDDVLGQLVIFFNLLLIAVLVWPMCRESWRDKESHSLRLLTITVLSIVPVAL

MVLTATGYFYTTLRLAGRWIETVYLVMIWNLLYQTVLRGLSVAARRIAWRRALARRQHLVKEGAEGAEPQ

EEPTIALEQVNQQTLRITMLVMVALFAVMFWAIWSDLITVFAYLDSITLWHYNGTEAGASVVRSVTMGSL

LFAIVASMVAWALIRNLPGLLEVLVLSRLNMRQGTSYAITTILNYAIIAIGAMTVFGALGVSWDKLQWLA

AALSVGLGFGLQEIFGNFVSGLIILFERPVRIGDTVTIGTFSGTVSKIRIRATTITDFDRKEVIIPNKAF

VTERLINWSLSDTVTRVVIRLGVAYGSDLDKVKEVLLKAAHDHPKVMQEPAPAVFFTTFGASTLDHELRL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004183208.1\_1426 [locus\_tag=BN49\_RS08520] [protein=Rpn family recombination-promoting nuclease/putative transposase] [protein\_id=WP\_004183208.1] [location=complement(1467553..1468452)] [gbkey=CDS]

MEKVSQTPHDAVFRQMLMHQAVAKDFLQLYLPAPFLAICELDSLQLVSGSFVEEDLRASYSDILYSLRTR

HGPGYVYALIEHQSTPDKLMAFRLLRYALAAMQRHLDAGHDTLPLVVPILFYHGKVSPWPWARNWQQLFA

DPALAKALYSNDFPLVDLTVMPDNQIARHRRMAMLELLQKHIRHRDLAELQVPLIALMTQGYLTEAQLNT

LLRYMLQAGTTEHPGALIRTLAAQSPRHKELMMTIAEWLEEKGRKQGQQEGEQEATRSIAARMLARGLER

QTVQELTGLSDEELAALAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002892136.1\_1427 [gene=rsmS] [locus\_tag=BN49\_RS08525] [protein=pleiotropic regulatory protein RsmS] [protein\_id=WP\_002892136.1] [location=complement(1468520..1468693)] [gbkey=CDS]

MSLENASDEVKLAVDLIMLLESHQIPAQTVLSALEIVRRDYANKLKNAESGSQNPEK

>lcl|NZ\_FO834906.1\_prot\_WP\_014599050.1\_1428 [gene=priC] [locus\_tag=BN49\_RS08530] [protein=primosomal replication protein N''] [protein\_id=WP\_014599050.1] [location=complement(1468706..1469233)] [gbkey=CDS]

MKTAQLLQTLNDQLSELSALVAPLAEHATLSPRFDRQLFHTRSTLMQAYLAEAQHNFNQLRQAVERQQLP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002892144.1\_1429 [locus\_tag=BN49\_RS08535] [protein=DUF454 family protein] [protein\_id=WP\_002892144.1] [location=1469303..1469680] [gbkey=CDS]

MPPVILTIIGWLAVALGTLGVFLPLLPTTPFILLAAWCFARSSPRFHQWLLYRSWFGGYLRHWQQYRAMP

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529842.1\_1430 [gene=apt] [locus\_tag=BN49\_RS08540] [protein=adenine phosphoribosyltransferase] [protein\_id=WP\_016529842.1] [location=1469831..1470382] [gbkey=CDS]

MTATAQQLEYLKNSIQSIEDYPKPGILFRDVTSLLEDPKAYALSIELLTERYKDAGITKVVGTEARGFLF

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>lcl|NZ\_FO834906.1\_prot\_WP\_032103329.1\_1431 [gene=dnaX] [locus\_tag=BN49\_RS08545] [protein=DNA polymerase III subunit gamma/tau] [protein\_id=WP\_032103329.1] [location=1470475..1472382] [gbkey=CDS]

MSYQVLARKWRPQTFADVVGQEHVLTALANGLSLGRIHHAYLFSGTRGVGKTSIARLLAKGLNCETGITA

TPCGVCDNCREIEQGRFVDLIEIDAASRTKVEDTRDLLDNVQYAPARGRFKVYLIDEVHMLSRHSFNALL

KTLEEPPAHVKFLLATTDPQKLPVTILSRCLQFHLKALDVEQIRHQLEHILGEEQIAFEPRALQLLSRAA

DGSLRDALSLTDQAIASGEGQLTAASVSTMLGTLDDDQALSLIEALVAADGERVMAGVNDAAARGVEWEA

LLVEMQSLLHRIAMVQLSPSALGADMAAVEVRMRELARTVPPGDVQLYYQTLLIGRKELPYAPDRRMGVE

MTLLRALAFHPRKPMPEPEVQPAQAAAPAPRQPVAPAAPPPQSPQSLPPTTSQVLAARSHLQRSQGATTP

KKSEPAAASRARPVNNAALERLSSITERVQARPAAAALEQAPAKKEAYRWKATTVVEESKVEVATPKALK

KALEHEKTPELAAKLAEEAVERDSWAAEVSQLAVPKLVEQVALNAWKEQEGSRVCLHLRPSQRHLNSASA

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SIRPI

>lcl|NZ\_FO834906.1\_prot\_WP\_002892173.1\_1432 [locus\_tag=BN49\_RS08550] [protein=YbaB/EbfC family nucleoid-associated protein] [protein\_id=WP\_002892173.1] [location=1472440..1472772] [gbkey=CDS]

MFGGKGGLGNLMKQAQQMQEKMQKMQEEIAQLEVTGESGAGLVKVTINGAHNCRRVEIDPSLLEDDKEML

EDLVAAAFNDAARRIEETQKEKMASVSAGMQLPPGFKMPF

>lcl|NZ\_FO834906.1\_prot\_WP\_002892177.1\_1433 [gene=recR] [locus\_tag=BN49\_RS08555] [protein=recombination mediator RecR] [protein\_id=WP\_002892177.1] [location=1472772..1473377] [gbkey=CDS]

MQTSPLLTQLMEALRCLPGVGPKSAQRMAFTLLQRDRSGGMRLAQALTRAMSEIGHCADCRTFTEQEVCN

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ILATNPTVEGEATANYIAELCAQYGVDASRIAHGVPVGGELEMVDGTTLSHSLAGRHKITF

>lcl|NZ\_FO834906.1\_prot\_WP\_004177228.1\_1434 [gene=htpG] [locus\_tag=BN49\_RS08560] [protein=molecular chaperone HtpG] [protein\_id=WP\_004177228.1] [location=1473489..1475363] [gbkey=CDS]

MKGQETRGFQSEVKQLLHLMIHSLYSNKEIFLRELISNASDAADKLRFRALSQPDLYEGDGELRVRVSFD

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EKREEKDGETVISWEKINKAQALWTRSKSEVNDDEYKEFYKHIAHDYSDPLTWSHNRVEGKQEYTSLLYI

PSQAPWDMWNRDHKHGLKLYVQRVFIMDDAEQFMPNYLRFVRGLIDSNDLPLNVSREILQDSSVTRNLRT

ALTKRALQMLDKLAKDDAEKYQTFWKQFGLVLKEGPAEDPSNQEAIAKLLRFATTHTDSSAQTVSLEEYV

SRMKEGQEKIYYITADSYAAAKSSPHLELLRKKGIEVLLLSDRIDEWMMSYLTEFDGKAFQSVAKADESL

DKLADEVDESTKEAEKALEPFVERVKNLLGDRVKEVRLTHRLTDTPAIVTTDADEMSTQMAKLFAAAGQA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002892184.1\_1435 [gene=adk] [locus\_tag=BN49\_RS08565] [protein=adenylate kinase] [protein\_id=WP\_002892184.1] [location=1475586..1476230] [gbkey=CDS]

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RIAQEDCRNGFLLDGFPRTIPQADAMKEAGITVDYVLEFDVPDELIVDRIVGRRVHAASGRVYHIKFNPP

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KILG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530883.1\_1436 [gene=hemH] [locus\_tag=BN49\_RS08570] [protein=ferrochelatase] [protein\_id=WP\_016530883.1] [location=1476359..1477321] [gbkey=CDS]

MHQTKTGILLANLGTPDAPTPGAVKRYLRQFLNDKRVVDTSRLLWWPLLRGVILPIRSPRVAKLYQSVWM

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DELARILAKKRAIPGISFIRDYAEHPDYIHALAASVRASFAVHGEPDLLLLSYHGIPQRYANQGDDYPQR

CRDTTRELVSALGLPPERVMMTFQSRFGREPWLTPYTDETLKMLGEKGTKHIQVLCPGFAADCLETLEEI

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MKFPGKRKSKHYFPVNARDPLLQQIQPENESSVSWGVGIDQTLVDIEAKVDEAFIVRYGLSAGHSLVIED

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YLQGVDGAIGRCFTLIGDSGERTFAISPGHMNKLRPESIPEAVIAGASALVLTSYLVRCKPGEPMPDATM

KAIEYAKKHDVPVVLTLGTKYVIADNPAWWQEFLQEHVSILAMNEEEGEALTGFADPLSAANKALDWVDL

VLCTAGPAGLYMAGFTEEEAKRKTQHPLLPGAIPEFNQFEFSRAMRHQDCVNPLRIYSHIAPYMGGPEKI

MNTNGAGDGALAALLHDITANNYHRNNVPNSSKHKCKWLTYSSLAQVCKYANRVSYQVLNQHSPRLTRGL

PEREDSLEEAYWDR

>lcl|NZ\_FO834906.1\_prot\_WP\_002892195.1\_1438 [locus\_tag=BN49\_RS08580] [protein=Kef family K(+) transporter] [protein\_id=WP\_002892195.1] [location=complement(1478725..1480401)] [gbkey=CDS]

MHHATPLITTIVGGLVLAFILGMIANKLRISPLVGYLLAGVLAGPFTPGFVADTKLAPELAELGVILLMF

GVGLHFSLKDLMAVKSIAIPGAIAQIAVATLLGMALSAALGWSLMTGIVFGLCLSTASTVVLLRALEERQ

LIDSQRGQIAIGWLIVEDLVMVLTLVLLPAIAGMAEKGNVGFASLALDLGITIGKVVAFIAIMMLVGRRL

VPWIMSRSAATGSRELFTLSVLALALGIAFGAVELFDVSFALGAFFAGMVLNESELSHRAAHDTLPLRDA

FAVLFFVSVGMLFDPMVLVQQPLAVLATLAIIIFGKSAAAFFLVRMFGHSPRTALTIAASLAQIGEFAFI

LAGLGMALNLLPQAGQNLVLAGAIISIMLNPVLFTLLEKYLDKTETLDEQTLEEVLEDEKQVPVDICNHA

LLVGFGRVGSLLGEKLMAQGIPLVVVETSRTRVDELRERGISAVLGNAANEEIMELAHLDCARWLLLTIP

NGYEAGEIVASAREKCPNIEIIARAHYDDEVDYIIDRGANQVVMGEREIARAMLRLLETPPAGEVVTG

>lcl|NZ\_FO834906.1\_prot\_WP\_002892200.1\_1439 [locus\_tag=BN49\_RS08595] [protein=MFS transporter] [protein\_id=WP\_002892200.1] [location=complement(1480627..1481847)] [gbkey=CDS]

MTTNQSAQPLSGPAAPPQKARTSFGILGAISLSHLLNDMIQSLILAIYPLLQAEFSLTFVQIGMITLTFQ

LTSSLFQPVIGYITDKRSMPWSLPVGMCFTLCGLILLALAGSFGMVLLAAALVGTGSSVFHPESSRVARM

ASGGRHGLAQSLFQVGGNFGSSLGPLLAAVIIAPYGKGNVAWFVLAALLAIVVLSQISRWYAAQHRMNKG

KPKPAIVNPLPRKKVILAVGILLMLIFSKYFYMASISSYYTFYLMHKFGLTVQNAQLHLFAFLFAVAAGT

VIGGPVGDKIGRKYVIWGSILGVAPFTLVLPYASLEWTGILTVIIGFILASAFSAILVYAQELLPGRIGM

VSGLFFGFAFGMGGLGAAVLGLLADHTSIDLVYKICAFLPLLGFLTIFLPDNRQKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042773.1\_1440 [gene=ushA] [locus\_tag=BN49\_RS08600] [protein=bifunctional UDP-sugar hydrolase/5'-nucleotidase UshA] [protein\_id=WP\_046042773.1] [location=1482143..1483795] [gbkey=CDS]

MHYFKHSVALALFAALSLGSLSAQAYEQDKTYKITILHTNDHHGHFWRNDYGEYGLAAQKTLVDGIRKEV

AAEGGSVLLLSGGDINTGVPESDLQDAEPDFRGMNLIGYDAMAVGNHEFDNPLSVLRQQEKWAKFPFLSA

NIYQKSTGERLFKPWALFKRGGLKIAVIGLTTDDTAKIGNPEYFTDIEFRKPAEEAKLVIQELQQNEKPD

VILATTHMGHYDNGNHGSNAPGDVEMARSLPAGSLTMIVGGHSQDPVCMAAENKKQVDYVPGTPCAPDRQ

NGIWIVQAHEWGKYVGRADFEFRNGEMKLVHYQLIPVNLKKKVTYDNGQSERVLYTPQIAENPQMMSLLT

PFQNKGKAQLQVKIGSVNGHLEGDRSKVRFVQTNMGHLLLAAQIARSNADFAVMSGGGIRDSIEAGDITY

KDVMKVQPFGNVLTYVDMSGKEVVDYLTAVAQMKPDSGAYPQFANVSFVAKDGKLNDLKIKGEPVDPAKT

YRMATLSFNATGGDGYPNIADKPGYVNTGFIDAEVLKEYIEKNSPLDAAAYEPKGEVSWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002892205.1\_1441 [gene=ybaK] [locus\_tag=BN49\_RS08605] [protein=Cys-tRNA(Pro)/Cys-tRNA(Cys) deacylase YbaK] [protein\_id=WP\_002892205.1] [location=complement(1483901..1484380)] [gbkey=CDS]

MTPAVKLLEKNKISFQIHSYDHDPNETNFGDEVVRKLGLNADQVYKTLLVAVNGDMKHLAVAVTPVAGQL

DLKKVAKALGAKKVDMADPMVAQRITGYLVGGISPLGQKKRLPTVIDAPAQEFATIYISGGKRGLDIELA

ASDLAQLLDAKFADIARRD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151327.1\_1442 [locus\_tag=BN49\_RS08610] [protein=TraB/GumN family protein] [protein\_id=WP\_004151327.1] [location=complement(1484583..1485377)] [gbkey=CDS]

MGLLNRIKMLWRAAVGSSYSWPAMDIVLPGERYLHLVGSIHMGTRDMAPPPAKLLKKIRQADALIVEADI

SGNETPFSNLPTYPPLAERLSDAQLSELEARAGELGLSVGLFDSQPLWQVAMVLQATQAQKLGLRPDYGI

DYQLLMAARESNIAVMELEGADSQIALLRDLPDGGMALLEDTLTHWRTNARLLQVMIGWWLEQPPSRGAV

SLPTTFSQSLYDVLMHQRNLAWRETLLALPPGRYVVAVGALHLYGEGNLPDMLT

>lcl|NZ\_FO834906.1\_prot\_WP\_046044023.1\_1443 [gene=copA] [locus\_tag=BN49\_RS08615] [protein=copper-exporting P-type ATPase CopA] [protein\_id=WP\_046044023.1] [location=complement(1485508..1488009)] [gbkey=CDS]

MSNTIDLTLDGLSCGHCVKRVKESLEQRPDVEQAEVTLTEAHVTGSASAQALIDTVKQAGYGAELSHPKT

KPLAESSIPSEALTAATPELPAAHDEDDSQQLLINGMSCASCVSRVQNALAAVPGVSQARVNLAERTALV

MGSASAAELVQAVEKAGYGAEAIEDDLQRRERQQETALATMKRFRWQAIVALLVGVPVMVWGMIGDNMMV

SDDNRSLWLVIGLVTLAVMVFAGGHFYRSAWKSLKNGTATMDTLVALGTGVAWLYSMSVNLWPQWFPMEA

RHLYYEASAMIIGLINLGHMLEARARQRSSKALEKLLDLTPPSARVVTPEGEKDLPLAEVQAGMTLRLTT

GDRVPVDGMISQGEAWFDEAMLTGEPVPQQKGDGDAIHAGTVVQDGSVLFTASAVGSQTTLARIIRMVRQ

AQSSKPEIGQLADKISAVFVPAVVVIALISAAIWYFFGPAPQIVYTLVIATTVLIIACPCALGLATPMSI

ISGVGRAAEYGVLVRDADALQRASELDTLVFDKTGTLTEGKPQVVAVKTFAGVDEHTALRLAAALEQGSS

HPLARAILDKAADGPLPEVSGFRTLRGLGVSGEAEGHRLLLGNQALLNEQHINTAEVESEMTAQASRGAT

PVLLAVDGQAAALFAIRDPLREDSVDALARLHRQGYRLVMLTGDNPTTAKAIAKEAGIDEVIAGVLPDGK

ADAIKRLQSQGHKVAMVGDGINDAPALAQADVGIAMGGGSDVAIETAAITLMRHSLHGVADALAISKATL

RNMKQNLLGAFVYNSLGIPIAAGILWPLTGTLLNPVVAGAAMALSSITVVSNANRLLRFKPKD

>lcl|NZ\_FO834906.1\_prot\_WP\_002892208.1\_1444 [gene=cueR] [locus\_tag=BN49\_RS08620] [protein=Cu(I)-responsive transcriptional regulator] [protein\_id=WP\_002892208.1] [location=1488116..1488526] [gbkey=CDS]

MNISDVAKKTGLTSKAIRFYEEKGLVTPPLRSENGYRTYSQQHLDELTLLRQARQVGFNLEECRELVALF

NDPSRHSADVKKRTLEKVADIENHIRELQNMRAHLLALAESCPGDDSAECPIIDNLSGCCHRKAQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004142979.1\_1445 [locus\_tag=BN49\_RS08625] [protein=NfeD family protein] [protein\_id=WP\_004142979.1] [location=complement(1488523..1488981)] [gbkey=CDS]

MIGMILAHPHLFWLSLGGLLLAAEMLGGSGYLLWSGVAGVVTGALTWLLPLSWEWQGTLFAVLTLLAAWL

WSKWLRKRVKTQRPADAQLNQRGQQLVGRRLTLDAPLVNGRGHVRVGDSSWPVIADEDFAAGSKVEVIAV

EGITLRIRPAVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002892258.1\_1446 [locus\_tag=BN49\_RS08630] [protein=SPFH/Band 7/PHB domain protein] [protein\_id=WP\_002892258.1] [location=complement(1488978..1489895)] [gbkey=CDS]

MLIFIPILIFVALVIVAAAVKIVPQGYQWTVERFGRFTQTLQPGLSLVVPFMDRIGRKVNMMEQVLDIPS

QEVISRDNANVTIDAVCFIQVIDAPKAAYEVSNLEQAIVNLTMTNIRTVLGSMELDEMLSQRDSINTRLL

HIVDDATNPWGVKITRVEIRDVRPPAELIASMNAQMKAERTKRAYILEAEGVRQAEILKAEGEKQSQILK

AEGERQSAFLQAEARERSAEAEARATQMVSSAIASGDIQAINYFVAQKYTDALQQIGAANNSKVVLMPLD

ASSLMGSIAGISELIKEGAGDRKKS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530372.1\_1447 [gene=fetA] [locus\_tag=BN49\_RS08635] [protein=iron ABC transporter ATP-binding protein FetA] [protein\_id=WP\_016530372.1] [location=1490036..1490713] [gbkey=CDS]

MKENNALLRLDGVGFKTDDAVILHNINFQLRAGEFKLITGPSGCGKSTLLKIIASLLSPTSGRLFFDDAD

VATLSPERYRQQVSYCAQTPALFGDSVYDNLIFPWQIRNKQPDPQALLADLQRFGLDENMLEKSINELSG

GEKQRVSLIRNLQFLPRVLLLDEITSALDESNKQNVNDIIHGYATEKQVAVLWVTHDRNEISHADEVITL

QPAGGNMQEVQHERA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177223.1\_1448 [gene=fetB] [locus\_tag=BN49\_RS08640] [protein=iron export ABC transporter permease subunit FetB] [protein\_id=WP\_004177223.1] [location=1490700..1491482] [gbkey=CDS]

MNGHNITNESLALSMVLVLIAILVSYREKLALEKDIIWSICRAIVQLIIVGYVLKYIFNVNHAVLTLLMV

LFICFNAAWNAKKRSKYIDKAFISSFIAITTGAGLTLAVLVFSGSIAFVPMQVIPIAGMVAGNAMVAVGL

CYNNMGQRFSSEQQQIQEKLSLGATPKMASARLIRESIRASLIPTVDSAKTVGLVSLPGMMSGLIFAGID

PVKAIKYQIMVTFMLLSTASLSTIIAGYLTYRKFFNARHQLVVTQLKKRP

>lcl|NZ\_FO834906.1\_prot\_WP\_002892263.1\_1449 [locus\_tag=BN49\_RS08645] [protein=co-chaperone YbbN] [protein\_id=WP\_002892263.1] [location=complement(1491590..1492444)] [gbkey=CDS]

MSEQNIVNISEANLQQTLQQSMNVPVLFYFWSARSQHCEQLTPVLERLAAQYNGQFTLAKVDCDAEQMLA

SQFGLRAIPTVYLFQNGQPVDGFEGPQPEEAIRALLDKVLPREEELKAQQALALMQEEKYADALPLLKEA

WQLSNQESQIGLLLAETLIALHRSDEAESVLKTIPLQDQDTHYQGLVAQIELLKQAADTPEIQQLQQQVE

QNPEDAQLASQLALQLHQVGRNEEALALLFSHLQKDLGAGDGQARKMLQEILAALGTGDALAAKYRRQLY

SLLY

>lcl|NZ\_FO834906.1\_prot\_WP\_004191621.1\_1450 [locus\_tag=BN49\_RS08650] [protein=SDR family oxidoreductase] [protein\_id=WP\_004191621.1] [location=complement(1492503..1493312)] [gbkey=CDS]

MTPERQGSLTGKVMQKTVLVTGCSSGIGLESALDLTRQGFRVLAACRKAEDVARMQDLGLTGILLDLDDP

QSVERAAAEVIALTDNRLYGLFNNAGYGVYGPLNTISRQQMEQQFSANFFGAHQLTMLLLPAMTPHGEGR

IVMTSSVMGLIASPGRGAYAASKYALEAWSDALRMELRHSGIQVSLIEPGPIRTRFTDNVNQTQSDKPVE

NPGIAARFTLGPEAVVEKVRHAFTSDKPKLRYPVTLVTHAVALLKRLLPARAMDKIIHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004196998.1\_1451 [gene=tesA] [locus\_tag=BN49\_RS08655] [protein=multifunctional acyl-CoA thioesterase I/protease I/lysophospholipase L1] [protein\_id=WP\_004196998.1] [location=complement(1493302..1493925)] [gbkey=CDS]

MNFKYVFRWHVPFLLLFLFTCRAMAADTLLILGDSLSAGYRMAANAAWPALLNEQWQAKTPVVNASISGD

TSQQGLARLPALLKQHQPRWVLVELGGNDGLRGFPPQQTEQTLRTIIKDIKAANAEPLLMQIHLPANYGR

RYNEAFGAIYPALAKEFAIPLLPFFMEEVYLKPQWMQDDGIHPNRDAQPFIADWMAKRLAPLVNHDS

>lcl|NZ\_FO834906.1\_prot\_WP\_004146399.1\_1452 [locus\_tag=BN49\_RS08660] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004146399.1] [location=1493896..1494582] [gbkey=CDS]

MPAENILEVHHLKKSVGQGEHQLSILTGVELVVKPRQTIALIGESGSGKSTLLAILAGLDDGSSGEVSML

GKPLHRMDEEARAALRAQHVGFVFQSFMLIPTLNALENVELPALLRGASDSQSRGDARALLEQLGLGKRL

HHLPAQLSGGEQQRVALARAFNGRPAILFADEPTGNLDRQTGDKIADLLFSLNREHGTTLILVTHDPLLA

ARCDRRLRLVDGQLREEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042777.1\_1453 [locus\_tag=BN49\_RS08665] [protein=ABC transporter permease] [protein\_id=WP\_046042777.1] [location=1494579..1496993] [gbkey=CDS]

MIARWFWREWRSPSLLIVWLALSLAVACVLALGSISDRMEKGLSQQSREFMAGDRTLRSWREVPAEWIAQ

ARKSGLTVGEQLSFATMTFAGDTPQLADVKAVDDRYPLYGTLETQPPGLKPQAGSVLLAPRLMALLNLKT

GDTIDVGDATLRIAGEVIQEPDAGFNPFQMAPRLMMNMADVAKTGAVQPGSRVAWRYKFAGDAEQLANYE

QWLLPKLGPEHRWIGLDQDDSALGKSLERSQQFLLLSALLTLLLAVAAVAVAMSHYCRSRYDLVAILKTL

GAGRSQLRKLIVGQWLLLLTLSVITGGVAGLALERLLLLVLKPVLPAALPAASGWPWLWAIGATGVISLL

VGLRPYRLLLATLPLRVLRQDVVANVWPLKIWIPAVSVVVVGLLAWLLGGSPLLWSVLAGAVVLALLCGL

VGWGLLWLLKRLTLKALPLRLAVNRLLRQPWSTLSQLAAFSLSFMLLALLLVLRGDLLDRWQQQLPPQSP

NYFLINIAPEQIVPVKTFLAEHQTRAAEFYPIVRARLTQINGQSTDGNKDEALNRELNLTWSEQRPDHNP

LVAGSWPPKPGEVSIEEGLAQRLGIKIGDTVTFTGDTQKFSAKVSSVRTVDWESLRPNFFFIFPAGALDG

QPQSWLTSFRWDNGPAMLTQLNREFPTVSLLDIGAILRQVGQVLSQVSRALEVMVGLVTACGVLLLLAQV

QVGMRQRHQELVVWRTLGAGKSLLRATLWAEFALLGLVSGLVAAIGAEVALAMLQTKVFDFPWAPDWRLW

VLLPLTGAVLLSLCGGGLGLRLLKGKALFRQFSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004219504.1\_1454 [locus\_tag=BN49\_RS30915] [protein=hypothetical protein] [protein\_id=WP\_004219504.1] [location=complement(1496970..1497083)] [gbkey=CDS]

MLLKINDLSICAFKIKAPPKTAAHHQNAIFLLAKLAE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529292.1\_1455 [locus\_tag=BN49\_RS08675] [protein=porin] [protein\_id=WP\_016529292.1] [location=1497175..1498320] [gbkey=CDS]

MAHTIKALAISIGAALALTSLPSHAEITLLKQDPQAGDPLSRLNFTVGGSIRPQLNMMTGDGDKGSYKRN

GFDGGTRFRFAADYYLFDDISWISYYELGVNIPALFDWDNHYAEGANNTTRRMLYTGLKSDTWGTLTYGQ

QNSIYYDVVGVKTDIWDYDMIGQAPGNGINGDYDGSYRSRNMLKYKKTVGDVDLYGSYLFEDSEYLPGNG

LRYKRKGGGSVGADYHIMKDLTWGTAWNYTRAEMRDPSSADSKTYDQNIVGTALSWTPDNWTFSFGGGWY

QNFLTTKKTDVHNYFAGDAWGIEYFAGYKFPINQYAVKSIQPYFMGDRLEYVNGRNYQRIDNGLGISFQL

DYGFRVDYEHVFTSSTDNLGDMNLVRLRYDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151323.1\_1456 [gene=mnmH] [locus\_tag=BN49\_RS08680] [protein=tRNA 2-selenouridine(34) synthase MnmH] [protein\_id=WP\_004151323.1] [location=complement(1498428..1499504)] [gbkey=CDS]

MTNGTDYRAILASDTPLIDVRAPVEFSQSAMPAAINLPLMNDEERAAVGTCYKRQGPEAALALGHKLVQG

DLRASRTQAWLEACARYPHGYLCCARGGQRSHIVQQWLKEAGVDYPLIVGGYKALRQAAIQATDELVQRP

IVLIGGCTGNGKTQLVCSRPDGIDLEGLAHHRGSSFGRTLQDQHPQATFENHLAVSLLKKAEQQTRWVLE

DEGHMIGANHLPESLRLRMAQSPLAVVEDPFDVRLERLREEYFDRMYRDFIAAYGEEKGWQAYGEYLHHG

LFAIRRRLGLQRFAQLTERLDEALVQQQRTASTEAHFAWLVPLLEEYYDPMYRYQLGKKAGKILFRGSWQ

EVAAWLAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004143002.1\_1457 [gene=purK] [locus\_tag=BN49\_RS08685] [protein=5-(carboxyamino)imidazole ribonucleotide synthase] [protein\_id=WP\_004143002.1] [location=complement(1499616..1500683)] [gbkey=CDS]

MKQVCVLGNGQLGRMLRQAGEPLGIAVWPVGLEADPEAVPFQQSVITAEIERWPETALTRELARHPAFVN

RDVFPIIADRLTQKQLFDKLGLATAPWQLLADKSEWPAVFARLGELAIVKRRVGGYDGRGQWRLRENEID

QLPADNYGECIVEQGINFSGEVSLVGARAHDGSTVFYPLTRNLHQDGILRASVAFPQANARQQEQAESML

TAIMNELNYVGVMAMECFVTAEGLLINELAPRVHNSGHWTQNGASISQFELHLRAITGLPLPPPVVNSPS

VMINLIGTDLNYDWLKLPLVHLHWYDKEVRPGRKVGHLNLTDSDTDRLSATLEAIKPLLPPEYTSGLFWA

QSQLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004893772.1\_1458 [gene=purE] [locus\_tag=BN49\_RS08690] [protein=5-(carboxyamino)imidazole ribonucleotide mutase] [protein\_id=WP\_004893772.1] [location=complement(1500680..1501189)] [gbkey=CDS]

MSSRNNSARIAIVMGSKSDWATMQFTAEILDALNVPYHVEVVSAHRTPDKLFSFAESAESHGYQVIIAGA

GGAAHLPGMIAAKTLVPVLGVPVQSAALSGVDSLYSIVQMPRGIPVGTLAIGKAGAANAGLLAAQILAQH

DAELHHRLSAWRQAQTDEVLDNPDPRGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004178781.1\_1459 [locus\_tag=BN49\_RS08695] [protein=hypothetical protein] [protein\_id=WP\_004178781.1] [location=complement(1501286..1501624)] [gbkey=CDS]

MSRKKWSQPLTWGMIIAILNPLGVSYIALIGVVIGNTLTFVWCAMLAWAIYFYAIYLLCTRPHDSRLVQI

YLLLMGTLMLPWGLVLLITCIMREIKVNQAPTPSPPGETKDG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151320.1\_1460 [gene=lpxH] [locus\_tag=BN49\_RS08700] [protein=UDP-2,3-diacylglucosamine diphosphatase] [protein\_id=WP\_004151320.1] [location=complement(1501732..1502454)] [gbkey=CDS]

MATLFIADLHLQTEEPAITAGFLRFLQGEARQADALYILGDLFEAWIGDDDPNPLHQQIASAIKAVVDAG

VPCYFIHGNRDFLVGQRFARQSGMILLAEEERLDLYGREVLIMHGDTLCTDDQGYLAFRAKVHTPWIQRL

FLALPLFIRRRIAARMRADSKAANSSKSMEIMDVNPQAVVDAMERHHVQWLIHGHTHRPAVHELQANGQP

AWRVVLGAWHSEGSMVKVTPDDVELIHFPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151319.1\_1461 [gene=ppiB] [locus\_tag=BN49\_RS08705] [protein=peptidylprolyl isomerase B] [protein\_id=WP\_004151319.1] [location=complement(1502458..1502952)] [gbkey=CDS]

MVTFHTNHGDIVIKTFDDKAPETVKNFLDYCREGFYDNTIFHRVINGFMIQGGGFEPGMKQKATKSPIQN

EANNGLKNTRGTLAMARTQAPHSATAQFFINVVDNDFLNFSGESLQGWGYCVFAEVVEGMDVVDKIKAVA

TGRSGMHQDVPKDDVIIKSVTVSE

>lcl|NZ\_FO834906.1\_prot\_WP\_004143010.1\_1462 [gene=cysS] [locus\_tag=BN49\_RS08710] [protein=cysteine--tRNA ligase] [protein\_id=WP\_004143010.1] [location=1503128..1504513] [gbkey=CDS]

MLKIFNTLTRQKEEFKPIHAGEVGMYVCGITVYDLCHIGHGRTFVSFDVVARYLRFLGYKLKYVRNITDI

DDKIIKRANENGESFVALVDRMIAEMHKDFDALNILRPDSEPRATHHIAEIIEITEQLIAKGHAYVADNG

DVMFDVPTDPNYGLLSRQDLDQLQAGARVDVVDVKRNPMDFVLWKMSKEGEPSWPSPWGAGRPGWHIECS

AMNCKQLGNHFDIHGGGSDLMFPHHENEIAQSTCAHDGEYVNYWMHSGMVMVDREKMSKSLGNFFTVRDV

LKYYDAETIRYFLMSGHYRSQLNYSEENLKQARSALERLYTALRGTDKSVDAAGGEAFEARFIEAMDDDF

NTPEAYSVLFDMAREVNRLKTEDAAAANAMAAHLRKLAAVLGLLEQEPEAFLQSGAQVDDAEVAEIESLI

QQRLDARKAKDWAAADAARDRLNEMGIVLEDGPQGTTWRRK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529287.1\_1463 [gene=ybcJ] [locus\_tag=BN49\_RS08715] [protein=ribosome-associated protein YbcJ] [protein\_id=WP\_016529287.1] [location=complement(1504559..1504771)] [gbkey=CDS]

MTTFSLGKHPHVELCDLLKLEGWSESGAQAKIAIADGLVKVDGAVETRKRCKIVAGQTVSFEGQSVTVTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004143017.1\_1464 [gene=folD] [locus\_tag=BN49\_RS08720] [protein=bifunctional methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase FolD] [protein\_id=WP\_004143017.1] [location=complement(1504773..1505639)] [gbkey=CDS]

MAAKIIDGKTIAQQVRSEVAEKVKARVAAGKRAPGLAVVLVGSNPASQIYVGSKRKACEEVGFVSRSYDL

PETTSEAELLELIDTLNADKTIDGILVQLPLPAGIDNVKVLERIAPDKDVDGFHPYNVGRLCQRAPRLRP

CTPRGIVTLLERYNIDTYGLNAVVIGASNIVGRPMSMELLLAGCTTTVTHRFTKNLRHHVENADLLIVAV

GKPGFIPGEWIKEGAIVVDVGINRLESGKVVGDVVYEDAAERASYITPVPGGVGPMTVATLIQNTLQACE

EYHDVEEA

>lcl|NZ\_FO834906.1\_prot\_WP\_227504844.1\_1465 [locus\_tag=BN49\_RS31375] [protein=site-specific integrase] [protein\_id=WP\_227504844.1] [location=complement(1506070..1507227)] [gbkey=CDS]

MTLRGGVWHCHFFTPSGKRVRRSLGTGDKKQAQELHDKLKAEAWRVDQIGDLPVRTFEECCIRWLREKDH

KRSLDDDKTKIEFWLQHFSGRDVSKITAEEVHEAVNGMINRKHLQVWESKRDAALRKGKPVPEYKPRQVS

QATKAQHLSFIRSLLRAAANDWCWIKTAPVIKTRKPISKRIRWLTREEAERLIECMPESIKPVVIFALAT

GLRRSNIIGLEWQQVDMQRKVAWVNPENAKAGKAIGVALNDTACRVLRDQIGKHSRWVFVHTTAKHRPDG

TLTPAVRKMRVDDNNAWRAGLKKAGIEDFRFHDLRHTWASWLIQSGVPLSVLQEMGGWESIEMVRRYAHL

APNHLTEHARKIDAIFGASDTNTTQGGNQAGLKLA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529284.1\_1466 [locus\_tag=BN49\_RS28755] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016529284.1] [location=complement(1507110..1507445)] [gbkey=CDS]

MASDKPITAQQAAVLLIVSARVIYRLIDSGELAGRKVGNKYRTTEEACIAYLKTPRDPVIANAGEHKGEV

LCQSPSGAACGTVISLRRQEKELGDLLARGTKSRLRSSTTS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529283.1\_1467 [locus\_tag=BN49\_RS08735] [protein=TraR/DksA family transcriptional regulator] [protein\_id=WP\_016529283.1] [location=complement(1507447..1507665)] [gbkey=CDS]

MSAEIIDQANELAERRLEMTIQNMRINHNAVSATHCRDCGEEIPERRRELVAGCQRCADCQEEEELRGKH

RR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529282.1\_1468 [locus\_tag=BN49\_RS08740] [protein=DUF2591 family protein] [protein\_id=WP\_016529282.1] [location=complement(1507662..1508039)] [gbkey=CDS]

MKVKTANLSGVQLDYAVACSINMGQPILHITSETLFVEMAMKVFSPSAKWNQCGELMEKYSISCYQSADP

ATGKVYHWVGVNELVAPGRRRGLTADNPRVAVCRAVVFAKFGDEIELPDELEGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529281.1\_1469 [locus\_tag=BN49\_RS08745] [protein=hypothetical protein] [protein\_id=WP\_016529281.1] [location=complement(1508036..1508758)] [gbkey=CDS]

MKERGMIFNGEMVRAILDGRKMQTRRPIKWKQTRFTEIGEREDGSKWPWSEDAEHACDFWHPCPFGAVGD

RIWVRETWGVVSHAFSDDGMMIDWVPDRPSTAIHEMPFGNGYYSGYAIYAADGDFTWGDDDGYEDGRSCW

KPSIHMPRAASRILLEITDVRVERLNAISEEDAEAEGIDMEALYDSQDCYDCIADHNMTGRPTVTGAFKY

LWESIYGAENWLANPWVWVIEFKRVEGGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529280.1\_1470 [locus\_tag=BN49\_RS31380] [protein=hypothetical protein] [protein\_id=WP\_016529280.1] [location=complement(1508755..1508976)] [gbkey=CDS]

MTPEEKENALRAQARRCAEEITKAMSVKPKPKWNAVCPPILRKHYEKVRPMGVSLVKFVSVIGRMNGRYG

VES

>lcl|NZ\_FO834906.1\_prot\_1471 [locus\_tag=BN49\_RS28050] [protein=phage N-6-adenine-methyltransferase] [pseudo=true] [location=complement(1508973..1509500)] [gbkey=CDS]

MTDYGGSKTPKNERDYWQTPIEIFNALDREFGFWLDAAASESNALCAHYLTELDDSLNSEWASCGAIWCN

PPYSDIGPWV\*KAAEQSRAQSQAVVMLLPADISTGWFISAMQSADELRLITGGRVQFVPASVTGKRQSNP

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529279.1\_1472 [locus\_tag=BN49\_RS28760] [protein=DUF1317 family protein] [protein\_id=WP\_016529279.1] [location=complement(1509497..1509655)] [gbkey=CDS]

MKHYRDAITVGKVKCMYSVLHRGWLMPSGEVVRNPLKVQRLAEELDTKRGAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529278.1\_1473 [locus\_tag=BN49\_RS08765] [protein=YqaJ viral recombinase family protein] [protein\_id=WP\_016529278.1] [location=complement(1509652..1510332)] [gbkey=CDS]

MTPDIILARTGIDVTRVEQGDEAWHRLRLGVITASEVHNVISKPRSGTKWTDMKMSYFHTLLAEVCTGAS

PEVNAKALAWGKQYEADARTLFEFTTDVKVTESPILFRDEGMRTACSPDGLCSDGRGLELKCPFTSRDFM

KFRLGGFEAIKSAYMAQVQFSMWVTGKDAWYFANYDPRMKREGIHHVVVERDDKYMSDFNEMVPEFISKM

DESLAEIGFTFGEQWK

>lcl|NZ\_FO834906.1\_prot\_WP\_029602661.1\_1474 [gene=bet] [locus\_tag=BN49\_RS08770] [protein=phage recombination protein Bet] [protein\_id=WP\_029602661.1] [location=complement(1510329..1511174)] [gbkey=CDS]

MANELVITASSLAERGIDCATWSALKNSIYPGAKDESVMMALDYCRARNLDPLLKPVHLVPMSVKDSKSG

KSEWRDVVMPGIGLYRIQADRSGDYAGAKEPEFGPDVTLTLTGIEVTVPQWCKYTVSKRMPSGEIVEFSA

KEYWVENYATAGRDTTAPNAMWKKRPYGQLAKCAEAQALRKAWPEIGQQPTAEEMEGKTLEVDARDVTPR

STTEALPLVASEETLQAITDLLTSLNKDWDQDFLPLCSNIFKRDIFQASQLTEEEAQKGFSFLQKKAQVA

A

>lcl|NZ\_FO834906.1\_prot\_WP\_016529276.1\_1475 [gene=gamL] [locus\_tag=BN49\_RS08775] [protein=host nuclease inhibitor GamL] [protein\_id=WP\_016529276.1] [location=complement(1511190..1511474)] [gbkey=CDS]

MNAYRAYDAIEERKWAEQSLTEEKQKWIDDRAQEIIDALPKEPSGLFRFSVPMDKSPYEGLRSDAAGEAY

NDLISAVAYAQAEYDWDHRTGCPF

>lcl|NZ\_FO834906.1\_prot\_1476 [locus\_tag=BN49\_RS08780] [protein=hypothetical protein] [pseudo=true] [partial=3'] [location=complement(<1511509..1511721)] [gbkey=CDS]

MSEIMDLVVIEIKPEQAPTPYRAGGLDAYLEQIRQAVNEVPDLTTKKGRDRVASLAAQVSRSKTAIEKPG

R

>lcl|NZ\_FO834906.1\_prot\_WP\_042940642.1\_1477 [locus\_tag=BN49\_RS08785] [protein=HNH endonuclease] [protein\_id=WP\_042940642.1] [location=complement(1511796..1512308)] [gbkey=CDS]

MNHIDKLSHARLKEVIKYDPETGVFTWLKRKQRKDLIGCHAGSVSGTGYRTIRVDGVLYQAHRIAFLYMT

GQFPSHDIDHINRDRSDNRWENLRPATRSQNCFNKAMISTNTSGVKGVYWHKKNKKWTVYVQINQKYTYL

GIYEDIELAELIANEARVKHYGDFIKSKVY

>lcl|NZ\_FO834906.1\_prot\_WP\_042940648.1\_1478 [locus\_tag=BN49\_RS30920] [protein=hypothetical protein] [protein\_id=WP\_042940648.1] [location=complement(1512516..1512626)] [gbkey=CDS]

MSKQGIRSLIYCLLICGVIWSAVAIKILHAAGVFNG

>lcl|NZ\_FO834906.1\_prot\_WP\_042940647.1\_1479 [locus\_tag=BN49\_RS08795] [protein=hypothetical protein] [protein\_id=WP\_042940647.1] [location=1512961..1513164] [gbkey=CDS]

MSNEDEFFAEMHPQIAQVIGIAVMQLLVEKREPSREALIEMIQVLWQDDQVDLAVELALDVLMLREE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042794.1\_1480 [locus\_tag=BN49\_RS08800] [protein=hypothetical protein] [protein\_id=WP\_046042794.1] [location=complement(1513205..1514125)] [gbkey=CDS]

MDNLPLALSGHQLQMELYPIKEADVDGIQMGVMNDGSPFLTQRGLARLCGVDHAALLRLASNWDDERTKP

RGQFIDQKLREQGLNLNRLFHKTVIQGTETNAFPDVVCMAFLEYYAFEATQGSREVALSNFRKLAGSQLR

RFIYLSVGIDPENPQRGALECFHERLLMNDQVPFGYFSVFREMADLSLKMVKGNFDFGPSAIPDISVGTM

WSKYWVANGCDEKYGQRTKSPHVYPDWFPQHRAGPVDAWIYPDDALGLFRRWMQNEYIPNRLGDYLSKKS

ADGAISAADALRIVEAVKKPELPKPH

>lcl|NZ\_FO834906.1\_prot\_WP\_223832624.1\_1481 [locus\_tag=BN49\_RS31385] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_223832624.1] [location=complement(1514204..1514611)] [gbkey=CDS]

MVSAGPGIVNQEFVEILRSVEYEPAEARHMFDGRKAESIRIINVRGDSMSGTIEPGDLLFVDISVKSFDG

DGIYAFLYDDTAHVKRLQKMKDKLLVISDNKSYAAWDPIEKDEMNRVFVFGKVIGSMPQTYRKHG

>lcl|NZ\_FO834906.1\_prot\_1482 [locus\_tag=BN49\_RS31390] [protein=helix-turn-helix domain-containing protein] [pseudo=true] [partial=3'] [location=complement(<1514690..1514902)] [gbkey=CDS]

MKKETLADRLNEAMASAGMSQGALAKASGIAQPTIWRLVSGNARGSTKIVEIANALGVRSEWLSTGNGPM

R

>lcl|NZ\_FO834906.1\_prot\_WP\_004201115.1\_1483 [locus\_tag=BN49\_RS08810] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004201115.1] [location=1515014..1515241] [gbkey=CDS]

MTNKTIQKAIDIAGSQKKLADLCGVAQPTVWRWLHGGGIDARYVMKIVSATNGKIKAAEIRPDLAQLLSA

HSPAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530548.1\_1484 [locus\_tag=BN49\_RS08815] [protein=CII family transcriptional regulator] [protein\_id=WP\_016530548.1] [location=1515282..1515566] [gbkey=CDS]

MENSTARNKHQARNIESWLHNQIAMKGTTNVANAMGLTKSSISKWKETWIPKIAMLLAVLEWGVVDDDMS

RLAKEVASLLRKEMAPKCSKHFEA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530549.1\_1485 [locus\_tag=BN49\_RS08820] [protein=replication protein] [protein\_id=WP\_016530549.1] [location=1515601..1516470] [gbkey=CDS]

MANTAEVINFPVPVVALQELRVADLDDGFTRIANELLEAVMLAGLSQHQLLVFMAVMRKTYGFNKKSDWV

SNEQLSELTGILPHKCSAAKSVLVKRGILTQTGRVIGINKTVSEWSSLPVKGTEKKPYLKKVTLPESGKK

SLPESGNAYYQNQVNTKDKHTKDKHTKDNKDNINNPPKSPRAVSFDALAVQLPGWLSAEIWSSWVAYRRD

LKKPIKSQQTVTQAINLLDRCRLNGYAPEEIINRSIANGWQGLFEPNGAKPQPSQQVRVAENFAGKDYGQ

TEIPSWARD

>lcl|NZ\_FO834906.1\_prot\_WP\_077261005.1\_1486 [locus\_tag=BN49\_RS08825] [protein=ATP-binding protein] [protein\_id=WP\_077261005.1] [location=1516473..1517324] [gbkey=CDS]

MELEEKITAIERMLDQLSKPPEDIPNCEVVIERVCCEKHGEYEQRKRILTSSIINLPSPPTSCPGCLKDE

LVFLRNEKAKTDDRTRTANVERLMLELKVPARFEACTLDNYLPVSEDAEFALKVCRAYASRWPDRRKNGG

GLVMCGKPGTGKNHLAYAIAKSVIADHQSPVVFTTALKIAREFKSTWSKTATLSEEDVIRFFTKPDLLII

DEVGIQFGSKAEEMIMFEIINTRYERLKPTILISNLPKDELTQFIGERVIDRMNDGGGCTISFTWDSYRE

NRS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530551.1\_1487 [locus\_tag=BN49\_RS08830] [protein=hypothetical protein] [protein\_id=WP\_016530551.1] [location=1517321..1517614] [gbkey=CDS]

MTGKDAILDYLKTHKTCSSPDVAAASGMTHTCINQAANILAKQGVLVAEARVWRTVYYRLATEEEISGRK

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530552.1\_1488 [locus\_tag=BN49\_RS08835] [protein=hypothetical protein] [protein\_id=WP\_016530552.1] [location=1517611..1518081] [gbkey=CDS]

MTITLQAVNELIASLESAGELSIREQKFLKLAKAFKQLAAENVEMKQIIDSVTNLDNEPQYHDEGMGCGL

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KFAKQLREGKSEEVKS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530553.1\_1489 [locus\_tag=BN49\_RS08840] [protein=hypothetical protein] [protein\_id=WP\_016530553.1] [location=1518078..1518440] [gbkey=CDS]

MSCGYQGYEFGAHYPDSICCDGYLWDADSGDEMGMDNGGDIPCPVCNRKEWLAFYRDEIIECGMEQAERK

RGPKTVKYGGFPEPIRFDAKAMRSIRRLLRRGWYQGRKYDAKQLREGADK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530554.1\_1490 [locus\_tag=BN49\_RS08845] [protein=site-specific DNA-methyltransferase] [protein\_id=WP\_016530554.1] [location=1518437..1519165] [gbkey=CDS]

MIHLHNADCFEVFPQIASGTVDLVCADIPYGTTQCRWDSVLDLTLMWKQLYRIAKPSSAIVLFSAQPFTS

VLVNSNLRDWRSEWIWEKPHATGFLNAKKQPLRAHENIEVFYRRQPTYNPQMTHGHARKTATRGTPNTDV

YGEALKKVTYDSTSRYPRDVQKFSSDKQKQSLHSTQKPLALVQYLIETYSNPGDTVLDFTMGSGTAGVAC

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MTDITELAQREKFENWARSQQLSLAYGDCGYFYSSTEMAWRAVKAQSAELVEALEKAKGMETYWKTQCRG

ITDHCEELQARIAQLESRTVTAAAADVLAERKRQVTREGWTPEHDDQHVNFEMAIAGGLYAISAVDSHHK

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530698.1\_1492 [locus\_tag=BN49\_RS08855] [protein=hypothetical protein] [protein\_id=WP\_016530698.1] [location=1519734..1519922] [gbkey=CDS]

MKMGEHMEPVIELLEELNGNNTDAKLKLLALVISEYMLNADVTGFEVTAGKMKVSVDISAEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530699.1\_1493 [locus\_tag=BN49\_RS31395] [protein=hypothetical protein] [protein\_id=WP\_016530699.1] [location=1519927..1520829] [gbkey=CDS]

MTKSTITREESVQAVFDLKVGYRLGFADIEILKRVARIALAAMDSEPVAYTDDELNAALQLHRLKVDGHS

QLSDAFRAGFRYTRRTTAQSAVESDFIPKNLDKALGVLAMAIPESREEFNFQTERWIQRLIDRVIRYADE

FQEQPAPAVPEEKPIPNTLSMYAVDAVAAIAEVKGWNACRTAMLQASNSPAQSDCFPAQNHVSPEQNSVD

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MTIAIDRLKEVTRDFGRRHIAYQMARELLEIYSGNGPLVWNVLSDFPPEVNGKYLVISSYGDIRTACYDC

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MKQQFCLINDNVKRNVVNFIQSLPVDHRSPLIIEAREESRTDKQNRLMWPLLKDLSDQVIWHGEKLEPAE

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ELRPNGYYKAQAQKAFNAYIRARDAALPCISCGETNPPDLHGGQWDCGHFKTVGAYPELRFEERNAHKQC

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A

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MSKSEKSITQELLRTLLEYDPQTGIFRWKIKASSSAHPGDIAGCIDGQGYRVIRIYGKNRKAHRLAWLYV

YGDGPEVIDHIDRNRSNNAIENLRAVTFSQNSANRAAKSKNKSGFTGVYWNELGKKWQASIVAKGRTHYV

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MNTQYLQYVRQQLIVATADLSGATKGQLVAFAENAQFTATARSRGRKKVADPVTGRMVNPSSPPIPGQQS

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MQRMNPTDGHNLPYWWSALLGIFSVLSLQDYVFIIGALISAFFTIKTYYAKRKEERERLDEEKKRTQLLA

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MTPSMRKKLIGVIAGGGGAIAIASALITGPTGNDGLEGVRYNPYQDVVGVWTVCYGHTGKDIMLGKKYTE

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MTRLTAIVSAVIISLIASMAWAIHHYRDNAITFKEQRDKATVRAETAETVSNSVVTAMNLINDISRVTQN

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MAENDNRRPYPPVNFTGENWLPYTRLIPATEIGEWVNQNILSEEGRIHNPDHAHLLEADVAFMWASGSFA

KSGRIVLGQCEQVMMRAGGWQKSRMEQQMHEWFGRIPKFIITLAADYCEQCNDLEFCALVEHELYHIAQA

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A

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MAALKGEVKAFIVQSLACFDTPSQVVESVKKEFGLSITRQQVESHDPTKANGRGLAQKWVAMFNATRERF

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MTTAEQKAFARKVECEEDGLYYARYFFKQRTGGKMIVAPHHKVIQKTLDRVIDGEIQRLIINVPPGYTKT

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GVYASSATGQVTGFRAGHMEPGWQGALIIDDPVKPDDAYSEIVRDGVNNRFNETIKSRLAIETTPMIVIM

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MERDIEARYYSIKVALKALFDQRLTGREREVNSHNWHFLCHDRGEDMRLYQVNAGKFIYDMSAQELADLL

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IDDSTVTLVGDSVEVVRKPTEYEVKTNGETNPMKEKMIAALNAAGVKTEGLTDDQVWDAYNQQVQKKAGD

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MALAPRFHTVIAGPARKNDPQVIEAIMAAAVKPGSLVMLDSTGKLAVHNVAGGAGVALALQHNYIGGGDI

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EWREWNGMQSENLDAMADDQEAHVAAIRADMADYMLSGDAKVKVKGYVGAGITNHANTNQVDLGASGLNI

DLTTSTPNESVAFFTGPFAKLLDDNYVQEKVKVWASPDIMRNLNRPYSDAAGFKEGTVLEYILRYGRIES

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AEQAEQAEQAEQAEQAEQAEQAEQAEQAEQAEQAEQQEESASKSKKAK

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MADPITAADVQAFLGELGYAIPAALLDPILCVVNKIIPCLDGAGYDECTAKLILMYAAALMATSSGARRI

KSQGAPSGASRSFDYGDDGITWLRDSLAKLDTSGCTSELPISAGNSVGLFMVVGGC

>lcl|NZ\_FO834906.1\_prot\_WP\_016528892.1\_1515 [locus\_tag=BN49\_RS08970] [protein=hypothetical protein] [protein\_id=WP\_016528892.1] [location=1535580..1535753] [gbkey=CDS]

MAWVSVQQRLPRTFTRVWVITDTGQQTTAYVKSDGEWFINCDRIRATGAVVLRWRDD

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528890.1\_1517 [locus\_tag=BN49\_RS08980] [protein=hypothetical protein] [protein\_id=WP\_016528890.1] [location=1536118..1536486] [gbkey=CDS]

MGAKVRGIRQAKANLDRIIKDVQGRKVVRAIQSAMLIGSAQAALYTPIDTSTLINSQAREITVNGTLVTG

RVIYSANYAVYVHDPAVKQNFTRATARKEFLTKGFEDTRSQIDAVVKRELSL

>lcl|NZ\_FO834906.1\_prot\_WP\_016528889.1\_1518 [locus\_tag=BN49\_RS08985] [protein=hypothetical protein] [protein\_id=WP\_016528889.1] [location=1536483..1536866] [gbkey=CDS]

MTPPMYMRLKDLFVAEGLTAGFKVQWRQWRDTGKDADQFIVFRPSGGTNIEYDRGGDWYVMVDVVSSKAN

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528888.1\_1519 [locus\_tag=BN49\_RS08990] [protein=immunoglobulin domain-containing protein] [protein\_id=WP\_016528888.1] [location=1536925..1537689] [gbkey=CDS]

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TDISTFSGEWKVADADTVVFEVAPPALAFTTNLPTTKSVAAGSALNMSVVVEGGRAPYTYVWKKDGTVVS

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528886.1\_1521 [locus\_tag=BN49\_RS09000] [protein=Panacea domain-containing protein] [protein\_id=WP\_016528886.1] [location=1538758..1539330] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_223177200.1\_1522 [locus\_tag=BN49\_RS28790] [protein=hypothetical protein] [protein\_id=WP\_223177200.1] [location=1539459..1539779] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_174893426.1\_1523 [locus\_tag=BN49\_RS31265] [protein=hypothetical protein] [protein\_id=WP\_174893426.1] [location=complement(1539822..1540289)] [gbkey=CDS]

MFRLDRKRQLLTLQILFNAYPRSLDDENKDELRELYDSHDDFLANLLYLEEHGLIVSGVRPVADGFRYNT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530532.1\_1524 [locus\_tag=BN49\_RS09010] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016530532.1] [location=complement(1540292..1541155)] [gbkey=CDS]

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FPPGTIVTFDSSLEAVSGDFVMCVLNDDSEAAFKQLILDQHQIYLKPLNRLYPMFQPDFIEIVGVAIHSQ

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RELMSMFPRLGESANQVIVATLVNPLLGHEVVPLPAIEEHYSTAGEVAAQLGCTANKIGRVANKHNLKTE

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MKKKILIFLCVLIISACGDKTESQLKNEAKETVTKKLSQNYKPDECRNWKVMASSGLAPMGRTVAICDDG

FNVSKGLTFSDLSVYRNDDGYVVCGIVSGQSDISRIGARFVYAVDSKNSLFIKMSKYPMFLSGGSTSRQL

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WQELSQQSLGYNMLTSAVDAFSGNASNAITGLLTGTMSAQEAMRSLGNTILNSVINSIVQVGVEALKNYI

LGQTLGAASVATSVGLAATTASAWAPAAAMASLASFGANAGPAAAGISSTVGLASGLALAGARYNGGQVS

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MATVQYPPFLPLPQRADQNMTQDTAWQTTQTAVGPLIITPITTDLKATWTLQWIFTLAQAERFKSWLRSP

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MPTLREWKERRPASDIKQTVEFYHPAFGYYRVVNNLFRPATFGGNSFEPARFSVTEPAQDGTAVISMTIT

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MTQDEFIRLVTGKPWANRSCSFGSMDCWALVVLYYRHVLGLELHHIPAYEAGADFITCHEQEVEHWRTIP

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ICNVARVSFNWIGDVLTFWRDERVSNPDAVFARSNMFWEDYKLSWKMSLPGGYDGVTLDYVDPSTNKKTY

IYLNVGTSGISEISDATVNAMQISLDGCRNATQATDRAWLEARKILYSRLTMTVKVLESTQVVRGTVVQC

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GDLYKLAGMNPGSAPRETGSQYTDGDSFLGSSYMLDRLGLNPDSDYRFLGDAAFDTRYVSNVVLNQTGSR

YLDGLGSDLDQMRYLMDNAADVQTTLGLTFGVALTAAQVAALNRSILWWEPATLNGRTVMVPKVYLSPKD

VSVRNGSVISGNTVQLAGGNISNSGSTLLARDGLAIDSSNSFSNLNAGLIRADGRLDLSASGDINNIGST

ISAKTLQLVSTGGSINNVTRTEQWRVGDDNRWGNIQFSGTDSEQTAAITASDGLYMAAANTINITGATVS

AGGDLAMETGSNINIAANQFTESRSQSGFWGQKHSRSSSTTYQSSSITAGGNAIMRAGSDLNVTASAINA

GHTAQLVAANDLNLNAAGNEQSSRTGGSESHQSGADRSTVTAGDKVTLVAGRDVTSQAAGIAAEGNVGIQ

AGRDVNLQAEATTAGSSSHSGKKTVIDESVRQQGTDIASGGSTTIIAGRDVNAEAAQVTASGNIGLAAGR

DVNLTTATESDYHYKEETKTKKGFLSKKTTHTIEEESATREAGTLLSGDQVQVLAENNLLLQGSAVVGEG

DVQLHAGNNVEITAATNTDTAWRFKEEKKSGLTGTGGIGFSIGSSKTTHELREAGTTQSQSASTTGSTGG

SVVISAGKQAHIDGSDVVAGRDIRITGDSVVIDPGHDTRTVDEKFEQKSSGLTVALSGSAGGAVNNAVSA

TQKAKESSDSRLSALQGTKAALSGIQAAQAVALDGARGGSDKDNNNTIGISASLGSQSSSSRSHSEQVMT

SGSTLNAGNNLAVTATGGDITVAGGQMKAGKDVTLDAFRDVNLRASQDTQQTTGSNKSSGGSIGVGIGAG

AGGAGISISANASSSKGHESGNGTWQNETTVDAGHQVIISSGRDTTLAGAQVSGHQVTADVGRDLTITSL

RDSDHYDSTQSSLSGGLGYTFGAGSWSGSLNASRDKMTSDWSSVQEQSGIFAGQGGFDVSVGSHTQLNGG

VIAATGSADKNSLNTGTLGFSDIHNQADYKTQHQGGGISTGGSIGSQFAGNMTSALLAGGGSKGHAEGTT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531314.1\_1543 [locus\_tag=BN49\_RS09095] [protein=hypothetical protein] [protein\_id=WP\_016531314.1] [location=complement(1566140..1566679)] [gbkey=CDS]

MPLPERLQPAKVNRQKLKQLADMAEEILAQIDNGAKEEDTGLKMLINDWNSQVINPYAFSDFRDFSSWTS

AKDFTGMAFNQEKYVADLSWDELIQIIQFVCQAEGKESEQSYALGLLEKNFDANPSDLIYWPNEWFQDKD

MLHVDLTPEEIAGYLMAKSGRWLSDAPQIELKYPIPSNS

>lcl|NZ\_FO834906.1\_prot\_WP\_002892366.1\_1544 [gene=uraH] [locus\_tag=BN49\_RS09100] [protein=hydroxyisourate hydrolase] [protein\_id=WP\_002892366.1] [location=1567061..1567462] [gbkey=CDS]

MKLVIASVISLLSFSALAAPEGTLSVHILNQQTGLPSPGVQIELDKQQGESWQHIATGKTDADGRIKSLY

PQAENMEPGVYKVTFKTGDYFKSQNMNTFFPVIPVIFNVTKQNQKLHIPLLLSQYGYSTYRGS

>lcl|NZ\_FO834906.1\_prot\_WP\_002892370.1\_1545 [locus\_tag=BN49\_RS09105] [protein=hypothetical protein] [protein\_id=WP\_002892370.1] [location=complement(1567541..1567711)] [gbkey=CDS]

MSGLINPHAAPEEAAYALLIELVRAQRVPQYEGEISGLLAMYDEAVKHFKEKETER

>lcl|NZ\_FO834906.1\_prot\_WP\_020804400.1\_1546 [locus\_tag=BN49\_RS30935] [protein=hypothetical protein] [protein\_id=WP\_020804400.1] [location=1568036..1568176] [gbkey=CDS]

MPLSGGGLGKDGLFPREGQQNILFVRVIVMTSMNKRHHIGYVGLSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004147414.1\_1547 [locus\_tag=BN49\_RS09115] [protein=citrate synthase] [protein\_id=WP\_004147414.1] [location=1568222..1569526] [gbkey=CDS]

MSTTPLTLSFAGQQPPIALPQVPGTRGPVGVDMRGLNQSGFCSYDPGFANTAGCQSAISWIDTENSVLLH

RGYPVDQLARQCDFLEVAYIMLNGDAPDEASYQTFRETITRHTLVHEQIARMCSGFRRDSHPMALMCALV

GALAAFYHDVLDVENPQHRALAATRLLSKMPTIAAMSYKYTIEQPAAYPRNDLSYAGNFLQMLFAIPAEK

YVLNPVIEQAMNQILVLHADHGQCASTTTVRAAGSSGANLFACVAAGLASLWGPMHGGANESSMRMLEEI

ESVDQVPAFLRQAKRDPQAFRRLGFGNSRYRHRDPRADILRETSHRVLAEVGMSDRLLQVAMALEDVALT

DPYFVDNGLSPSVDFYTAVILKAMNLPSSMFAVVTAVGRTVGWVAHWNEMHQAPLTIYRPRQIYVGEGYR

DYVSRRGERSAELR

>lcl|NZ\_FO834906.1\_prot\_WP\_002892375.1\_1548 [locus\_tag=BN49\_RS09120] [protein=hypothetical protein] [protein\_id=WP\_002892375.1] [location=complement(1569579..1569884)] [gbkey=CDS]

MKSYLYAKNRLMLIILSWLSADEALPSRHDFQQTETILSTLHIPYVLKPDLDQLRATLQQLLATPRPQAC

EVGAFLSALLALYTRLTEYTAVEHYLLSRHL

>lcl|NZ\_FO834906.1\_prot\_WP\_002892378.1\_1549 [locus\_tag=BN49\_RS09125] [protein=LuxR C-terminal-related transcriptional regulator] [protein\_id=WP\_002892378.1] [location=complement(1569862..1570524)] [gbkey=CDS]

MLICIADSEYFNIALKAYINEPNSKPLDIKEILCYPFSGQSEMFYTFFATDAGARLSTILIDYSSVSIEV

LQVALSLKSFNPLIRIFIFAKSGYPLSELERSLAIVLGAEFITSFAGLSAALARGPRLTSPPADKLYIAI

PDSYNLTRKETFLISLLMGGMPLCHVASTMQLTIKRVYYYRSRVLSKLAVKNNVELMNKVQGMVLRHYRQ

ETGHEIVSLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529341.1\_1550 [locus\_tag=BN49\_RS09130] [protein=type 1 fimbrial protein] [protein\_id=WP\_016529341.1] [location=1570998..1571558] [gbkey=CDS]

MKKYSRGMASFVVMMMLSPVAAQAADGKVTFNGEVIENTCTVVNKDKTVTLPTVQRSALSSAGETAGVVP

FTIDLTSCTPGADVSVYFEKDQYVSTEGRLKNTLSDGTEAENVDVELLNTRFTPINLAETPAVAADGTIA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529340.1\_1551 [locus\_tag=BN49\_RS09135] [protein=molecular chaperone] [protein\_id=WP\_016529340.1] [location=1571617..1572312] [gbkey=CDS]

MRRMVLALLLSSYLPSADASMVIDGTRIIFSGDKKEIAVRAPNMGETPSLTQVWVDDGRVQNQPEKDAAP

FIVLPPIVRIEPGKGQSWRLVFNGSRLPQDRESLFWFNLLDIPPEPKNGKTDNYLQLAIRSRIKLFYRPA

GVAAEKIAAEKALSWALAPTGNGLRVSNASARYITIDSITLNGQKHAVGMVAPFSSLEIAPKGVALRTLP

AKFSFTTINDYGAVVNHNYPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042821.1\_1552 [locus\_tag=BN49\_RS09140] [protein=fimbrial biogenesis outer membrane usher protein] [protein\_id=WP\_046042821.1] [location=1572323..1574758] [gbkey=CDS]

MKLREIKVGLMLLLPWQEAWAAEAFSFNRAHLHGAAQVDLQKYQYGNPLHAGQYRSTLSVNGRDLGEETF

VIQEHDGQLEPCISPSLFDALQLKDAQWPTAATCLRFSQIDKAIGWEYDSGENVLRVNMPQALLQPHYRG

AVNLKKVDSGVPAAVLRYQANSYQSIVDGDSSSHHYLGLDASLRAFGWRLHHQSSYQAQEGNTHWDSIAT

WAERSVVNWASTLRLGQGWTDGTFFDSVSFIGGRLATDVRMLPGSRRGFAPSVSGVARTNARVTVTQNGA

LLYEATVPPGKFTFDDLYPTNAGGDLQVTIHEADGSQDTFTVPYATLPGLVRAGAVYYDLSLGYLDEDGI

AGRPGFGEATLQYGFNDYISGYTGANATTDYYSTLVGSAFNTYWGALAVDLSRSAAKGREHGWQEGYRWR

VSASKSFTSDTRMLLSMSHSNDGNYRSIRDAAWEHDRHPNDWREMTRYSATLSQQAGSGSLSFNGIWSED

VRHHRWRSYQLGYANRYGQLNYYLYAQQSQDIHHRNNQVVGVSFSLPFGQAGSLTTRFNHDKNYGSQLQS

SYTGSAGEKNAFSYGLTASYDMPRENPNEASVAANGSLRTDYAYLNASASAGRHQQQYSLGASGALVAHQ

GGMTATPELGETFAIVEAPGAAGARVANRPGQPINRQGFTIIPYLDPFTANWLDLDPQGLNDHVEIVSSS

TTVVPDSGAAVKVKFVTRTGYSWFAHVTLPDGAAPPLGAEVFDDNGRAVGAVGQGGLLYARVPQDHGSVS

VVWGERSGQRCRLAYAIRDDAVQQVSSGTPHQVCRPGIKEK

>lcl|NZ\_FO834906.1\_prot\_WP\_004147417.1\_1553 [locus\_tag=BN49\_RS09145] [protein=type 1 fimbrial protein] [protein\_id=WP\_004147417.1] [location=1574760..1575785] [gbkey=CDS]

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WEIACSGSEPGGFQSIGGSRVGPAGDGKPGDIYSIDRLPGIGYSFQMGEQDGINFDPLFTAWPSAPVFSG

QRAFQAENKKPTIYFWRIADNGGLPPPGEYCLNDYLGDIYLGGVQAMRFSVSGLCIQVKSPTCKITDDSK

NINVFLGRHNKTAFTGLNSTTAPVPFNINLTNCENVGSVFMQFNATVDSAVAANEVIKIDDQPEGASGLG

VQILSAGGSLVPLNQVSQVWSGKKGSQTNYRLSYQARYIQTQPAVTAGEANASATFVVTYN

>lcl|NZ\_FO834906.1\_prot\_WP\_020316411.1\_1554 [locus\_tag=BN49\_RS09150] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_020316411.1] [location=complement(1575808..1576674)] [gbkey=CDS]

MNYQLVKQVRENNPLRKSFIDLAVKTFDLSFEEWYQQGYWTDAYIPYAFVERNKVIANASANIIDLRWQG

EPRRYIQIGTVMTEPDHRNKGLAGQLIHHILQDWQQEADAFFLFANPTTVDFYPKFGFTRSEEYQYIMPV

SPRAGDFRKLDMDSADDVALLRHYYEKSNPFSPLRVEHNFGLLMFYCSAFMKHFVYYSAKNEAVVIAMQN

GPVLICFDLFCDVGKSLSTLVNELADDHVYQAILGFTPSEDRLGEYEKIEGEDILFVYDQKENLFKDRKL

MFPLLAHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002892400.1\_1555 [locus\_tag=BN49\_RS09155] [protein=LpxL/LpxP family Kdo(2)-lipid IV(A) lauroyl/palmitoleoyl acyltransferasee] [protein\_id=WP\_002892400.1] [location=1577185..1578105] [gbkey=CDS]

MSNLPKFSRALLHPRYWLLWLGIGFLWLLVQLPYPVIYRLGTALGRLAMRVMKSRARIARRNLELCFPEM

SAADREALLVKNFESLGMGLMETGMAWFWPTHRVARWTETSGVNEVVELLEEKQGILLIGIHFLTLEMGA

RMYGMFTPGIGVYRPNDNPLIDWLQTWGRLRSNKTMLDRKNLKGMVRALKEGEILWYAPDHDYGPASSVF

APLFAVEQAATTTGTWMLAKMSGATIVPFVPRRKPNGMGYELISLTPERTPPLASAEVTAAWMNQIIEQC

ILMAPEQYMWLHRRFKTRPEGVPPRY

>lcl|NZ\_FO834906.1\_prot\_WP\_002892402.1\_1556 [locus\_tag=BN49\_RS09160] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_002892402.1] [location=1578206..1578478] [gbkey=CDS]

MKKVIVALALSAVAFGASAAQLITKEEVKHFKLTKVGPISVGPSGGEFSSPSDLHDQLSKLADEKGGKYY

VITAAREHGPNFEATAEVYK

>lcl|NZ\_FO834906.1\_prot\_WP\_004147422.1\_1557 [gene=cadC] [locus\_tag=BN49\_RS09165] [protein=lysine decarboxylation/transport transcriptional activator CadC] [protein\_id=WP\_004147422.1] [location=1578772..1580340] [gbkey=CDS]

MLQPVVRVGEWLVTPSVNQISRKGRQLTLEPRLIDLLVFFARHPGEVLSRDELIENVWTRNVVTSHVVTQ

SISELRKSLKDGDDVSLEYIATVPKRGYKLTVPVIWCTEEGEELAPSMEALTPSPSTAVPAPPAAGAPSD

VSVPLPDAAAPPPAPTVASAPSGRKRLTTALVWGLFLLALGTCVALVALSSMESRPPVNKARLLLNPRDI

DIHLVNGNSCANWSSQHSYAVGLASLITTSLNTFSTFMVHDKTDYNINEPSSSGKTLTIEFVNQRHYRAQ

QCFMSVQLVDNADSSTMLDKRYFVTNDNQLTIQNDLMNSLSDALAQPWPARMQAMLRQYQPSQSVALTYF

YQSHQLLMKGDVDSLSKASSLLDDVIKRAPDFIYAYAEKTLVDVLRHSQQPLDDKQLAALYSEVERVGAM

PGIKDMAIYYQIKAVDSLGKGKVDEANTAINSAIDLEMSWLNYVLLGKVYEMKGENRLAADSYITAFNLR

PGEDTLYWIENGVFQTSVNRVVPYLDNFLSSE

>lcl|NZ\_FO834906.1\_prot\_WP\_002892484.1\_1558 [gene=cadB] [locus\_tag=BN49\_RS09170] [protein=cadaverine/lysine antiporter] [protein\_id=WP\_002892484.1] [location=1580706..1582040] [gbkey=CDS]

MSSAKKIGLFACTGVVAGNMMGSGIALLPANLASIGGIAIWGWVISIIGAMSLAYVYARLATKNPQQGGP

IAYAGEISPAFGFQTGVLYYHANWIGNLAIGITAVSYLSTFFPILNNPVPAGIACIAIVWIFTFVNMLGG

TWVSRLTTIGLVLVLIPVVMTAVVGWHWFDVATYQANWNTSSTTDSHAVIKSILLCLWAFVGVESAAVST

GMVKNPKRTVPLATMLGTAMAGIVYIAATQVIAGMYPASQMAASGAPFAISASTILGGWAAPMVSAFTAF

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>lcl|NZ\_FO834906.1\_prot\_WP\_002892486.1\_1559 [gene=cadA] [locus\_tag=BN49\_RS09175] [protein=lysine decarboxylase CadA] [protein\_id=WP\_002892486.1] [location=1582123..1584270] [gbkey=CDS]

MNVIAIMNHMGVYFKEEPIRELHRALERLDFRIVYPNDRDDLLKLIENNSRLCGVIFDWDKYNLELCEEI

SKMNEYMPLYAFANTYSTLDVSLNDLRMQVRFFEYALGAAEDIANKIKQNTDEYIDTILPPLTKALFKYV

REGKYTFCTPGHMGGTAFQKSPVGSIFYDFFGSNTMKSDISISVSELGSLLDHSGPHKEAEEYIARVFNA

ERSYMVTNGTSTANKIVGMYSAPAGSTVLIDRNCHKSLTHLMMMSDITPIYFRPTRNAYGILGGIPQSEF

QHATIAKRVKETPNATWPVHAVITNSTYDGLLYNTDFIKKTLDVKSIHFDSAWVPYTNFSPIYEGKCGMS

GGRVEGKVIYETQSTHKLLAAFSQASMIHVKGDVNEETFNEAYMMHTTTSPHYGIVASTETAAAMMKGNA

GKRLIDGSIERSIKFRKEIKRLKGESDGWFFDVWQPEHIDGPECWPLRSDSAWHGFKNIDNEHMYLDPIK

VTLLTPGMKKDGTMDDFGIPASIVAKYLDEHGIVVEKTGPYNLLFLFSIGIDKTKALSLLRALTDFKRAF

DLNLRVKNMLPSLYREDPEFYENMRIQDLAQNIHKLIEHHNLPDLMFRAFEVLPSMVMTPYAAFQKELHG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151795.1\_1560 [gene=dtpD] [locus\_tag=BN49\_RS09180] [protein=dipeptide permease DtpD] [protein\_id=WP\_004151795.1] [location=1584330..1585805] [gbkey=CDS]

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LLYAAGNVGSIAAPIACGLAAQWYGWHIGFALAGIGMFIGLMIFLSGSRHFRHTRGVDKPALRAVKFVLP

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AQQGGSSISLFIDHFVNRRLLNWDVPTALFQSVNAIAVMAAGVVLAWLMRPEGSVRSVLRVWLKFSFGLL

LMGGGFMLLALNARHGAADGQASMGMMVAGLAMMGFAELFIDPVAMAQITRLNMPGVTGVLTGIYMLATG

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A

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MSEQQAQGADEAIDLNNELKARREKLAALREQGVAFPNDFRRDHTSDQLHAEFDAKDNDELASLNVEVAV

AGRMMTRRVMGKASFVTLQDVGGRIQLYVARDDLPEGVYNEQFKKWDLGDIIAARGKLFKTQTGELSIHC

TELRLLTKALRPLPDKFHGLQDQEVRYRQRYLDLIANEESRHTFRIRSQILATMRQFMVARGFMEVETPM

MQVIPGGASARPFITHHNALDLDMYLRIAPELYLKRLVVGGFERVFEINRNFRNEGISVRHNPEFTMMEL

YMAYADYKDLIELTESLFRTLAQTVPGKTEVPYGDQVFDFGKPFEKLTMREAIKKHRPETNMADLDNFDA

AKALAESIGIQVEKSWGLGRIVTEIFDEVAEAHLIQPTFITEYPAEVSPLARRNDVNPEITDRFEFFIGG

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MNKTWLFTTLTLALVAAAPAHAISAKYREQLERSGCTQMTDGTTCDIHKTKAENAAAAQHASSGFAPWVG

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L

>lcl|NZ\_FO834906.1\_prot\_WP\_016532364.1\_1563 [gene=iolE] [locus\_tag=BN49\_RS09195] [protein=myo-inosose-2 dehydratase] [protein\_id=WP\_016532364.1] [location=1588728..1589648] [gbkey=CDS]

MATEQLRWGVSPLCWTNDVLEDLGGDIPLDTCLREAREAGYQGIELGRKFPRQASTLGPLLAAADLRLAS

GWYSGMLADRSVEAELEAVREHAQLLRQLGAKVMVYGECGQLPGETPLDEPISLSPPLSRVSLAAYCHKL

NTFADLLLRDYDLQLAYHHHLMMLVEHDEELERFLSHTHDNVGLAFDTGHAFVAGVEIPRVLHKYGHRIR

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042840.1\_1564 [locus\_tag=BN49\_RS09200] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_046042840.1] [location=1589645..1590817] [gbkey=CDS]

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GTEGTLYMDGERFNELQVYRFNDDKHDRGFKTLYAGSQIPAYAGFFGFDFGGGGLGYFDVKVIEVHDLVQ

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MFPSHLPTPRRPAAQSIPILRWGIIGPGWIAERFVHSLKTYSRQQVVAVVSRSQAKADRVAAEWGIPQAY

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CDYAPKYDVIRQLLEDGALGDLHTLLADHGEYFTRDHRIFNADLAGGPMMDLGSYVTSFALMVGGMPQEI

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MICKRFALVGSGFIGQVHAASLARHEGSALTMVADTAPERAQALAARYGARAVTVSEAIHSDAIDAVLIA

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IGRVELVQMVCRASSMPPLDYLRSSGGQMRDQAIHFFDLLRFLTGDEVRTVAAMGAALALPDIAEFGDVD

TSILMMQMRGGALAQLDNTRRTGHGYDERITLLGAEGALESGSQSPAGPTLWRGNQRIEPGLWPDWFSRV

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LAKAMNGKGNVAILLGDLANESTRDRTKGVEEVVAKYPNIKIVQKQTAKFTRNDAVDVVSNWMTSGEDIQ

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MNAFALEAEGISKFFPGVKALDNVSLRVRPGTVHALMGENGAGKSTLMKCLIGIYRPDKGSIRVKGEPVE

FTDTMDALRSGISMIHQELNLVPHMTVAENIWLGREPMKYGFVDHGQLTRQTQALLDKLNIRLTADRLVG

DLSIAAQQMVEIAKAVSWNADIVIMDEPTSALTEGEVAHLFTIIRDLRAQGKAIIYISHKIDEIFAITDE

ISVFRDGTWVGSKNTTEFTRQSLITQMVGRELTQLFPKFNNTIGEEVLTVRNLTRQGVFHDVSFSVRRGE

ILGVAGLVGAGRSEVMESLFGMERFDSGEVLIDGAPVTIDSPSVAIEKGMALLTEDRKKSGLFLVLSVLE

NMSIVKMPEYIGKSGFVQHVKMAEDCMEQIRRLNIKTPTMDQIINNLSGGNQQKVLIARWLLAQPKILIL

DEPTRGIDVGAKAEIYHLISELANRGVAVIMVSSELPEILGMSDRVMVMHEGRITGILEKDEADQETILS

LASH

>lcl|NZ\_FO834906.1\_prot\_WP\_004152946.1\_1570 [locus\_tag=BN49\_RS09230] [protein=ABC transporter permease] [protein\_id=WP\_004152946.1] [location=1597684..1598706] [gbkey=CDS]

MKLTAAPASEGSSFFANLRHKMPKDTGIFVVMLVIALTFEIAGWYVRDQSFLLNTNRLVLIVLQVAIIGI

IAVGVTQVIITTGIDLSSGSVIALAAVVAASLAQTSDSLSPMFPALVNLPAVIPICAGIGVGLLCGLTNG

FLVTRTGIPPFIATLGMMVSARGLAQYYTQGNPISFLSDSFTAIGQGAMPVIIFFVIAAVFHIALKHTRY

GKYVYAIGGNMTSAKVSGINVNKYLVIVYTIAGALSGLAGVVLAARVSSGQSSMGMSYELDAIAAAVIGG

SSLMGGVGRITGTLIGAMILGLIKSGFTFVGVDAYVQDIIKGIIIVAAVTIDMRRNRKKH

>lcl|NZ\_FO834906.1\_prot\_1571 [locus\_tag=BN49\_RS09240] [protein=hypothetical protein] [pseudo=true] [location=1598890..1599499] [gbkey=CDS]

MNTPSFGKFSPRWLAGKRGLIVTLLAGLAILALGRGMNLPAREVYRERQIRQLEEDAQWVAERLERRMNI

PAPQREATWPLAAMRAALQTLAQERHYQLLLVNGDEHLLAASHALPASVLAQVQAQFPREMQPPLFGSHY

QTIQPFAPHQRMLSRALNGNAGLAGWNLVMLAPDGGLPSLLVAYRWPVTIGLGAVLASALLAL

>lcl|NZ\_FO834906.1\_prot\_WP\_025368379.1\_1572 [locus\_tag=BN49\_RS09245] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_025368379.1] [location=complement(1599547..1600557)] [gbkey=CDS]

MLMKTKRVTIKDIAELAGVSKATASLVLNGRGKELRVAQETRERVLAIAREHHYQPSIHARSLRDNRSHT

IGLVVPEITNYGFAVFSHELETLCREAGVQLLISCTDENPGQESVVVNNMIARQVDGLIVASCMHSDADY

QKLSEQLPVVLFDRSPSDSALPLVMTDSVTPTAELISRIAPQHADEFWFLGGQPRLSPSRDRLAGFTQGL

AQAGITLRPEWVINGNYHPSSGYEMFAALCARLGRPPKALFTAACGLLEGVLRYMSQHHLLDSNIHLASF

DDHYLYDSLSLRIDTVQQDNRQLAWHCYDLLSQLIDGQAPEPLQRYLPATLQIRHP

>lcl|NZ\_FO834906.1\_prot\_WP\_004199626.1\_1573 [locus\_tag=BN49\_RS09250] [protein=sucrose-6-phosphate hydrolase] [protein\_id=WP\_004199626.1] [location=complement(1600581..1601981)] [gbkey=CDS]

MSLPSRLPAILQAVMQGQPQALADSHYPQWHLAPVNGLLNDPNGFCQVAGRYHLFYQWNPLACDHTYKCW

GHWSSADLLHWRHEPIALMPDEEYDRNGCYSGSAVEFEGALTLCYTGNVKFPDGGRTAWQCLATENADGT

FRKLGPVLPLPEGYTGHVRDPKVWRQDGRWYMVLGAQDVQQRGKVLLFTASDLREWRLVGEIAGHDVNGL

ANAGYMWECPDLFPLADTHLLICCPQGLAREAQRFLNTYPAVWMAGRFDAERGIFDHGPLHELDSGFEFY

APQTMQADDGRRLLVGWMGVPDGDEMHQPTRAQGWIHQMTCVRELEWQAGTLYQRPLRELVALRGEAQGW

CGQTLPLAPMELAFDIAPNSTLGLDFAGALQLTVNRDGLRLSRRGLQTAEMHHRYWRGEARRLRIFIDRS

SVEIFINDGEGVMSSRFFPGYPGQLIFSGATPVAFCRWLLRPCMVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002892640.1\_1574 [locus\_tag=BN49\_RS09255] [protein=sucrose-specific PTS transporter subunit IIBC] [protein\_id=WP\_002892640.1] [location=complement(1601981..1603351)] [gbkey=CDS]

MDFEQISRSLLPLLGGKENIASAAHCATRLRLVLVDDALADQQAIGKIDGVKGCFRNAGQMQIIFGTGVV

NKVYAAFIQAAGISESSKSEAADLAAKKLNPFQRIARLLSNIFVPIIPAIVASGLLMGLLGMVKTYGWVD

PSNALYIMLDMCSSAAFIILPILIGFTAAREFGGNPYLGATLGGILTHPALTNAWGVAAGFHTMNFFGIE

VAMIGYQGTVFPVLLAVWFMSMVEKRLRRVIPDALDLILTPFLTVIISGFIALLLIGPAGRALGDGISFI

LSTLISHAGWLAGLLFGGLYSVIVITGIHHSFHAIEAGLLGNPSIGVNFLLPIWAMANVAQGGACFAVWF

KTKDAKIKAITLPSAFSAMLGITEAAIFGINLRFVKPFIAALVGGAAGGAWVVSMHVYMTAVGLTAIPGM

AIVQASSLLNYIIGMAIAFAVAFALSLTLKYKTDAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004147437.1\_1575 [locus\_tag=BN49\_RS09260] [protein=carbohydrate porin] [protein\_id=WP\_004147437.1] [location=complement(1603456..1604973)] [gbkey=CDS]

MYKKRKLAILIALLTGTAAAHGQTDLNSIEARLAALEKRLQDAETRASTAESRAASAEQKVQQLTQQQQQ

TQATTQQVARRTTQLEEKAERPGGFEFHGYARSGVIMNDSAASTKSGAYMTPAGETGGAIGRLGNQADTY

VEMNLEHKQTLDNGATTRFKVMVADGQTTYNDWTASSSDLNVRQAFVELGNLPTFEGPFKGSTLWAGKRF

DRDNFDIHWIDSDVVFLAGTGGGIYDVKWNDSLRSNFSLYGRNFGDIADSSNSVQNYIVSMNNFAGPVQM

MVSGMRAKDNDDRQDANGNLVKGDAANTGVHALLGLHNESFYGLRDGTSKTALLYGHGLGAEVKGIGSDG

ALRPGANTWRFASYGTTPLSDRWFIAPAVLAQSSKDRYVDGDSYQWATLNLRLIQEVTQNFALAWEGSYQ

YMDLQPEGYNDRHAVNGSFYKLTFAPTFKVGSIGDFFSRPEIRFYTSWMDWSKKLDNYANDDALGSNGFK

SGGEWSFGMQMETWF

>lcl|NZ\_FO834906.1\_prot\_WP\_004177006.1\_1576 [locus\_tag=BN49\_RS09265] [protein=aminoimidazole riboside kinase] [protein\_id=WP\_004177006.1] [location=complement(1605138..1606061)] [gbkey=CDS]

MNGKIWVLGDAVVDLLPDGEGRLLQCPGGAPANVAVGVARLGGDSGFIGRVGDDPFGRFMRHTLAQEQVD

VNYMRLDAAQRTSTVVVDLDSHGERTFTFMVRPSADLFLQPEDLPPFAAGQWLHVCSIALSAEPSRSTTF

AAMEAIKRAGGYVSFDPNIRSDLWQDPQDLRDCLDRALALADAIKLSEEELAFISGSDDIVSGIARLNAR

FQPTLLLVTQGKAGVQAALRGQVSHFPARPVVAVDTTGAGDAFVAGLLAGLAAHGIPDNLAALAPDLALA

QTCGALATTAKGAMTALPYKDDLQRSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151802.1\_1577 [locus\_tag=BN49\_RS09275] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004151802.1] [location=1606300..1606941] [gbkey=CDS]

MNPSFGDIYDRYQKLTLTTHLPAVIACSETLSLGKDQGFIPQPGYLYFLLQGQMTLAFGDEQNLVGIVIA

HMPLGLLEHYCPSVALYYQCLGECQLAKITASDFERIFFHSSPGYMQELTTILAYMGIFALDAHYERGSQ

TSFQTIKSMLSRYLYRGEIDGGQHESLSAFIIKRTNLSRSYVYQVLAALREGGYITVKKGKLISIDRHIP

EKF

>lcl|NZ\_FO834906.1\_prot\_WP\_002892695.1\_1578 [locus\_tag=BN49\_RS09280] [protein=DUF3302 domain-containing protein] [protein\_id=WP\_002892695.1] [location=1607077..1607421] [gbkey=CDS]

MTLDYVALAILIAVALILFYGVIVIHDIPYEIAKERRHPHQDAIHYAGWVSLFTLHALWPLLWIWATLWR

EDRGWGMRHIADEQQALHQRLETVVQQLEQVQREVDVLKAKEAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002892697.1\_1579 [locus\_tag=BN49\_RS09285] [protein=HlyD family secretion protein] [protein\_id=WP\_002892697.1] [location=1607421..1608563] [gbkey=CDS]

METLMLLTYAALCIVVFKVFRIPLNKWTVPTAVLGGIALIGAVIFGMNYNFPYTDVGNQVFRTVPIVSQV

RGRVQSVPVKPNQMLHKGDVLFTLDPTPFQAKVDDLQAQIKAASQDALSLNAALSQAQAELSRAVAQRDQ

SRREYARYREGHAQGAFSDQMVDTRLQTWKADEASVSAAQAKVVQARNALDSVVKGKNTTVASLLAQLQK

AQFQLENTVVRAPEDGYVSTVGLRPGTMSTALGMIPLMTFVPVEGAASREYVAAFRQNALQRLHKGEPAE

LMFPAIPGTVFRGEVADVLPAIGESQFQGQGKLLTTDALNTHGRALVVLKVTDPRFAEYALPQGATLEAA

VYSDHLKELSLIRKILIRMKSWENYIYLDH

>lcl|NZ\_FO834906.1\_prot\_WP\_002892698.1\_1580 [locus\_tag=BN49\_RS09290] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_002892698.1] [location=complement(1608604..1609401)] [gbkey=CDS]

MSDQTLSGLSLSHFSAGYPRRKVIENLTVPHLPRGKITALLGPNGSGKSTLMRAMAGLGPCRGELLLEGE

NLLTQPFSRRAEQVVYLPQTLPAGVHLHVLESIIVAQRAAGGRHSPQRQEEVMALLRQLGIAHLAMSYLD

QLSGGQKQLVGLAQSLIRQPRLLLLDEPLSALDLNYQFHVMDLVRRETRRRNIVTLVVVHDINIALRHAD

HVLMLKAGQLLGDGTPAAVITPETLAAVYGVRGRIEPCSQGVRQVIIDGLVDSEA

>lcl|NZ\_FO834906.1\_prot\_WP\_072143255.1\_1581 [locus\_tag=BN49\_RS09295] [protein=iron ABC transporter permease] [protein\_id=WP\_072143255.1] [location=complement(1609398..1610426)] [gbkey=CDS]

MMDDYRRIVRRRLLLILLLALLIVASLLLDFMLGPSGLPLQSLWQTLTDPASADPGTRAIVWDIRLPYAV

MAIIVGLALGLAGAEMQTILNNPLASPFTLGVSSAAAFGAALAIVLGIGLPGIPGQWFISANAFIFALLA

ALLLDGITRWTQVATSGVILFGIALVFTFNALVSMLQFIANEDTLQGLVFWTMGSIDRASWSKVAILLVA

LALVMPLSLRSAWKLTALRLGEDRAISFGINVRRLRLTTLLRISILSALSVAFVGPIGFIGLVAPHIARM

LFGEDHRFYLPASALIGALVLSLASIASKNLIPGAIIPVGIVTSLVGVPFFLSIILRHRGQV

>lcl|NZ\_FO834906.1\_prot\_WP\_023312805.1\_1582 [locus\_tag=BN49\_RS09300] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_023312805.1] [location=complement(1610487..1611605)] [gbkey=CDS]

MARKSVRSLLLTALLATPLLSYATQYPLTVTDLDGRQVTLAKEPQRIILQDGRDIMTLALLDRDNPFKRL

VAWNNLAKKQDVATWQMLKTTWPQSATILDMGFSDKGNVDLESVIARQPDLMIAQLRARPALMESGVIDK

LSALHVPVLFVDYEIAPAKDTAPSIDLLGKVLNRESQAKAFTDYYSQQLQTIRQKTAAITPKANVFVEAL

AGNSDACCFTHGHSGWGGLVEAVGANNIGSQLLPGASGFVSLEKIISMKPDAWIMTGSKRGNSQVLPLGY

AVKPEAVKAQAQTLLARPGVSQIPAVQEKRAYGVYHHFYNHPWNIVGMEYLAKDIYPQAFGDLNPDETYH

YIVRHFTDLPDQPFVFSWQQSE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529849.1\_1583 [locus\_tag=BN49\_RS09310] [protein=hypothetical protein] [protein\_id=WP\_016529849.1] [location=1611877..1612266] [gbkey=CDS]

MKKAMIALSAILVAAPVFAATTHATDDTVAAANANANTAKEKLHQAQHEGEEQQLKAKRAAEGKQDSVGS

QVSEGAQKTWNKTKEGTEKGWDKTKEVSEKGWNATKSGAEKGWDKTKTGAEELKNKVTE

>lcl|NZ\_FO834906.1\_prot\_WP\_002892701.1\_1584 [locus\_tag=BN49\_RS09315] [protein=RcnB family protein] [protein\_id=WP\_002892701.1] [location=1612435..1612890] [gbkey=CDS]

MKKMISLAVILSCVLSVPAFADGPNDGHRPGQPTVWQNGPDHDGHAPQGGPDAHHQGDHDQRGPDRDGHD

KRDLARHEQDHFAWRGNDFRKGHPAPAPFRGDEYRVRDWSDRGLPPPPEGHHWSYIDGNYVLIAAATGII

TSILVSGALGH

>lcl|NZ\_FO834906.1\_prot\_WP\_016831715.1\_1585 [locus\_tag=BN49\_RS30940] [protein=hypothetical protein] [protein\_id=WP\_016831715.1] [location=complement(1612955..1613080)] [gbkey=CDS]

MASDTASLLSKVNVYHLTEKELSTQATINGYKYWPDAALDP

>lcl|NZ\_FO834906.1\_prot\_WP\_012737575.1\_1586 [locus\_tag=BN49\_RS30945] [protein=hypothetical protein] [protein\_id=WP\_012737575.1] [location=1613043..1613180] [gbkey=CDS]

MTFESNEAVSDATPLEAAAIGALQPASATIARRKSLCNCLPVYFI

>lcl|NZ\_FO834906.1\_prot\_1587 [locus\_tag=BN49\_RS09330] [protein=M20 family metallopeptidase] [pseudo=true] [location=1613396..1614574] [gbkey=CDS]

MSDYVIPEIKATEAEMISIRHYLHANPELSLEEFNTSELVASKLT\*WGYQVTRGLGKTGVVGSLSKGDSP

RTIGLRADMDALPIEETTGLPWASTAPGKMHACGHDGHTTILLAAAKYIASPACQFNGTVHLIFQPAEEA

IGGADLMIKDGLFEQFPCERIFGLHNMPGLPVGKLGFYAGNFMASADTVKITITGYGGHGAHPERTVDPI

VAGAALVMALQSIVARNVPPGETAVVSVGTFQAGIASNVIPESAVMELSVRAMKPEIRDLLIKRIHELAD

FTAKSYGASSVVEVYDSYPVLTNSPEETDFARALALEVFGREGVLESVSPMNASEDFAFMLRERPGSYFL

LGNGEKGEKGGCMVHNPGYDFNDDIITTGATLFARLVEKHCR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042859.1\_1588 [locus\_tag=BN49\_RS09335] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_046042859.1] [location=1614594..1615370] [gbkey=CDS]

MKKSLLLWRALMASTSALAEGGKEIRFGVDPTFAPFEWKDPQGKLAGFDIDLGNAICQQLQAKCVWVESN

FDGIIPALKARKFDAILSGMYMTEKRKAQIAFSDKLYNGPVFLVARKNTLQGNTPEQLKGKTIGVEQGSA

QETYVNQHWRPQGINIVAYQGADSVVRDLESGRIDGAVLSGMMADYSFLQQPQGKEFAFVGGHLQDDTLF

GAGAAIGLRKDDEALRQEINGAIAKILADGTYKKLAGKYFSFDVYSGT

>lcl|NZ\_FO834906.1\_prot\_WP\_016530490.1\_1589 [locus\_tag=BN49\_RS09340] [protein=aldo/keto reductase] [protein\_id=WP\_016530490.1] [location=1615499..1616452] [gbkey=CDS]

MMTRPLGKTGFSIAPLVFGGNVFGWTIDEKTSFALLDAFVDHGFDAIDTADVYSRWAEGNQGGESETIIG

RWLQARPGMRDKVKIFTKVGSDLGLPGHKGLSKAWIQQAVDDSLRRLNTDYIDLYFSHWPDPQNPVAETL

EAFHSLQQAGKIRAMGASNLDAMQLAGALEVARKGGLPAWQVLQPEYNLYHRSAFEGALCDLCVSRDIGV

VTYYSLASGFLTGKYRQPSDLTQSQRGSGIGKYLNPRGMRIIDTLAAVADEQGAKPAEVALAWLIGREGV

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530492.1\_1590 [locus\_tag=BN49\_RS09345] [protein=MoaF N-terminal domain-containing protein] [protein\_id=WP\_016530492.1] [location=complement(1617002..1617793)] [gbkey=CDS]

MTSEAVFIQVGALADGFAPHGNLLATASLPAGERFTFYADGSEPQQLVIENDQTLLWNGKRAPWRATALR

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QPGPLPGFTDALIGMRNQYTYSPTERYEHIYLNDNFYAWQCLDGVEKGLADVDRCHYVQVAEDLYLFVWR

EKIIPTLGVILIDLQQMRTDGKIMGYQGSDFGALSNFPVGASAKILNVTRHQE

>lcl|NZ\_FO834906.1\_prot\_WP\_023302214.1\_1591 [locus\_tag=BN49\_RS09350] [protein=SDR family oxidoreductase] [protein\_id=WP\_023302214.1] [location=complement(1617819..1618595)] [gbkey=CDS]

MARVVVITGGGTGIGAACARLMRAAGDRVFITGRREAPLQAVADETGATALVGDAADGEVWRQRLLPTIL

DQTGGIDVLICSAGGMGNSPAAETSDRQWREALDANLNSAFVSVRACLASLIACRGNVLFVASIASLAAG

PQACGYVTAKHALIGLMRSIARDYGPQGVRANAICPGWVTTPMADEEMIPLMQEHGLSLTEAYQRVCRDV

PLRRPASPEEIAQACQFLCSPQAAIISGATLVADGGASIVDVPTLAFT

>lcl|NZ\_FO834906.1\_prot\_WP\_004893684.1\_1592 [locus\_tag=BN49\_RS09355] [protein=arylsulfatase] [protein\_id=WP\_004893684.1] [location=complement(1618683..1620416)] [gbkey=CDS]

MNKKAMAAAVSMILAGGAHAAQQERPNVIVIIADDMGYSDISPFGGEIPTPNLQAMAEQGMRMSQYYTSP

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ATPKDRGFNHAFAFMGGGTSHFNDAIPLGTVEAFHTYYTRDGERVSLPDDFYSSEAYARQMNSWIKATPK

EQPVFAWLAFTAPHDPLQAPDEWIKRFKGQYEQGYAEVYRQRIARLKALGIIHDDTPLPHLELDKEWEAL

TPEQQKYTAKVMQVYAAMIANMDAQIGTLMETLKQTGRDKNTLLVFLTDNGANPAQGFYYESTPEFWKQF

DNSYDNVGRKGSFVSYGPHWANVSNAPYANYHKTTSAQGGINTDFMISGPGITRHGKIDASTMAVYDVAP

TLYEFAGIDPNKSLAKKPVLPMIGVSFKRYLTGEVQEPPRGNYGVELHHQAAWVDGEWKLRRLVPRGLTA

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MLNIAALRQQQIPLAAEPRSPVPFHILMKPIGPACNLACRYCYYPQDETPVNKMDDARLEQFIRRYIAAQ

PAGAREINFVWQGASRCWPA\*ASTKKRSPCRRAMPPTA\*LSATACRPTGR\*STTHGADCSANMALLSG\*A

SKATKRCRTTIVRINAAGRPGRRRCAALTCSISIRWTLICWWWCITRWRPTRRRFMTGWSASARAICSFS

R\*\*AKARPCAKDTSSAPITGDVLWSASGDSGGSAAIEGGCSLSISNRRGRSISLIPAAAACTAPAAAATW

\*WSPMDSSTPAII\*STPNIGWVALTSRRSPPQLTPRCNCLSVSRKVCAANARLAR\*KWSARAAARRISTP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002892774.1\_1594 [locus\_tag=BN49\_RS09365] [protein=LuxR family transcriptional regulator] [protein\_id=WP\_002892774.1] [location=1622073..1622756] [gbkey=CDS]

MSALLKASRNDAIIARCLQTISQLIPLTSAVFYRVNNRLKPENYILHNISDNTHQQYLENFQPLDPLLPS

HFSHQNTTVAAMTPRLCDRNRHYYHEFMLPNNVRDMTEIFIRRERRIVAGISLMRDVPFSSEERQRAQAV

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ELVSRTWMPAAQRTLHL

>lcl|NZ\_FO834906.1\_prot\_WP\_020316359.1\_1595 [locus\_tag=BN49\_RS09370] [protein=MFS transporter] [protein\_id=WP\_020316359.1] [location=1622874..1624046] [gbkey=CDS]

MSSTPLTDNALSRPAGLVVSLRLLAAIVIFAAIAPGILMTAPAVAAQLASEWQLKPGQIGWLFSAELGAM

SLATLPAWWWMSRLDWRRVALTAGVVFLAANLVSAVVTQYETLLAARFIASLAGGTLMILCISCAAGTPN

PSRVYAFWVLGQLLLGMLGLLALPGLFATFGLKVVYLILAAIMLCCLPLVSAFPPRFQPLSVSRQQPSTA

LWRQALAVLAVLTFYISLSAVWTFIGTIGSAAGLSPTQVGLVLAAATVCGIIGAGGAALRGTRRADRLPV

WLGYGLLIVSVGLLIGQPLLVRYAIAALLFKFTWTFVLPFILARVAGLDNSGRLMNSINLVIGGGMAAGP

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531822.1\_1596 [locus\_tag=BN49\_RS09375] [protein=class II histone deacetylase] [protein\_id=WP\_016531822.1] [location=1624063..1625178] [gbkey=CDS]

MKRKTGFFFDERCFWHSTGLHAVTLPVGGWVQPPAGGGHAESPETKRRMKNLMDVSGLTPQLALRSAAPA

SLEDLRRIHPDSYLERFKAISDNGGGMLGKEAPLGPGSYEIACLSAGLACAAVEAVLKGELDNAYSLSRP

PGHHSLPDQSMGFCFLANIPIAVERAKAQLGLGKVAIIDWDVHHGNGTQHIYLQRDDVLTISLHQDGCFP

PGYAGEDDRGVGAGEGYNINIPLLAGAGDDSWRYALETIVIPALARFEPELIIIACGYDANAMDPLARMQ

LHSDSFRAMTEQVQQAADRLCGGKLVMVHEGGYAESYVPFCGLAVMEALSGIRTEVQDPLLEFIQQQQPR

ATFAQFQRQAIDRLAQQFGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531823.1\_1597 [locus\_tag=BN49\_RS09380] [protein=DUF3156 family protein] [protein\_id=WP\_016531823.1] [location=complement(1625185..1625778)] [gbkey=CDS]

MSSVPWFETPLMNAVQRDLAGWPSEKLSERSALLRLNDATAVTFSVRQKRLFMASIHSCEFVVEGPVTRP

ARGKIRAHQSGWLKRLPIRFIGSKESAELAGYLNGFPNLQQTLSELDYRRFSLTFDSSGWRCSIEPWAAS

EVVCKMPPLRRYLRLEAQQRMLLLSVLAMVNQAVSQWMRGEIAEEKALTSPPSPRGS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042865.1\_1598 [locus\_tag=BN49\_RS09385] [protein=APC family permease] [protein\_id=WP\_046042865.1] [location=complement(1625756..1627255)] [gbkey=CDS]

MFSNRLASHLERGVVGFPTTLASSVGLIMASPVILTVTSGFGMGGDTFALAVLLAFIMMQAQVTTFAEAA

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VGMVVIFGLLNAIGVEIFGKVEVVLTFGMWTTLTIFGLCGIFMAPVTHLSGWFGTPLNVSDINGLFGYIG

MAMFMFVGCELVTPMAPEIKQAHRTIPRAMALGLLGVASCMFIYGAAINRQVENTVLDAANNVHLLDTPM

AIPAFAERVMGHAGQYWLGVGLLLAGCATINTLMAAVPRIIYGMALDGALPRFLTWLHPRFKTPVIAIAI

GVAIPCLHAWYLNGDLDRIVPLILAAVCAWGVAYLLVTLSVVMLRIRRPDLPRAYRSPWFPLPQIISSVG

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MPDVLRPLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002892824.1\_1599 [locus\_tag=BN49\_RS09390] [protein=cupin domain-containing protein] [protein\_id=WP\_002892824.1] [location=complement(1627630..1627995)] [gbkey=CDS]

MHAFKLKHPVPDLQPIGSVSLLGATPTAGDPQVAGAMIYGEPQDAFTCGLFSSTEGSFTMTYPFTEHATV

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531587.1\_1600 [locus\_tag=BN49\_RS09395] [protein=FAD-binding oxidoreductase] [protein\_id=WP\_016531587.1] [location=complement(1628009..1629310)] [gbkey=CDS]

MNIKIDALNYYGATKKYHLHFPALREDIEADVVIIGGGFSGINTALELAEQGITNVVVLEARHLGYGGTG

RNGGQVMAGIGHDIEAVKKHVGKEGLETLFKIANLGAGIIRERIRKYNIDADFVPGYGYLAYNQRQLKTL

RQWEKEFKAATPDEEIELYTGKEVQQVVGSEVYCGALKHMGCGQIHSLNMLLGSAQAAHSLGVKIFESSP

VVEVNYGKQVRVRTAMGSVKAAKLLWACDSFLNNMEPEIYNKTLVTYSYQVSTEPLSDELIERISPLRGA

FSDIRPVINYYRVTRENRLLFGSATRFVEYTPNDFAAWNRTLLAEVFPYLRDVKIDFAWGGPMACSANLF

PQIGTLRDHNNVFYVQGYSGFGVTPSHIVCKILAEGINGGSDRYRLLSSIPHATIHGRDSLRLLLVTAGK

LMHQTAGFWKGRS

>lcl|NZ\_FO834906.1\_prot\_WP\_023279211.1\_1601 [locus\_tag=BN49\_RS09400] [protein=aldehyde dehydrogenase family protein] [protein\_id=WP\_023279211.1] [location=1629469..1630953] [gbkey=CDS]

MSEITLLAEVTAFLRQPHGQFIAGQREAGRGAPFAVINPATGQAIAEVTAADSDQADRAMESARQAFSQW

REMPTLARGALLLKLADTLAEHREALAQLESLCSGKTITLARMLELDQSVAFLRYFAGWAGKVTGETLDV

SLPSMAGEKYTAFTRRQPLGVVVGIVPWNFSIMIAIWKLAAALVCGCTIVLKPSEYTPLTLLRVAELAKA

VGIPDGVINVVNGAGGEIAQRLITHPACAKVSFTGSVATGEKVQQSASASGKRVTLELGGKNAALFLDDL

TPEAMVNGIIEAGYLNQGQICAAAERFYLPQGKLDAVLALLKDKLSAFAPGSPLDERTLMGPLANRQQYD

KVLRLIQTARDEGDTIVCGGEALPGEGYFLQPTAVKVRSEESTLMREETFGPVCSFIGYRSEEEALARMN

ASPYGLAASVWSDNIRQALRYSEAIEAGIVWVNMHTFLDPAVPFGGMKGSGIGREFGSAFIDDYTELKSV

MVRY

>lcl|NZ\_FO834906.1\_prot\_WP\_042942170.1\_1602 [locus\_tag=BN49\_RS09405] [protein=YncE family protein] [protein\_id=WP\_042942170.1] [location=1631349..1632431] [gbkey=CDS]

MKYTLPALTLTISAALSGCATPHSSAVSQPVVDSPVPNVAQPLQRQLAEGLYEMALSPQGDALYVASAEG

FKNVQGGAVYTLDPHTLNTIGLTHTDLKNFALQLSAEGKTLYVSNSLDGGISAIDTATGKVKNRLLFSER

NEKGRPYGARQLLLLNNTLYVGAVADPAQIWVVDATTLKLKTRIKNTGKWMTGLHYSAQTGRVYAANGSG

EILVINPHNQRIEQRWKPLGDKPALLLNMAEDSDTGRLFVTDNSKAKTTLVLDIHSGKLLKQLDVGDSLA

VQFNKKRHEIYISQRESGKVISLDASRYTLKKSWALPANPNSLLLSADGQTLFVTVKQPFNKDHSTKGPD

SVVRIDLNAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046042867.1\_1603 [locus\_tag=BN49\_RS09410] [protein=TonB-dependent siderophore receptor] [protein\_id=WP\_046042867.1] [location=1632491..1634404] [gbkey=CDS]

MHTTHYSSFPLRKTLLALAIGAASQTAMAADAAAAKQPGEETLIVEANETSDFKSGGDLVVPAFLDGQIA

HGGRLGMLGEQKAMDVPFNVIGYTSKLIQDQQAKTIADVVSNDAGVQTVQGYGNFAETYRIRGFKLDGDD

MTMGGLAGVVPRQVMDTQMLERVEIFKGANSLLNGAASSGVGGTMGVNISGVDFVPALPDNSKNYSQKWG

YSDIESEFGMAKAEYDLTNSWTVYSALGGQHSHEIGTYSAPKLLNKNGDATVGRLDTNRIIDAISGMGGV

RGDFNTGAISHKVNLGYAAQVHTDATAWRMSARNPTTNIYDNHDVAMPDNAYFGGNYHDPLVTSRSRTQG

WLLSDTLGFFNDKVLFTAAARHQKVVVRNYSNATGLEDTSSRYTQSRWMPTFGLVYKPWEQLSLYANHTE

ALQPGSVAPTTAANAGQSTGIAHSKQDEVGVKIDYGTIGGSLALFEIKKPNAISDTAGNYGLDGEQRNRG

VEMNVFGEPMLGLRLNASTVWLDAKQTKTAEGATDGKDAIGVANFYAVLGAEYDIKPVEGLTATALVNHS

GSQYADAANTKKLDSYTTLDLGLRYRMRLNADQNEMIWRVGVTNVTNEKYWSGIDDTGTYLFEGDPRTVR

VSMSYDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151811.1\_1604 [gene=pheP] [locus\_tag=BN49\_RS09415] [protein=phenylalanine transporter] [protein\_id=WP\_004151811.1] [location=1634513..1635889] [gbkey=CDS]

MKDASTSSETVTESGPTLHRGLQNRHIQLIALGGAIGTGLFLGIGPAIQMAGPAVLLGYAVAGIVAFLIM

RQLGEMVVEEPVSGSFAHFAYKYWGPFAGFLSGWNYWVMFVLVGMAELTAAGIYMQYWLPDVPTWVWAAA

FFIIINAVNLVNVRLYGEAEFWFALIKVLAIIGMIAFGLWMLFGGHGGSKAGFDNLWKHGGFLATGWHGL

ILSLAVIMFSFGGLELIGITAAEAQNPEKSIPKAVNQVVYRILLFYIGSLVVLLALYPWVEIKSDSSPFV

MIFHNLDSNLVASALNFVILVASLSVYNSGVYSNSRMLFGLSVQGNAPKFLARVSKRGVPVNSLLLSGII

TSLVVVLNYLLPHEALGLLMALVVATLLLNWIMICMAHLKFRAAQRRKGRESKFKALLAPASNYFCIAFL

GLILALMCTIDGMRLSAILLPVWILFLFIAFKLLRRPA

>lcl|NZ\_FO834906.1\_prot\_WP\_171819467.1\_1605 [locus\_tag=BN49\_RS09420] [protein=MFS transporter] [protein\_id=WP\_171819467.1] [location=1636077..1637282] [gbkey=CDS]

MSHRFLVPRLSLMMFMQFFIWGSWSVTLGLVMTRYEMSLLIGDAFSAGPIASILSPFVLGMLVDRFFASQ

KVMAVMHLAGAAILWFVPQALVAQNGALLIGLLFGYTLCYMPTLALTNNIAFHSLANVDKTFPVVRVFGT

IGWIIAGICIGVTGISDTTGIFTLSALCSVALALYSLTLPHTPAPAKGMPVQFRDLLCADAFALLKTRHF

LIFSLCATLISVPLGTYYAYTASYLADAGVKDVSTAMSFGQMSEIVFMLVIPLLFRRLGVKYMLLIGMAA

WFVRYAFFALGVSEEGRFLLYLGILLHGVCYDFFFVVGFIYTDRVAGEKVKGQAQSMIVMFTYGIGMLLG

SQISGALYNHLVAGQSVPQAWVTFWWIPAVAAAVIALIFLFSFQYNEKEPH

>lcl|NZ\_FO834906.1\_prot\_WP\_016532202.1\_1606 [locus\_tag=BN49\_RS09425] [protein=sugar phosphate isomerase/epimerase] [protein\_id=WP\_016532202.1] [location=1637299..1638321] [gbkey=CDS]

MKTIKGPGIFLAQFIGPQAPFNTLAGIAQWAAGLGYKALQIPCNHPAIFDVERAAASQTYCDEVSGILAE

HGLVISELSTHLEGLLVAVHPAYDAAFDAFAPAALHGDPQARQRWAVEKVRQAAVASGRLGLQAHATFSG

ALAWPFFYPWPPHNQPLLDEAFAELARRWRPLLDLFDEQGVDVCYEIHPGEDLHDGVTFERFLALVDNHP

RCNMLYDPSHLHLQQMDYLAYIDIYHARIKAFHVKDAEFRRNGRNGVYGGYQPWQQRAGRFRSPGDGQID

FKGVFSKLTEYDFAGWAVLEWECCLKDSETGAREGSEFIRRHIIPVAGRAFDDFAAGGRE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532201.1\_1607 [locus\_tag=BN49\_RS09430] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_016532201.1] [location=1638323..1639474] [gbkey=CDS]

MIQVAIIGAGFIGPAHLEALRRLGDVEVVALCDSRLEAAQRKAQALNIAHAYDSVEALLAHPGLQVVHNC

TPNHLHAQINRQILAAGLHVFSEKPLCMTVEEARELVALAARAGVVHGVSFVYRQFAMVQQAAAMIRHGE

VGRIFAAHGSYLQDWMLLETDYNWRVDSAQGGASRTVADIGSHWCDTVQFMTGRRIVEVMADLSIVWPTR

KAPVNGKATFSAVHEAQAYETRPVDTEDFGSVLLRFDDGSKGSFMVSQVSAGRKNRLAVEINGSLCSLAW

DQEVPQRLWIGHREQPDRLLSDDPSLLRSEIADSAHYPGGHIEGWPDAFKNMMGHFYQAVRAGKMPAAGA

RRFAAFDDGADVMYIIEAIVKSHQEQRRVSVER

>lcl|NZ\_FO834906.1\_prot\_WP\_004202462.1\_1608 [locus\_tag=BN49\_RS09435] [protein=Exc2 family lipoprotein] [protein\_id=WP\_004202462.1] [location=complement(1639494..1639910)] [gbkey=CDS]

MRLSTAILALSCALATITGCTSSKSSPERHAYAFVAHRSDFVGGNFTVNRQENYRLNLPTFTAMYARGQQ

DKAAGMSESDARRTAEAIKQQAAQGTRTEHAFTGNASDKWDNAMENKDAVLFGNELSGAYLDGYLGVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002892939.1\_1609 [locus\_tag=BN49\_RS09440] [protein=LacI family transcriptional regulator] [protein\_id=WP\_002892939.1] [location=1640159..1641139] [gbkey=CDS]

MSIQKIARLAGVSVATVSRVLNNSDTVKAKNRERVLQAIKESNYQPNLLARQLRTARSNMILVMVSNIAN

PFCAEVVKGIEEEAEKNGYRILLCNSGSDLARSTSGLQLLSGKMVDGIITMNALSSLPELTTMIGDAPWV

QCAEYADTGSISCVGINDVEAAQGAVSRLADSGRRRIALINHDLSYRYARLRERGYKSVLHVHGLAYQQV

TYAQDLSAAAGKRAMEQLLSQDEKPDAVFAVSDSLAAGALRAIAQAGLRVPGDIAVIGFDGTELAEVVSP

QLTTVEQPSRAIGRTAVSLLMKRIDDPDAAVERVMMDWRVIDRASV

>lcl|NZ\_FO834906.1\_prot\_WP\_004142570.1\_1610 [locus\_tag=BN49\_RS09445] [protein=mechanosensitive ion channel family protein] [protein\_id=WP\_004142570.1] [location=complement(1641143..1642387)] [gbkey=CDS]

MQELISQIAALGIEITPTRSLMIIFGIILFTAVVVHLILHKVVLRAFEKRALASSHLWLQIITQNKLFHR

LAFTLQGIIVNVQAVLWLQKGSEAAEILTTVAQLWVMIYAMLSFFSLLDVILKLAQKFPAASQLPLKGIF

QGIKLVTAIIIGILIISLLIGQSPAILISGLGAMAAVLMLVFKDPILGLVAGIQLSANDMLKLGDWLEMP

KYGADGAVIDIGLTTVKVRNWDNTITTIPTWSLVSDSFKNWSGMSASGGRRIKRSLNIDTTSIHFLDEQE

QQRLIRAKLLKPYMDSRHEEISAWNQQYAGEQSILNERRMTNVGTFRAYLQEYLRHHPRIRQDMTLMVRQ

LAPDANGLPIEIYCFTNTVVWAEYEGIQADIFDHVFAVVDEFGLRIHQTPTGNDIRALTGAFSR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042875.1\_1611 [locus\_tag=BN49\_RS09450] [protein=MFS transporter] [protein\_id=WP\_046042875.1] [location=complement(1642458..1643885)] [gbkey=CDS]

MNTSAVSPGRAGLLLLLSGQMLPLIDTSITNVALDAITHTLAASATQQELIVALYGVAFAVCLAMGSKLG

DNYGRRRLFMWGVALFGIASLLCGMANSIGALLAARTLQGAGAALIVPQILATLHVTLKGPAHARAISLY

GGIGGIAFIVGQMGGGWLVSADIAGLGWRNAFFINVPICLLVLALSRRYVPETRRETPSRIDWQGTLYLA

LILCCLLFPMALGPELHWPLWLQLMLVAVLPLLFAMRQSALRQQQRGDHPLLPPRLLQLTSIRFGMAIAL

LFFSAWSGFMFCMALTMQEGLGMAPWQSGNSFIALGVAYFISALYAPRLIARYSMGRILLTGLAVQIAGL

LLLCATFSRFGVATNALTLVPATALIGYGQALIVNSFYRIGMRDISASDAGAGSAILSTLQQATLGLGPA

ILGSLFLALARRGGGNYPQALIDFLLVEVAMMLLLGAIALWLRHHLNRQPATVAS

>lcl|NZ\_FO834906.1\_prot\_WP\_032105285.1\_1612 [locus\_tag=BN49\_RS09455] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_032105285.1] [location=1643994..1644860] [gbkey=CDS]

MTTMPQRESTIAVPDDRRKQLGAFLRARRESLDPQRLGLPRVGRRRTPGLRREEVAMLADVGVTWYTWLE

QGREVNPSEAVLVGVANALQCSPLETRHLFVLAGLTPPEATQVTVCEGISPGTRRMLDSLMPQPASIQKP

NFDIVAWNDSFCRLMGVDFATLPEEDRNCIYLYLTHETWRSRIENRDVLPTFVSYFRAAMAEHRGDPAWE

NKLARFFAASSEFEALWHQRYEVRGVENQIKHFNHPQLGRFSLQQMYWYSAPRNGSRLLVYLPMDEAGEQ

ALAWLDQH

>lcl|NZ\_FO834906.1\_prot\_WP\_046042877.1\_1613 [locus\_tag=BN49\_RS09460] [protein=DUF2157 domain-containing protein] [protein\_id=WP\_046042877.1] [location=1645527..1646561] [gbkey=CDS]

MNVTRKEQRIIQRALNAWQASGELTPSDSQRLAQTMRVSPFDWRRLSRYAFWTALACVLISLGSLFADSE

LVAWLLSLFSHSALMRILLPALLAVACYGWGFRRQRRETQWHYSTEAILFLGVVFTAVALWQLGERLDNG

SGHIAPLFLAGCVIYCAIGYIARSGLAWLFFLLALGNWFGAETGYVSGWGAYWLGMNYPIRFVLFGGALL

ALCYGAQSLLRQRQLFTVSKAMGLTYLFIALWIMSIFGNYDADSWYQVSQARLLPWGLLFAVAAGVCIFI

SLKTDDGMLRGFGLTFLAINLYTRFFEFFWNGMHKVLFFLILAVSLAVIGRYAERIWHAGNVKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002893000.1\_1614 [locus\_tag=BN49\_RS09465] [protein=sigma-54-dependent transcriptional regulator] [protein\_id=WP\_002893000.1] [location=1646658..1649387] [gbkey=CDS]

MNKESIFRQLEQRIAGRALTAEALGEFNAMAIADSLKQKRSIISHHLNNLHREQRVVKVNGRPVLFLPVT

VLRDHHRLAVRHGEYASIQALCADRQDSLAQLIGAQGSLQEALRQCKAAISYPGAGLPLLLRGPTGTGKS

FLARQLWHYAIDEGILPADAPFTVFNCAEYANNPELLTSKLFGHAKGAFTGADKAVPGLIETSNGGVLFI

DEVHRLPPEGQEKLFHFMDNGSWRRLGESADERSATVRLIFASTEDLEKHFLATFIRRIPVIVKILPIAE

RGQFERLAFIHHFFRREAQRLNHDLALDGEIVSQLMRETLEGNVGGLENLIRNICASAWTFGERDSGLLH

IKAGLLPDRLLADAPFTLQQNSERVMIYRDGDAQPLFSGRHHEYQRLTENICSLCEELAQDNISVRTFEK

LIYQNVTLYLDALMNQESTVSLQDKRLRFIEDVGKAIAVNYDLQLNVEFAYLTGRYLTSLPLAPRSVAEP

VRLVMQRWLDSSAGLAQRIAEKLLDVVNNKYDLLIDTLDRLAITAIVSNAIDATSGGKVKALIIAHGYST

ASSIAGVANRLIGEKIYQAMDMPMEVAFNDVSRAVVDYLQHTDTRAGVMVLIDMGYTKEIADALLSVING

PLVVVDNVTTRMALNVASEIALGKNIEQIAEEIVPLNQSRWDVFWPAEKKERVLLVTCITGIGTAFKFKN

LMEKSLLNDFDINIIACEYTRLKNSRTAVSLLHQYEVIAVVGTHDPQLAGVPWVGIEELLGEQGHRHLSQ

LLSGYLNEKQIALINKNMVREFSLHNVVNSLTILNAGKTMGHIETIIAEWQNTLGFHFNNNLIISLYVHL

SCMIERLVMRNEISHYKDLEQFTRQHGEFIAMVNHSFQRLKILYNVALPVAEIGYIHDIFELRIEDFSW

>lcl|NZ\_FO834906.1\_prot\_WP\_004147471.1\_1615 [locus\_tag=BN49\_RS09470] [protein=SIS domain-containing protein] [protein\_id=WP\_004147471.1] [location=complement(1649440..1650426)] [gbkey=CDS]

MSIAHQNAHTIIRDILSKQHIERVWFVGCGGSLTGFWPGKYFLDCEAKKLAVGYVTSNEFVHATPNALGK

NSVVILASQQGNTAETVEAARIARQKGAATIGLVYTPGTPLCEHSDYTIEYCWARYPETVDPTQQKAAYS

LWLALEVLAQTEGYAHYDEMVSAFASFESVVRGAQQQVQADARHFAEAWKTEKVIYMMGSGPSFGAAHQE

SICILLEMQWINSASIHSGEYFHGPFEITETGTPFILLKSSGRTRPLDDRAIRFIERYQGKLQIIDVEKV

GIDALHASVREYFCGLLHNCVLDVYNLALATARNHPLTTRRYMWKVEY

>lcl|NZ\_FO834906.1\_prot\_WP\_004183293.1\_1616 [locus\_tag=BN49\_RS09475] [protein=SIS domain-containing protein] [protein\_id=WP\_004183293.1] [location=complement(1650491..1651552)] [gbkey=CDS]

MHVEDYMNETPACLLAMLTQTREDLWQAAKALTERGVTRIILTGSGTSYHGALTARSFMQQWCGLPVDVY

WPFLLDDSALTLSDKALVIGISQGGGSLSTLAAMERARAAGHLTASMAGEAPAVIDRAADLVLTVPCGEE

RAGAKTKGYHCTILNLMLLGLAVASRQRRLSDEERKALLIRMDTTFNHLPTLIEASQAWVLNHARPLIDS

ADIRLTGPARLFGTVQEGALKMLETLRCPVAGYEFEEFIHGIYNAFDERSTLIMLDPFPDERQDRLAEIL

GGWTQHIYRIGPQVENNGKNMPFAFINDPDFAVFEYIIPLQMVCARLPPVKGIDPAIPKDPQFHQKMKSK

QLN

>lcl|NZ\_FO834906.1\_prot\_WP\_004176976.1\_1617 [locus\_tag=BN49\_RS09480] [protein=PTS system mannose/fructose/sorbose family transporter subunit IID] [protein\_id=WP\_004176976.1] [location=complement(1651570..1652424)] [gbkey=CDS]

MSEMTQTVTGATQPQSDDASRITARDLRSVFWRSFTLQGSWNYERQQHMGYAFAMSPALKRIYQDPTELG

RALQRHLVLFNTTPHLSTFIFGLSIAMEEENQRNPEFNEESINAIKTSLMGPLAGIGDSIFWGSLKVIAA

GMGIYFAQQGSLLGPILALLVYNLPHLLCRWYGLKLGYRAGTTWLMRIYQSGLMDRVTYIASIVGLMVVG

AMTASMIDITTPLSFTAGQTTMKAQEFIDKILPSLLPLLFTLGMYKLIRKGVNINWILLGTVAFGMAASA

LGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002893012.1\_1618 [locus\_tag=BN49\_RS09485] [protein=PTS mannose/fructose/sorbose/N-acetylgalactosamine transporter subunit IIC] [protein\_id=WP\_002893012.1] [location=complement(1652427..1653170)] [gbkey=CDS]

MLLTATLLGLIAALGILDGRLLGVSMIDRPLVMCALTGLVCGNLHEGILIGATLELIFLGNVAIGAAHPP

DIVTGSVLATAFSIMSGRGPEAALTIAIPVSMLAQTLGILVRVVNARFGHLADRYAAQGNTRMVGLMHLA

GPTLLYFLNGFLPVFFAILLGSSAVSWFLEAIPPVITNGLIVASKILPALGFALLISMMLSSKLMPYLGL

GFLIAAYTKLDIIAIALFAVVLAFIISQFLNLNQQES

>lcl|NZ\_FO834906.1\_prot\_WP\_004176974.1\_1619 [locus\_tag=BN49\_RS09490] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_004176974.1] [location=complement(1653185..1653655)] [gbkey=CDS]

MIKLVRIDYRLLHGQVVFAWTRALDIDHIIVANAKAAADAFITMSLNLAKPAGVTLDIATVEQAAEKLNS

GKLDHKKVMVVLGNTAETLALVEKVPGISAINYGGLPQKEGARQFGKAIYLTEEEIAHSRALKEKGIRLE

MRQVPAHSAELLNDQL

>lcl|NZ\_FO834906.1\_prot\_WP\_002893017.1\_1620 [locus\_tag=BN49\_RS09495] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_002893017.1] [location=complement(1653648..1654082)] [gbkey=CDS]

MKHIYVASHGHFARGLVNSLSLLIGDEHGVIPVCAYDEDIVTTEQLEQTLEHLIVQANGDEVVIFTDLLG

GSINNSAVSVLMRHRNVFVVAGINLTLLLEFLLCEEATTEAAIIYATSAARESIVFINPLITQPSSDPQG

ESHD

>lcl|NZ\_FO834906.1\_prot\_WP\_004178896.1\_1621 [gene=nfsB] [locus\_tag=BN49\_RS09500] [protein=oxygen-insensitive NAD(P)H nitroreductase] [protein\_id=WP\_004178896.1] [location=complement(1654330..1654983)] [gbkey=CDS]

MDIVSVALKRYSTKAFDATKKLTAGEAEQLKTLLQYSPSSTNSQPWHFIVASTDEGKARVAKAASGTYVF

NERKILDASHVVVFCAKTAMDDAWLQRVVDQEEADGRFATPDAKAANHKGRTFFADMHRKELKDDDQWMA

KQVYLNVGNFLLGVAAMGLDAVPIEGVDFAILDEEFDLKAQGYTSLVVVPVGHHSVEDFNATLPKSRLPQ

STTITEI

>lcl|NZ\_FO834906.1\_prot\_WP\_004142557.1\_1622 [locus\_tag=BN49\_RS09505] [protein=MmcQ/YjbR family DNA-binding protein] [protein\_id=WP\_004142557.1] [location=complement(1655103..1655471)] [gbkey=CDS]

MTPETLHPCAHRIALTYPFTEHCWPFGPEYDVFKVDGRIFMITMTIRGRALVNLKAEPQKSLLNQQIYRS

IEPGYHMNKKHWITVVPGEDISEDLLAELIDDSWHQVVNKLSKKAQQRLRPR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176968.1\_1623 [locus\_tag=BN49\_RS09510] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_004176968.1] [location=complement(1655471..1656052)] [gbkey=CDS]

MARPKSEDKKQALLEAATAAFAQSGIAASTSAIARSAGVAEGTLFRYFATKDELLNELYLAIKLRLVRTM

IAGLDPDEKRPKENARNIWNSYIDWGVRNPMEHKAIRRMALSERITDETRRQVKESFPELNEMCQLSVKE

IFLSEAYRAFGDALFLSLAETTIEFASHDPQRAREIIALGFEAMWHALHEADA

>lcl|NZ\_FO834906.1\_prot\_WP\_012737592.1\_1624 [locus\_tag=BN49\_RS09515] [protein=MBL fold metallo-hydrolase] [protein\_id=WP\_012737592.1] [location=1656232..1657347] [gbkey=CDS]

MSGQDMNRVTFSVVAIMLLAAATTLPFVLNAGFGKAPQGAQLSQVEASPHYRDGQFHNQLPTPGFTGQKN

MLAAWWDFLMTKRENARPAQPLPLVKTDLATLPLGQDVMVWLGHSSWYLQLAGKRILIDPVFSDYAAPFS

FINKAFPGDYPWRAEGMPEIDLLIISHDHYDHLDYATIRALLPKIKRVITPLGVGSHLRYWGMDGALITE

ADWQQAVPASDELTVHVLPARHFSGRGLKRNQTLWASFLFVTRQQKIYYSGDSGYGPHFKAIGDEFGPVD

LAIMENGQYDQDWKYIHMMPDETAQAADDLRARAVLPGHAGRFVLAKHSWDEPYQRLAAASEGRAWRLLT

PVQGEPVWVADKTQSFNAWWR

>lcl|NZ\_FO834906.1\_prot\_WP\_002893035.1\_1625 [locus\_tag=BN49\_RS09520] [protein=RamA family antibiotic efflux transcriptional regulator] [protein\_id=WP\_002893035.1] [location=1657378..1657719] [gbkey=CDS]

MTISAQVIDTIVEWIDDNLHQPLRIDDIARHAGYSKWHLQRLFLQYKGESLGRYIRERKLLLAARDLRDT

DQRVYDICLKYGFDSQQTFTRVFTRTFNQPPGAYRKENHSRAH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529803.1\_1626 [locus\_tag=BN49\_RS09525] [protein=DUF1158 domain-containing protein] [protein\_id=WP\_016529803.1] [location=complement(1657737..1657985)] [gbkey=CDS]

MKHPLETLLSAAGILLLALLSCLLLPAPSLGLTLAQKLVETFHMMDLNQLYTVLFCLWFLALGAIEYLVL

RWIWRRWFSLER

>lcl|NZ\_FO834906.1\_prot\_WP\_046042883.1\_1627 [locus\_tag=BN49\_RS09535] [protein=cation-transporting P-type ATPase] [protein\_id=WP\_046042883.1] [location=1658488..1661211] [gbkey=CDS]

MTKMNNPKFTTPSGDTAPRQVWQQTVDAVLAQTKSQAAGLSSADAAERLNTCGPNALPEKKGKPGWLRFL

AHFNDVLIYVLLAAVALTAIMGHWVDTLVILGVTVINALIGHIQESNAEKSLQGIRNMLSSDARVQRNGK

HETIPTRDLVPGDIVILRAGDRVPADMRLIETHNLRVEEAILTGESTVVDKITDALEGDLPLGDRVNMVF

SGTTVSAGGGVGVVTATGAQTELGHINQMMAGIEKHRTPLLVQMDKLGKAIFAIILAMMVALFIFSLALR

DIPMGELLLSLISLAVAAVPEGLPAIISIILSLGVQTMARKRAIIRKLPTVETLGAMTVVCSDKTGTLTM

NEMTVKAIITADCCYRVEGDSYEPQGRIFLEGSDEPVQVQPGTVLETWLRTIDLCNDSQLTQDERGLWGI

TGGPTEGALKVLAAKAQLPAVEARLVAKIPFDSQYKYMSTLQHIDGNARVLITGAPDVIFAMCREQMSRH

GAVPFEAQYWEEEMARFARQGLRMVAAACKPASLDATTLNHEDLQEGLIFLGIAGMMDPPRPEAIDAIHA

CQTAGIRVKMITGDHPQTAMSIGQMLGITNSSQAMTGYQLEHMDDAALAKAAVEYDIFARTSPEHKLRLV

KALQDNGEVVGMTGDGVNDAPALRQADVGIAMGIKGTEVTKEAADMVLTDDNFATIASSVKEGRRVYDNL

KKTILFIMPTNLAQGLLIIIALLAGNIIPLTPVLILWMNMATSATLSFGLAFEAAERNVMNRPPRKTGQH

VMDGFAVWRVAFVGSMIAIAAFILEAWLAPRGHSPEFIRTVLLQMLVTAQWVYMINCRSSDSFSLSMGLL

RNKGIWLVTGVLLLMQLVIIYVPLMQSMFGTEALPLRYWFVTLVIGVAMFLVVEVEKRLTRRFRKTA

>lcl|NZ\_FO834906.1\_prot\_WP\_014907946.1\_1628 [locus\_tag=BN49\_RS09540] [protein=efflux RND transporter periplasmic adaptor subunit] [protein\_id=WP\_014907946.1] [location=1661264..1662343] [gbkey=CDS]

MIKTFRFALLACGLVGGALTATAAPAVPVRVATVELAPHAEERAIPGRVEAIRAVDIRARTEGVIVQRHF

QDGQYVTEGDLLFTLDDAQPRAALALAQAELKSAEASLRQSQQLLTRYERLINNHSISRNDVDTARMQRD

VAAAAVQQAKARVEAQQIVLSYTQIAAPVTGRVGHSAFHVGTLVNSSSGVLVDIVQLDPVRVSFALDEAA

FFSKTGQHADIHALKQAWLAQIEVDGKRRDGVLTSIDNRIDARTGSVAVRAEFANPQHRLLPGGSVTILF

RPQELPSRVMVPAAAVQQDPQGFFSWVLKPDHTAGQRRLTLAGQQGQQFAVEKGLQAGEQVITDGAQRLR

EGAAVQVLN

>lcl|NZ\_FO834906.1\_prot\_WP\_046042886.1\_1629 [locus\_tag=BN49\_RS09545] [protein=efflux RND transporter permease subunit] [protein\_id=WP\_046042886.1] [location=1662357..1665449] [gbkey=CDS]

MLTFFIRRPRFAMVIALLLTFVGAVSLKLIPVEQYPAITPPVVNVSASWPGASASDVAEAIAAPLETQLN

GVDHMLYMESTSSDEGTYRLSITFAAGTDADLAAIDVQNRVAQALAQLPAEVQQNGVQVRKRASNLLMGV

SLYSPLGTLTPLFVSNYASTQVREALARLPGVGEVQMFGARDYSMRIWLRPDRMNALNITTDDVAQALRE

QNVQGAAGQVGTPPVFNGQQQTLTINGLGRLNEAASFGEIILRRGAQGQLVRLADVATIELGARSYSSGA

QLNGKASAYLGIYPTPTANALQVASAVRAELNRLHTRFPADLTWEVKFDTTRFVAATIKEIGVSLALTLL

AVVVVVSLFLQSWRATLIVVLAIPVSLIGTFAVLYLLGYSANTLSLFAIILALTMVVDDAIVVVENVETK

MAEGLDRLQATAQALRQIAGPVIATTLVLLAVFVPVALLPGIVGELYRQFAVTLSTAVALSSLVALTLTP

ALCALLLRPRPARPAAVWRAFNRLLDGTRYGYGRLVGRMNRRPWLALAATVAAGALVAFSFTSMPKGFLP

QEDQGYLFASVQLPEAASLERTEAVMTQARKLLMANPAVEDVIQVSGFNILNGTSASNGGFISVMLKDWH

QRPPLDAVMADIQRQLLSLPEATIMTFAPPTLPGLGNASGFDLRILAQAGQSSAELEQVTREILQLANQH

SQLSRVFTTWSSNVPQLTLTVDRDRAALLDVPVAQIFSSLQTAFGGTRAGDFSRNNRVYHVVMQNEMQWR

ERAEQISELYVRSRDGERVRLSNLVTITPTVGAPFIQQYNQFPSVSVSGSAAEGVSSRTAMAAMEQILQA

HLPPGYDYAWSGISWQEQQTGNQAVWIVLAAVAMAWLFLVAQYESWTLPASVMLSVLFAIGGALLWLWTA

GYANDVYVQIGLVLLIALAAKNAILIVEFARSRREEGLSIVDAAREGATRRFRAVMMTAVSFIIGIMPMM

LATGAGAQSRRIIGTTVFSGMLVATMVGILFIPSLYVLFQRMREWAHRRG

>lcl|NZ\_FO834906.1\_prot\_1630 [locus\_tag=BN49\_RS30335] [protein=IS3-like element ISKpn1 family transposase] [pseudo=true] [location=1665745..1667109] [gbkey=CDS]

MAKPKYSPETKLAVVNHYLSGKDGEQSTADLFGIERTSVRRWVRAWQFHGAEGLTAKNNHYSDEFKLVVV

RAVISDRLTMREAAARFNLSAEILVRRWLDVYNDAGAEGLLNMQCGRPGQMTKPKNIPPLTDKELEKLSP

EELRAELRYLRAENAYLKKLKALVQSEKNGKKP\*\*SVN\*GMNTLCGTFCGRPVCPVARGITI\*MH\*SKGT

GMRVLKRTSGRYTTITKVVYGYRRITLALRKQGLRINHKTVQRLMAELSLRSVIRAKKYRAWKGRTGEAA

PNILSRNFGASKANEKWVTDVTEFPVQGKKLYLSSVLDLFNREVIAYSLSERPVMEMVNTMLDGAFPKLR

PGDAPLLHSDQGWHYRMRSYQERLKAHGMTQSMSRKGNCLDNAVMENFFGTLKSECFYLREFRSVSALRK

AVEDYIHYYNNERISLKLKGLSPVEYRTQALRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042888.1\_1631 [locus\_tag=BN49\_RS09560] [protein=phosphodiester glycosidase family protein] [protein\_id=WP\_046042888.1] [location=complement(1667248..1667967)] [gbkey=CDS]

MLLRCLLPLALLPLAAVASAACTLTDPTLTLQSYRVDAQKERIAMYWQYRHGKAWGSLRSLLAGIDGDGR

VQMAMNGGIYDKAYAPLGLYIEDGKRLTPVNRSAGGGNFFIRPGGVFLVENGRAKIVPLPAYKPSPAIRY

AVQSGPMLIENGVINWRLKPSASSRKLRNGVGIDKQGRVVFMLSDRETNFYDFACYAQSKLGVRQMLYLD

GTLSKMYRKGGSVPWQYHPFVTMITVERK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176954.1\_1632 [locus\_tag=BN49\_RS09565] [protein=YbdK family carboxylate-amine ligase] [protein\_id=WP\_004176954.1] [location=complement(1668014..1669129)] [gbkey=CDS]

MPLADFHRSDPFTLGIELELQVVNPPGYDLSQDASTLIADVQHELTVGEAKHDITESMLEIATGVCRDIS

HAQIQLSAIQQAVQRAALRHHLQICGGGSHPFHAWQRQQISDNPRYVKTVEHFGYLAQQATVFGQHVHVG

CQSGDDAIYLLHGLSRFVPHFIALNAASPWFDSTDSRFACSRLNRFSSYPDNGPMPWVADWQGFRRLFRQ

LSYTSMIDSMKDLHWDIRPSPQFGTVEVRVMDTPLTLAQAIHIAGFIQTLACWLLTERPFKHQPDDYLLY

PFNRYQACRYGLDGTLTDVRSGEQRSIRQEILQLADRLAPFAHQLKATAALEAVVRQAKSPHSEAQQMRD

FIANGGSLSGLVQKHCEIWAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004191441.1\_1633 [locus\_tag=BN49\_RS09570] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004191441.1] [location=1669456..1671123] [gbkey=CDS]

MHKKTLFSRAGRLAVAVSGALALAGAALPANASTLRIAMTAADIPLTLGQPDQGYEGNRFTGIPLYDALV

EWDLSQGEKPSGLVPGLATEWHIDPQNTSRWIFTLRPGVKFHDGTEVNADAIVWNVDKVLNKAAPQYAPG

QIGNTLSRMPTLTGAEKIDDHTVALTTSEPDALLPYNITNLFIVSPTAWQKQYDAVPASVGDSAARSKQA

WTAFAAHAVGSGPFKLEKLVPRQQLILDKNPDYWNKDRIPRVDKVVLIPLPEANARTAALLSKQVDWIEA

PAPDAIDQIKSQGFHLYANTQPHLWPWQFSFEKGSPWQDIRVRKAANLCLNRAELKSYLGGYMTEATGVY

EADSPWHGKPTFQIKYDPDAARQLMTEAGYSASKPLHVTVATSASGSGQMQPLPMNEYIQQSLKSCFFNV

DIKVVEWNTLFTNWRLGARDPSAKGIDAINVSAAVNDPYFGLIRFSTAKAFPPVATNWGYFSTPETEKLA

AAVKHAFTPAEMNKAAGELHAALVDQVPFLFVAHDVGPRAISPAVTGVVQPQSWFIDLSLVSKKE

>lcl|NZ\_FO834906.1\_prot\_WP\_004178910.1\_1634 [locus\_tag=BN49\_RS09575] [protein=ABC transporter permease] [protein\_id=WP\_004178910.1] [location=1671142..1672095] [gbkey=CDS]

MINTLLYRILLAIPTMLGVAVICFMLVQIAPGDPLVSVMPPDASEALRQTLMQAYGFDKPLPLQFIHWLW

RALHGDLGMSVATGRPVIDEVMTAVAYSLRLALLATAIGFVLGSLFGFVAGYFRNSVIDRLASVLSVFGV

SVPHYWLGMLLVILCSVKFALLPATGGGPIGEVGWQWDWAHLQFMLLPALTLSVIPTGIIARTVRSQVAD

ILSQEFIVGLRARGLNESRIFVHVMKNAAPTALAVMGLQVGYLMGGSILVETVFSWPGTGLLLNTAIFQR

DLPLLQGTIWVLALFFVLLNLLVDILQTTLDPRIKRS

>lcl|NZ\_FO834906.1\_prot\_WP\_008805546.1\_1635 [locus\_tag=BN49\_RS09580] [protein=ABC transporter permease] [protein\_id=WP\_008805546.1] [location=1672098..1672991] [gbkey=CDS]

MVDTATTKAVPAAAAHASRQGYWRGVLRRLLRDPGGVVVGVVILLLLALALFGPWLIVKDPYQTSMFLRL

KPIGSDGFPLGSDELGRDMLSRLILGTRLSLFMGIVPVVFAFFIGGAIGIIAGYTGGKTNTVIMRTVDVF

YAFPSVLLAIALSGALGAGIGNALLSLTLVFVPQVARIAESVTAQVRHMDYIDAARATGASALTIIRVQV

LGNVLGPIFVFSTGLISVCMILASGLSFLGLGVRPPEPEWGLMLNTLRTAIYTQPWVAALPGLMIFITSI

SFNILADRLRAAMAIKE

>lcl|NZ\_FO834906.1\_prot\_WP\_004223507.1\_1636 [locus\_tag=BN49\_RS09585] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004223507.1] [location=1672995..1674032] [gbkey=CDS]

MQPFINIDLGGPAQPLLKVNHLLKYFRGGKGREVVQAVDDISFTVMKGETLGVVGESGCGKSTTARLLMQ

LLTQDSGELIFDGQGVGSSRLPLKAYRRQVQMVFQDSYASLNPRLTMEESIAFGQRVHGVSAREASEYAR

YLLAHVGLEPARFADRYPHALSGGQRQRVNIARALAMKPRLVILDEAVSALDKSVEAQVLQLLQELKRTL

ELTYVFISHDLHVVRWLSDRILVMYLGEVVEIGPAEQLFTASAHPYTRALLSSMPSMDPENRTLTSPLSG

DPPSPIAPPSGCRFHTRCPHAKAVCAEVKPRLEAVGEGHQSACLMAQPASPWHQSIPLKEVSHVG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532221.1\_1637 [locus\_tag=BN49\_RS09590] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016532221.1] [location=1674022..1675032] [gbkey=CDS]

MSDNAFVHVRDLRVVFRRDGQTINAVNGVSFEVQKGEVMALIGESGSGKSVTLRALMRLHPPGSSELSGT

LQVGDDEVLTMSASQLRRYRGGRCAMIFQEPLLAFDPVYTVGQQIIEGLRRHEGLSRQAARDRALEALSQ

VRIPSPERRLDAYPHEMSGGMRQRAMIALALSCNPKLLLADEPTTALDATVQIQILILLREQQKQRGLSI

VFVTHDIGAAVEIADRVAVMYAGRIVEEASMSEILRHPRHPYTQVLLGSRPKEGLKKGDALHCIPGAPPD

LARLPPGCAFAERCPHRRPVCEQSLPPTESVAERHAVSCHRWRELAIDANAQALAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016532222.1\_1638 [locus\_tag=BN49\_RS09595] [protein=Zn-dependent hydrolase] [protein\_id=WP\_016532222.1] [location=1675130..1676398] [gbkey=CDS]

MSSDVLFTPATDTTGWRINGDRLWASLMDLAQIGATPKGGCRRLTLTDLDRQGRDKVIGWAREAGMSVTI

DKIGNVFMRREGRNPGLPPIVSGSHIDTQPTGGKFDGNYGVLAALEVVRTLNDLQIATDAPIEVVFWTNE

EGSRFVPVMMGSGVFAGVFPLEETWAVTDKEGVSVGEALEQIGYIGEQTPGDHPIGAYFEAHIEQGPILE

DEAKTIGIVQGVLGIRWYDCVVTGQASHAGPTPMRLRQDALQVATRIMQEVVAIAGRSEEGRGTVGSVQV

WPNSRNVVPGEVTFSIDMRNLSDALVDEMDRQLRAFIAEVERESGLQVALKQVSHYPAAPFDAECQQAIA

DAAQRLGYPARPIVSGAGHDAVYMSYLAPTGMIFIPCKDGISHNEIEYASPEHVAAGANVLLQVMLQYAR

PV

>lcl|NZ\_FO834906.1\_prot\_WP\_046042890.1\_1639 [locus\_tag=BN49\_RS09600] [protein=DMT family transporter] [protein\_id=WP\_046042890.1] [location=complement(1676502..1677410)] [gbkey=CDS]

MDKSAPGPWSGWLHGLLGVIIFSGSLPATRLAVQDMDPLLLTFLRASIAGLLAIALLVGFRQKRPRLAQL

VSLIIVSSGVVLGFPLLTALALQHITSAHSIVFIGLLPLMTALFGVLRGGERPRRAFWIFSLLGSLLVVG

FALTQSAAASLSGDLLMLAAVIACGLGYAEGAKLTRELGGWQVICWALVIALPLMLPASLLVQPASWHAI

SASSWVALGYVSLFSMLIGFIFWYKGLAAGGIAAVGQLQLLQPFFGLGLSAALLHETVSPLMLAVTLGVV

LCVVGSRKFGRQRVGAGSPSRD

>lcl|NZ\_FO834906.1\_prot\_WP\_046042892.1\_1640 [locus\_tag=BN49\_RS09605] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_046042892.1] [location=1677535..1678869] [gbkey=CDS]

MKARYKAVVDRYAQAIRSGQLPAGSRLPTHRTLAAGERISLATATRVYRELEEMGLVSGETGRGTFVRDL

SLPPGHGVDQQVVAADVVDLNFNYPSLPEQGDALREALRQLAMAGDIDSHLRYQPHAGRLAERDIIARHL

TCQHFAPDAENVLIVNGAQHGLAVTVMGLLRPGDVVAVDALTYSGFKILAALYHLELAAIPCRPEGPDLR

ALHTLCQQRRVRAVYTMPTLHNPLGWVLNTGQRQALADLARQHDLLIIEDAAYARLVSRPPPPVVSYAPE

RTVYVTGFSKNIATGLRVGVVISPPRYRPEIERAIRATTWNTPTLISSLICAWIEDGTVARFETQKRQDA

RQRQQVARELLCGLPVVSHPDSYFVWLPLGEESRADRLANALMERRISVSTAEPFCVSATIPQALRIALG

SVPFDSLCPALRSVRDAVEYEQYR

>lcl|NZ\_FO834906.1\_prot\_WP\_004191435.1\_1641 [locus\_tag=BN49\_RS09610] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_004191435.1] [location=complement(1678866..1680329)] [gbkey=CDS]

MIRHLLHVDFQPGRGLQEQVRETLVNAILSGIFAADTPLPSCRQLASQLRVSRNTTALVFESLVNEGYLI

SRPRSGYYLHPDYHEASPAAVESAPQREAAAPRWGDRLQMTPSQQESILKPAGWMHYRYPFIYGQPDTRQ

FPLATWRSAANWLHGGVRDPAWVIDHIDQDVPMLIEQIRTRVLPKRGIVAAPDEILITLGSQNALYLLTR

LLLSSTTRIGVENPCFREAINTFLLADAEVVPHPVDEEGIVLNERPCDYYYVTPGHQVPTGVTMSSARRR

QLLEHAARHDAVIIEDDYDSESNFTLNPLPALKASDRSGRVVYVSSLSKALSPGLRLGFMVADPDLIDEA

RALRRLVYRHPPTNIQYQMAHFLAQGHYETHLRRYHYDSAQRWERLHAALQRYLPSCRALAGSEHANAFW

LQTPAQINTQQLTWRAAHAGVLIEPGARHFLNAAPPDNYFRMGFHAINPDAIAQGVEVLRGQLEQMG

>lcl|NZ\_FO834906.1\_prot\_WP\_004178926.1\_1642 [locus\_tag=BN49\_RS09615] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_004178926.1] [location=1680571..1681422] [gbkey=CDS]

MKKSLASMCLSAVLTVAFSYHAVAADLPEIEKSGTLKVATEDDYAPFNFMNNGQADGFNKDMLEELRKYA

KFHVDQSILPWTGLLAAVSTGQYDMALTGAVITDERLKVFDFTPPWASAQHYFVKRAGDTSLNTIADLSG

KKVGLQAGSALLARLPELKAMLEKTGGKLGPVVEYPSYPEAYADLANKRLDYVINVVISVNDLAKAKPKV

FAKGLAVSGPGYMAWPIPKNSPQLLAYMTRFMNHMKETGKLAELQKKWFGETYDNLPTEAITSPEQFHKL

AGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002893187.1\_1643 [locus\_tag=BN49\_RS09620] [protein=amino acid ABC transporter permease] [protein\_id=WP\_002893187.1] [location=1681470..1682111] [gbkey=CDS]

MDAISWQLLIEGAWTTLWISAIAIAFGVVAGLLIALVRMLRLPVIDQLLVVYISLARATPLVTLVLFLFL

SLPTMGINLDKNVAAIVALTLNTSAFNAEIWRNAFRTFPREQREAAESVGMRRWTYFRYIMLPQMWIESL

PALVNEMSFLIKGSPAIAVIGVVDLTRVTNRISSVTYEPLSPILAAGLLYVAIIGCLLKLQGIAERKARR

LAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002893189.1\_1644 [locus\_tag=BN49\_RS09625] [protein=ABC transporter permease subunit] [protein\_id=WP\_002893189.1] [location=1682126..1682791] [gbkey=CDS]

MNQWGVIWSVRDSFIAGLFATLELFITAALAALIIGIALCYFSEYQKKVINRIIIGFVSLMRAIPFLILA

YLLYYGLPQLGISMEPWTAGLLALIIYHGAYFFEILRSQRRVFSGGYIEAAIAQGFSRYAIFRRIILPNI

VSSALPLIGNQLIICLKDTAFLSIITVQEITAAANSVQATYFIPFNAFIVAIGLYWAISILLELLIKRLT

AWGAKRGMSHA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151676.1\_1645 [locus\_tag=BN49\_RS09630] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_004151676.1] [location=1682784..1683545] [gbkey=CDS]

MPESIAVSVKNVSKQFDNVEVLRDINLTVEKGTVVSILGSSGSGKSTLLRCMNWLEQPDRGEIHIGGQRL

GIDEQRGRAMSHRQLAKIRERVGMVFQSFNLWPHLTVQQNVSEALLRVKGMKRDEAKAMAMQQLEKVGMA

HKADVYPITLSGGQKQRVAIARSLAMSPEVILFDEPTSALDPELVNEVLGVMKALAAEGYTMVVVTHEMD

FARQVSNEVVFLEKGLLIEKAPPEKFFTQPDSERVRQFLQSSR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176941.1\_1646 [locus\_tag=BN49\_RS09635] [protein=SDR family NAD(P)-dependent oxidoreductase] [protein\_id=WP\_004176941.1] [location=complement(1683599..1684363)] [gbkey=CDS]

MATSNVVFITGATSGFGEAAAQVFADAGWSLVLSGRRYPRLKALQDRLAARVPVHIIELDVRDSEAVAAA

VASLPADFADITTLINNAGLALSPLPAQEVALEDWKTMIDTNVTGLVTVTHALLPTLIRHGAGASIINIG

SIAGQWPYPGSHVYGASKAFVKQFSYNLRCDLLGTGVRVTDLAPGIAETEFTLVRTKGDQAASDKLYRGT

TPLSARDIAEQMFYIATLPAHMNINRVEVMPVRQAWQPFAIDRD

>lcl|NZ\_FO834906.1\_prot\_WP\_016531493.1\_1647 [locus\_tag=BN49\_RS09640] [protein=aspartate aminotransferase family protein] [protein\_id=WP\_016531493.1] [location=1684544..1685881] [gbkey=CDS]

MKLAIHNEVAVSNDEVRQLDRTYVFHSWSMQGNLNPLVIAGAQGCELWDYEGNTWLDFSSQLVNVNIGYQ

HPRVLAAMKSQLETLVTIAPATANLARGEAAKRIVDLAPAGFSKVFFTNAGADANENAIRMARLYTGRDK

VLSAYRSYHGNTGSAIAATGDWRRVPNEFSRGHVHFFNPYLYRSEFNAATEEEECQRALAHLRRIIECEG

PTAIAAILLESIPGTAGILVPPAGYMQGVRALADEFGIVLILDEVMAGFGRTGSWFAFEQDGVVPDLVTF

AKGVNAGYVPAGGVLISEPIARYFDDHFFAGGLTYSGHPLAMAAIVATIDAMKEEKVVENAASIGNEVLR

PGLEALAEKHAIIGEVRGRGLFQALELVSSREQKTPLTAADMAAIKGALTEAGLLAFVVENRIHVVPPCT

ITAEQVAQGLAIFDAVFARFASLAK

>lcl|NZ\_FO834906.1\_prot\_WP\_021313382.1\_1648 [locus\_tag=BN49\_RS09645] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_021313382.1] [location=complement(1686623..1687327)] [gbkey=CDS]

MAIVNLQDLQVTFGAKTAVSAASFRVDAGETFSLIGASGCGKSTILRVLAGLQREWRGSVDLLGQAITPG

FRFQGDLRRNVQMVFQDPYASLHPNHTLWRTLAEPLQIHGIRDVTPRVTTALEQVGLAADAVRRYPHQLS

GGQRQRVAIARALLLRPQILLLDEPTSALDMSVQAEILNLLNRLKQEHGMTYLLVSHDADVIAHMSDRAA

FMAEGVIQRFFDREALVNGEHRMR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042895.1\_1649 [locus\_tag=BN49\_RS09650] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_046042895.1] [location=complement(1687314..1688150)] [gbkey=CDS]

MTDIRLTVQGLAVDYPTARVVDNVSFTLGNERLALVGESGSGKSMTARALMGLVRKPGVVSAERLEVLGR

DVLTLSARGWRELRGNDIAMVLQDPRYALNPVQSIQTQLEEALTLHQRLSRRGRAEAVKDAIAAVGLDLP

VLSRYPGELSGGMGQRVIIALALLNNPKVLIADEPTSALDARLRNQILELLVEQSAQRQMAMLLISHDLP

LVAAHCDRVLVMYQGRQVDEMPARALPSATHPYTRTLWTCRPNAHTYGQMLPTLDRTLDFTETAYGDR

>lcl|NZ\_FO834906.1\_prot\_WP\_004142505.1\_1650 [locus\_tag=BN49\_RS09655] [protein=ABC transporter permease] [protein\_id=WP\_004142505.1] [location=complement(1688143..1688976)] [gbkey=CDS]

MPTYLFLRRLRRSPAAFSGLTLVILLVLTALFAPWLAPHDPNWQDAAARLQGPGAGHWLGTDSYGRDLLS

RLLYGARPALGLVALVTAITLPVGLLVGILSGYYGGWLERILMRFTDVVMSMPRLILAFAFVAMLGPGLV

NGALALALTTWPAYARQARSEIQRLRHSDYLAAAEMLGIRGGRLLVGHILPLCLPSAIVRLALDLAGIIL

AAAGLGFLGLGARPPMAEWGAMIADGMQVIFDQWWIAAIPGAAILLASLAFNLLGDGLRDILEPQHD

>lcl|NZ\_FO834906.1\_prot\_WP\_023279735.1\_1651 [locus\_tag=BN49\_RS09660] [protein=ABC transporter permease] [protein\_id=WP\_023279735.1] [location=complement(1688976..1689998)] [gbkey=CDS]

MPSFSTHLTRLLQGLFTLLLTLFGLLLVTFSLSALSPVDRVLQIVGDHASQSTYDQVRHQLGLDQPLPVQ

FWHYLVNLAHGDLGIASATGQPVLHDLLAVFPATLELATLALIVGAVLGIVAGVLCARYAGSPWDLAVRT

FTLLGNSVPIFWLGLLMLALFYARLQWAPGPGRLDDIYQYTVEPRSGFALIDTWLSGDTAAFKNAIGHLA

LPVLVLAYYSLASITRLTRSACLSEMNKEYILLARAKGAGEMTILLRHVLPNIRGTLLTVIALAWTSMLE

GAVLTETVFSWPGIGRYLTTALFAGDTTAIMGGTLLIGVSFVLINNLTDLLVRLTDPRVR

>lcl|NZ\_FO834906.1\_prot\_WP\_004142499.1\_1652 [locus\_tag=BN49\_RS09665] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004142499.1] [location=complement(1690118..1691686)] [gbkey=CDS]

MTKKLLPLLLLSALSAAAHAATPPNTLVVAQGLDDIVSLDPAEANELSSIQTVPSLYQRLVQPDRNNPEK

IVPILAESWQADPAAKTLTIKLKPDAKFASGNPLRPEDVIFSYTRAVTLNKSPAFILNVLGWQPDNIASQ

LKKVDDHTLTLHWTADVSPAVALNILSTPIASIVDEKQVAPNAKNNDFGNDWLKMHSAGSGAYKMRVYQP

HQAIVLEANASSPTGAPKIKSIIIKNVPDPASRRLLIQQGDADVARDLGADQIAALQDKPGVKVLSIPSA

EQNYLVFNTANSANPLLNNPAFWEAARWLVDYEGITKNLLKGQYFIHQSFLPAGLPGALETNPFTFDPQK

AKAILDKAGIKDAHFTLDVENKPPFITIAQSLQASFAQGGVKVDLLPAAGSQVYARVRAKQHQAAIRLWI

PDYFDAHSNASAFAWNDGKSSTVAGLNGWQIPELNKATLAAVAEPDPAKRLGLYKTMQETLLQHSPYVFI

DQGKTQIVVRDNVKGYQQGLNADMVWYDNVTK

>lcl|NZ\_FO834906.1\_prot\_WP\_002893466.1\_1653 [locus\_tag=BN49\_RS09670] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002893466.1] [location=1691892..1692587] [gbkey=CDS]

MPEINEYGQQVNDLVPGWQGAQVLRRTALNGRFCRLEPLDVDRHAADLFAAYALGDNSDWTWLASTRPES

VAATAHWIAGKVNDDALVPYAVVDLRSEQAVGIVSYMAIEREMGTVEIGHVTWSRRMKNTPLGTEAVWLL

LKNGFDHGYRRLEWKCDSMNVASRRAAERLGFSWEGRLRQRLVRKGRTRDSDMLSIIDGEWPARDAALRA

WLAAENFTADGQQIKRLEAFR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530003.1\_1654 [gene=betA] [locus\_tag=BN49\_RS09675] [protein=choline dehydrogenase] [protein\_id=WP\_016530003.1] [location=complement(1692708..1694372)] [gbkey=CDS]

MQFDYIIIGAGSAGNVLATRLTEDPNTTVLLLEAGGPDYRFDFRTQMPAALAYPLQGKRYNWAYETEPEP

YMNNRRMECGRGKGLGGSSLINGMCYIRGNAMDLDNWAKEPGLEHWSYLDCLPYYRKAETRDIGPNDYHG

GDGPVSVTTPKPGNNPLFEAMVEAGVQAGYPRTDDLNGYQQEGFGPMDRTVTPQGRRASTARGYLDQARG

RPNLTIRTHALTDHIIFAGKRAVGVEWLEGESTIPSKATANKEVLLCAGAIASPQILQSSGVGNPELLRQ

FDIPVVHDLPGVGENLQDHLEMYLQYECKEPVSLYPALQWWNQPKIGAEWLFGGTGIGASNQFEAGGFIR

SRAEFAWPNIQYHFLPVAINYNGSNAVKEHGFQCHVGSMRSPSRGHVRLKSRDPHAHPAILFNYMSHEQD

WQEFRDAIRITREIMNQPALDKYRGREISPGIECQSDAELDEFVRNHAETAFHPCGTCKMGYDEMAVVDG

EGRVHGLEGLRVVDASIMPQIITGNLNATTIMIGEKMADAIRGRQPLPRSTATYYVAGDAPVRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530004.1\_1655 [gene=betB] [locus\_tag=BN49\_RS09680] [protein=betaine-aldehyde dehydrogenase] [protein\_id=WP\_016530004.1] [location=complement(1694386..1695858)] [gbkey=CDS]

MSRMAEQQLYINGGYTSATSGRTFETINPATGEVLATVQAAGREDVDHAVESAQRGQKIWAAMTAMERSR

ILRRAVDLLRQRNDELARLETLDTGKPLSETAAVDIVTGADVLEYYAGLIPALEGSQIPLRDSSFVYTRR

EPLGVVAGIGAWNYPIQIALWKSAPALAAGNAMIFKPSEVTPLTALKLAEIYSEAGLPDGVFNVLPGIGA

ETGQYLTEHPDIAKISFTGGVASGKKVMANSAASSLKEVTMELGGKSPLIIADDADLDLAADIAMMANFY

SSGQVCTNGTRVFVPAKRKAEFEHKILERVARIRAGDLFADDTNFGPLVSFPHRDNVLRYIESGKREGAR

LLCGGEALKGDGFDNGAWVAPTVFTDCSDEMTIVREEIFGPVMSILSYADEAEVIRRANATEYGLAAGVV

TPNLNRAHRIIHQLEAGICWINSWGESPAEMPVGGYKHSGIGRENGVMTLQSYTQVKSILVEMGKFQSIF

>lcl|NZ\_FO834906.1\_prot\_WP\_004176934.1\_1656 [gene=betI] [locus\_tag=BN49\_RS09685] [protein=transcriptional regulator BetI] [protein\_id=WP\_004176934.1] [location=complement(1695872..1696459)] [gbkey=CDS]

MPKLGMQPIRRRQLIDATLDAINEVGMHDATIAQIARRAGVSTGIISHYFKDKNGLLEATMRDITSQLRD

AVLNRLHALPNGSASQRLQAIVGGNFDETQISSAAMKAWLAFWASSMHQPMLYRLQQVSSRRLLSNLVYE

FRRELPREQAQEAGYGLAALIDGLWLRAALSGKPLDKTLAQSLTSHFIRQHLPNP

>lcl|NZ\_FO834906.1\_prot\_WP\_004142478.1\_1657 [gene=betT] [locus\_tag=BN49\_RS09690] [protein=choline BCCT transporter BetT] [protein\_id=WP\_004142478.1] [location=1696588..1698621] [gbkey=CDS]

MTDLSQSREKDKINPVVFYTSAGLILLFSLMTIFFRDFSAEWIGRTLDWVSKTFGWYYLLAATLYIVFVV

CIACSRFGSVKLGPEQSKPEFSLLSWAAMLFAAGIGIDLMFFSVAEPVTQYMQPPEGAGQTIEAARQAMV

WTLFHYGLTGWSMYALMGMALGYFSYRYNLPLTIRSALYPIFGKRINGPIGHSVDIAAVIGTIFGIATTL

GIGVVQLNYGLSVLFDIPDSLAAKAALIALSVIIATISVTSGVDKGIRVLSELNVALALGLILFVLFMGD

TSFLLNALVLNVGDYVNRFMGMTLNSFAFDRPVEWMNNWTLFFWAWWVAWSPFVGLFLARISRGRTIRQF

VMGTLIIPFTFTLLWLSVFGNSALYEIIHGDAAFAQEAMAHPERGFYSLLAQYPAFTFSASVATITGLLF

YVTSADSGALVLGNFTSKLKDINSDAPNWLRIFWSVAIGLLTLGMLMTNGISALQNTTVIMGLPFSFVIF

FVMAGLYKSLKVEDYRRVSASRDTAPRPMGLQDRLSWKKRLSRLMNYPGTRYTKLMMETVCYPAMEEVAQ

ELRLRGAAVELKSLPPEEGENLGHLDLLVHMGDEQNFIYKIWPQQYSVPGFTYRARSGKSTYYRLETFLL

EGSQGNDLMDYSKEQVITDILDQYERHLNFIHLHREAPGNSVMFPDG

>lcl|NZ\_FO834906.1\_prot\_WP\_004178946.1\_1658 [gene=ivy] [locus\_tag=BN49\_RS09695] [protein=Ivy family C-type lysozyme inhibitor] [protein\_id=WP\_004178946.1] [location=complement(1698667..1699113)] [gbkey=CDS]

MFKALTAIVALAASASVMAQGDVTLNSLAHDAATRASFNQMVKGHQLPAWVTTGGTGSPAQTVKLGSESW

QVLSACKPHDCGHERIAVIWSEKSKQMSGVYSVVDEKTDQEKLTWLNVSDALSIDGKTVLFAALSGSLDN

HPDAFNYQ

>lcl|NZ\_FO834906.1\_prot\_1659 [locus\_tag=BN49\_RS31405] [protein=hypothetical protein] [pseudo=true] [location=1699338..1699758] [gbkey=CDS]

MAYVNHLLTFIESNPALAVGFNLILLLLSGIFAHLLCKFLLIKVVRKVFFSSHKQDVPLEKDRRIAEKLS

NFIPVIIVYYVLQFMPAMPASLVTAINTICGILFFIFMSVFFNEMLDIVNSSYLRKTKRKNHSIKGYIQI

>lcl|NZ\_FO834906.1\_prot\_WP\_223176074.1\_1660 [locus\_tag=BN49\_RS09700] [protein=mechanosensitive ion channel family protein] [protein\_id=WP\_223176074.1] [location=1699680..1700594] [gbkey=CDS]

MLDIVNSSYLRKTKRKNHSIKGYIQIGKILVHILAAIMILAVMSNKSPIIIISSLGAVAAVLMIVFQHTL

LSLVANVQLSSNDVLQLGDWIEMPDKNLSGEVTDIALHTITIRNWDNTISRIPTKNFLTETYTNWQAMFS

SGARRIMRSIAIDQHSVRFLDQEMLSSMLTIRGVSEPLATLLDGRDPGGVADRWFVDNGLTNLTLFRHYL

MHYLAERPDIIKEMYIVARTLKPSPSGIPLEIYCFTTSTLWKDYENTQSAIFEYITAVAGQFSLRLYQYP

AGHDFWRLSQEHAARTGLPPSAEG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530005.1\_1661 [locus\_tag=BN49\_RS09705] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_016530005.1] [location=complement(1700591..1701484)] [gbkey=CDS]

MADFPPVASLRSFEAVARLGSVTQAAHELSVTHSAVSQHIKQLEALVGVTLFIRHGRGVRITEEGRLYAL

QIREALQHIADATRMVQIKPRTLEVSLATLPSFGCHWLLPRLARFQARHPQIAVRLLTSLAVVNLQQEGI

DLAIRMGQGDWEGMESRHLFADEQLVVAAPGYRGGNLPTTPQAIAASDIFFSMESWNAWCSQAGLEKPIV

PAGLRLNDSNLVLEAVRLGAGVALERRSLVAGAIARGELVQLTAVTVPYPWHYWLTVSPQAENRPEVARF

IAWLEEEIALWRQQISV

>lcl|NZ\_FO834906.1\_prot\_WP\_046042900.1\_1662 [locus\_tag=BN49\_RS09710] [protein=glutathione S-transferase] [protein\_id=WP\_046042900.1] [location=1701739..1702344] [gbkey=CDS]

MKLIGMMDSPYVRRVAVSLALYGVEFESLPLSVFSGFDEFSRINPVVKAPTVVLDNGTQLMDSTLILHYF

ETTNPAGRRLLPVHPEALARDLHLLGVILAACEKAVQHVYEHRLRPEEKQHQPWIARVTGQLLAACREWD

ARLADRAAAAQPDQVMVTSTVVWSFIQLMIPAVVSAAAFPHICALAEKGEALPAFQQYPLG

>lcl|NZ\_FO834906.1\_prot\_WP\_021313378.1\_1663 [locus\_tag=BN49\_RS09715] [protein=SDR family oxidoreductase] [protein\_id=WP\_021313378.1] [location=complement(1702397..1703182)] [gbkey=CDS]

MIGKDFAQHLFSLRDRVAFVTGAGSGIGQTIACSLASAGARVVCFDLRDDGGLAETVSHIESIGGQACSY

NGDVRQIADLRAAVALAKSRYGRLDIAVNAAGIANANPALEMESEQWQRVIDINLTGVWNSCKAEAELML

ESGGGSIINIASMSGIIVNRGLDQAHYNCSKAGVIHLSKSLAMEWVGKGIRVNSISPGYTATPMNTRPEM

VHQTREFESQTPMQRMAKVEEIAGPALFLASDAASFCTGVDLVVDGGFVCW

>lcl|NZ\_FO834906.1\_prot\_1664 [locus\_tag=BN49\_RS09720] [protein=SDR family oxidoreductase] [pseudo=true] [location=complement(1703383..1704180)] [gbkey=CDS]

MQRDFQNKTVVITGACRGIGAGIAERFARDGANLVMVSNAERVHETAETLRQRYQADILSLQVDVTDEAQ

VQGLYEQAAARFGTIDVSIQNAGVITIDYYDRMPKADFEKVLAVNTTGVWLCCREAAKYMVKQNHGSLIN

TSSG\*GRQGFIYTPHYAASKMGVIGITQSLAHELAPWNITVNAFCPGIIESEMWDYNDRVWGEILSTEQK

RYGKGELMAEWVEGIPMKRAGKPEDVAGLVAFLASDDARYLTGQTINIDGGLIMS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042902.1\_1665 [locus\_tag=BN49\_RS09725] [protein=ABC transporter permease] [protein\_id=WP\_046042902.1] [location=complement(1704241..1705308)] [gbkey=CDS]

MNQKYMIYMYLLKARTFIALLLVIAFFSVMVPNFLTASNLLIMTQHVAITGLLAIGMTLVILTGGIDLSV

GAVAGICGMVAGALLTNGLPLWNGDILFFNVPEVILCVAIFVVLVGLVNGAVITRFGVAPFICTLGMMYV

ARGSALLFNDGSTYPNLNGMEALGNTGFATLGSGTLLGVYLPIWLMIGFLVLGYWLTTKTPLGRYIYAIG

GNESAARLAGVPIVKAKIFVYAFSGLCAAFVGLIVASQLQTAHPMTGNMFEMDAIGATVLGGTALAGGRG

RVTGSIIGAFVIVFLADGMVMMGVSDFWQMVIKGVVIVTAVVVDQFQQKLQSKVILMRRHEEKLAAIPPN

GATSS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176928.1\_1666 [locus\_tag=BN49\_RS09730] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_004176928.1] [location=complement(1705326..1706870)] [gbkey=CDS]

MAPHDLVAPQPVESEVIIETRGLSRVYPGVTALDNVNYRVYRNKVNVLIGENGAGKSTMMKMLAGVETPS

SGQIILDGEAVSLQSTHQAEKLGISIIFQELNLFPNMNVMDNIFMANEFFQKGRINEKYQYALAKSLLER

LELDVDPYAPLGELGIGHQQLVEIARALSKDTRVLIMDEPTSALSQSEVKVLFKVIAQLKRRGVTIIYIS

HRLEELMEIGDNITIFRDGRFISERHVSDASVPWIIEQMVGDKKKHFDYQPAPKGDAVLDVKGLTALHPS

GGYKLNDVTFTLSKGEVIGIYGLLGAGRTELFKGLVGLMPCQRGEVHLNGESIGKSRFQQRLKKGLALVP

EDRQGEGVVQMMSIQANMTLSDFSLQGFRRAWRWLNPQKEETCVKEMIQQLAIKVSDATLPITSLSGGNQ

QKVVLGKALMTQPQVVFLDEPTRGIDVGAKTDVYHLIGKMAQQGLAVMFSSSELDEVMALADRILVMADG

RITADLPRHAVTREQLIAASTPQD

>lcl|NZ\_FO834906.1\_prot\_WP\_002893596.1\_1667 [locus\_tag=BN49\_RS09735] [protein=DUF2291 domain-containing protein] [protein\_id=WP\_002893596.1] [location=complement(1706872..1707492)] [gbkey=CDS]

MFKKTCLTLAVLALGGCRIVSQQELADLKSPPNPHMANMDKTWQQSIVPQVVTKARPAAELMSALKAAKD

IDSACKTLGYRAQDENPCIFYVKVSGTVSKLDTASRSGKMTLTDASVGKVTVQIGPTLRGTQLRDGYSGA

SYQDFNDQVLFGEYSKNINSQAVKMIQTANVKTGDSVEVYGVFSAWDIPQTLPEITPAKIIHAGGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002893597.1\_1668 [locus\_tag=BN49\_RS09740] [protein=D-ribose ABC transporter substrate-binding protein] [protein\_id=WP\_002893597.1] [location=complement(1707536..1708471)] [gbkey=CDS]

MKLRITLLTAATLTAFSFAAHAAEKGTIMIMVNSLDNPYYASEAKGASEKAQALGYKTTVLSHGEDVKKQ

NELIDTAIGKKVQGIILDNADSTASVAAVEKAKKAGIPVVLINREIPVDDVALEQITHNNFQAGSEVANV

FVEKMAEKGKYAELTCNLADNNCVTRSKSFHQVIDQYPDMVSVAKQDAKGTLIDGKRIMDSILQAHPDVK

GVICGNGPVALGAIAALKAANRSDVIVVGIDGSNDERDAVKAGTLQATVMLQAQAIAAQGVTDLDNYLQK

GEKPAKQRVMFRGILITQDNADKVQDFNIKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002893599.1\_1669 [locus\_tag=BN49\_RS09745] [protein=FGGY-family carbohydrate kinase] [protein\_id=WP\_002893599.1] [location=complement(1708631..1710151)] [gbkey=CDS]

MQATAKEFIIALDEGTTNAKAVVLDSRGKVIVKFSQPLAIQTPRDGWVEQSGEALVTASLTVIASAVAHV

GAENVAALAISNQRETAIGWYRDSGEPINAAITWQCTRSAAFCDTLRHDRQEQHIKRATGLPIAPLFSAS

KMRWLLDATVDGHLRAERGEICLGTIDSWLLWNLTAGEAFCCDYSNASRTQLLNLHRGEWDDEMLALFGI

PRAALPEIKPSSGLFGHTKGLAAIPDGIPIMSMIGDSHAALFGHALGEAGCVKATYGTGSSVMAPVKSAQ

CDIDALATTVAWHDGDQLVWGLEGNIPHTGDAVAWMADSTGLSELSAAELAHELNTLPASVDSTLGVYFV

PALTGLGAPWWDDSARGVICGLSRGVKRAHLIRAALESITYQIADVVVAMRQHEEFTLTALMVDGGPTNN

DWLMQYQADLLGCPVMRSDVPELSAIGAALLARKALHPGSTADLQAFLTEHSTFQPDMARHQRLQTRWQE

WRHAVDRTLWKPDSPA

>lcl|NZ\_FO834906.1\_prot\_WP\_002893602.1\_1670 [locus\_tag=BN49\_RS09750] [protein=sugar-binding transcriptional regulator] [protein\_id=WP\_002893602.1] [location=complement(1710501..1711451)] [gbkey=CDS]

MAKQDEQRLLVKIATLYYLEGRKQSDIAQLLSLSQSFVSRAITRCQKEGVVKISVVQPSNIFLKLEKGLE

DRYGLKQAVVVDTEEEASDHTIKRAIGSAAAHYLETRLRPKDLIGVSSWSSTIRAMVDEVHAQNLKASGV

IQLLGGVGPNGNVQATILTQTLAQRLNCDAWLLPSQSIEGSMEERNRLLASKDVADVVSRFDEVDIAIVG

IGILEPSQLLKTSGNYYHEDMLQVLAARGAVGDICLHYYDKNGHPVLRDDEDPVIGMALEKVKKCPNVVA

LAGGTDKVAAIKGALTGGYIDVLITDYPTARMLVSD

>lcl|NZ\_FO834906.1\_prot\_WP\_002893603.1\_1671 [locus\_tag=BN49\_RS09755] [protein=transketolase] [protein\_id=WP\_002893603.1] [location=1711826..1712656] [gbkey=CDS]

MNPYRYDIQTLERKARAVRRHIVRLNANSPAGGHTGADLSQVELLTALYFRVLNVAPDRLDDPQRDIYIQ

SKGHAVGCYYCVLAEAGFFPVEWLETYQHANSHLPGHPVRQKTPGIELNTGALGHGLPVAVGLALAAKKS

NSTRRIFLITGDGELAEGSNWEAALAAAHYGLDNLVIINDKNNLQLAGPTREIMNTDPLADKWRAFGMEV

SECQGNDMASVVSVIEGLKQEGKPNVIIANTTKGAGISFIQGRPEWHHRVPKGEEIALALEELKDE

>lcl|NZ\_FO834906.1\_prot\_WP\_023282274.1\_1672 [locus\_tag=BN49\_RS09760] [protein=transketolase] [protein\_id=WP\_023282274.1] [location=1712649..1713584] [gbkey=CDS]

MSNAEHLANVMVEAFIAAVERGVDLVPVVADSTSTAKIAPFIKQFPGRLVNVGIAEQSMVGTAAGLALGG

KVAVTCNAAPFLISRANEQIKVDVCYNNTNVKLFGLNAGASYGPLASTHHAIDDLAVMRGFGNIQIFAPS

SPRECRQIIDYAIGYQGPVYIRLDGKALPELHDESYRFVPGAIVTLREGDDIALVATGSTVHEIVDAAQM

LADAGIQAKVVSVPSLRPCDTAALLAALKPCKAVITVEEHNVNGGVGSLVAEVLAEAGVGIPLKRLGIPD

GEYAAAADRGWLRKHHGFDAASVAELAQKMR

>lcl|NZ\_FO834906.1\_prot\_WP\_019705360.1\_1673 [gene=entD] [locus\_tag=BN49\_RS09765] [protein=enterobactin synthase subunit EntD] [protein\_id=WP\_019705360.1] [location=complement(1713636..1714259)] [gbkey=CDS]

MRHHRTVLPLAGYTIQQIDFDPATFQPEDLFWLPYHASLTGWGRKRQAEHLAGRIAAAYALREVGEKRLP

AIGDQRQPLWPTPWFGSISHCGQRALAVIADRPVGVDIERRFTPQLAAELESSIISPAEKTALLHSGLPF

PLALTLAFSAKESGFKACHPDVQAGVGFNDFTLAAIKEGNLRLRLSTVEYRLQWIQAGEYIITLCAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004210903.1\_1674 [gene=fepA] [locus\_tag=BN49\_RS09770] [protein=siderophore enterobactin receptor FepA] [protein\_id=WP\_004210903.1] [location=complement(1714326..1716554)] [gbkey=CDS]

MNNRIKSLALLVNLGIYGVAFPLSAAETATDDKNSAAEETMVVTAAEQNLQAPGVSTITADEIRKRPPAR

DVSEIIRTMPGVNLTGNSTSGQRGNNRQIDIRGMGPENTLILIDGKPVTSRNSVRLGWRGERDTRGDTSW

VPPEIIERIEVIRGPAAARYGNGAAGGVVNIITKKTGDEWHGSWNTYMNAPEHKDEGSTKRTNFSLSGPL

GGDFSFRLFGNLDKTQADAWDINQGHQSERTGIYADTLPAGREGVKNKNIDGLVRWEFAPMQSLEFEAGY

SRQGNLYAGDTQNTNSNDLVKENYGKETNRLYRNTYSVTWNGAWDNGVTTSNWAQYERTRNSRKGEGLAG

GTEGIFNSNQFTDIDLADVMLHSEVSIPFDYLVNQNLTLGSEWNQQRMKDNASNTQALSGGEIPGYDSTG

RSPYSQAEIFSLFAENNMELTDTTMLTPALRFDHHSIVGNNWSPSLNLSQGLWDDFTLKMGIARAYKAPS

LYQTNPNYILYSKGQGCYASKDGCYLQGNDDLKAETSINKEIGLEFKRDGWLAGVTWFRNDYRNKIEAGY

APVYQNNKGTDLYQWENVPKAVVEGLEGTLNVPVSETVNWTNNITYMLQSKNKETGDRLSIIPEYTLNST

LSWQVRDDVSLQSTFTWYGKQEPKKYNYKGQPVTGSEKNEVSPYSILGLSATWDVTKYVSLTGGVDNVFD

KRHWRAGNAQTTGGATGTMYGAGAETYNESGRTWYLSVNTHF

>lcl|NZ\_FO834906.1\_prot\_WP\_046042907.1\_1675 [gene=fes] [locus\_tag=BN49\_RS09775] [protein=enterochelin esterase] [protein\_id=WP\_046042907.1] [location=1716814..1718022] [gbkey=CDS]

MLRTGSEEWWQTLRGPQCRAVDDAIEVTFWWRDPAGDETRSPHRRVWLYITGVTDHHQNARPQSLQRLPG

TDAWFWRTTLSPTWRGSYCFIPSDRDDDFSPEVFSADAPDRALLREGWRKLLPRAIADPLNPHSWRGGRG

HGVSALEMPQAPAQPGWDPLNEAHPAARCLEWRSARLGNHRRVWIYTPGEAVDPQTRPLAILLDGQFWAE

SMPVWSPLAALTREGRLPPAVYLLIDAIDNQRRGVELPCHRDFWLAVQEELLPLVHGYAPFSDRPDRTVV

AGQSFGGLAAMFAALNWPQRFGCVLSQSGSYWWPHRDGRGKGFIGEQLRQGEVSAAGLRVWLEAGQREPI

IFRANQALLAQLTTTQQTIFWRQVDGGHDALCWRGGLTAGLIQLWQPLLSHP

>lcl|NZ\_FO834906.1\_prot\_WP\_004176919.1\_1676 [locus\_tag=BN49\_RS09780] [protein=MbtH family NRPS accessory protein] [protein\_id=WP\_004176919.1] [location=1718050..1718253] [gbkey=CDS]

MQFSNPFDNPQGQFYILRNDQQQYSLWPAHCDLPAGWTVVCPPQSAEACNAWLAANWSTLTPAHHAS

>lcl|NZ\_FO834906.1\_prot\_WP\_046042909.1\_1677 [gene=entF] [locus\_tag=BN49\_RS09785] [protein=enterobactin non-ribosomal peptide synthetase EntF] [protein\_id=WP\_046042909.1] [location=1718264..1722145] [gbkey=CDS]

MTTRLPLVAAQPGIWMAERLSTLPGAWSVAHYVELRGALDPTLLGKAIVAGLQQADTLSLRFEEEEGEVW

QWLAADRTFAEPSIIDLRTAPDPHRAATEWMQADLAQDLRVDGGNPLVCHQLLRVGDDRWYWYQRYHHLL

VDGFSFPAITRQIAAIYRAWQRGEATPESPFTPFAEVVDEYQRYAGSEAWQRDKAFWQAQRQALPAPASL

SAAPLGGRAAGSDIWRMKLEMNADAFRRLASHAPQCQPADLALALTTLWLGRLCNRMDYAAGFIFMRRMG

SAALTSTGPVLNVLPLAVHIDARETLADLAMRLAAQLKKMRRHQRYDAEQIVRDSGKAAGDEPLFGPVLN

VKVFDYQLDIDGVQAVTHTLATGPVNDLELALFPDETGGLSLEILANKARYDEAELRRHMARLTALLAQF

AADPALRCGEAEMLSADELARLAAVNDTAVPLPATTLSALVADQARKTPDAPALADARWQFSYREMRQQV

VALAQLLRQRGVKPGDSVAVALPRSVFLTLALHGIVEAGAAWLPLDTGYPDDRLRMMLEDARPSLLIATE

DQLARFSDIPGLESLCYQQPLAAGDDAPLALSKPDHTAYIIFTSGSTGRPKGVMVGQTAIVNRLLWMQDR

YPLSADDVVAQKTPCSFDVSVWEFWWPFIAGAQLVMAEPEAHRDPQAMQQFFARYGVTTTHFVPSMLAAF

VASLDADSVAACRTLRRVFCSGEALPTELCREWERLTGAPLHNLYGPTEAAVDVSWYPACGSELAAVTGS

SVPIGWPVWNTGLRILDAAMRPVPPGVAGDLYLTGIQLAQGYLGRPDLTASRFIADPFAPGERMYRTGDV

ARWLTNGAVEYLGRSDDQLKIRGQRIELGEIDRVMSALPDVGQAVSHACVFNQAAATGGDARQLVGYLVS

DYGLPLDTAALKAQLAEQLPPHMVPVVLMQLAELPLSANGKLDRKALPLPTLGGERSGRPPEPGMETLVA

AAFSQLLGCEVNDIDADFFALGGHSLLAMRLAAQLSRQLARQVTPGQVMVASTVGKLSALLAADLSDEQA

QRLGLDTLLPLRESDGPTLFCFHPASGFAWQFSVLARYLSPRWSITGIQSPRPQGPMASAASLDEVCEHH

LRTLLAQQPHGPYYLFGYSLGGTLAQGIAARLRQRGEAVAFLGLLDTWPPETQNWAEKEANGLDPEVLAE

IDREREAFLAAQQGQASGELFSAIEGNYADAVRLLTTAHSAKFDGKATLFVAEKTRQEGMDPQVVWGPWV

GELEVFSQNCAHVDIISPQAFEAIGPVVREILG

>lcl|NZ\_FO834906.1\_prot\_WP\_002893737.1\_1678 [gene=fepC] [locus\_tag=BN49\_RS09790] [protein=iron-enterobactin ABC transporter ATP-binding protein] [protein\_id=WP\_002893737.1] [location=complement(1722210..1723004)] [gbkey=CDS]

MSAVPSRLRGEQLTLAYGNKTIAESLNVTIPDGHFTAIIGPNGCGKSTLLRTLSRLMTPASGHVWLDGAQ

IQQYASKEVARRIGLLAQNATTPGDITVQELVARGRYPHQPLFTRWRKEDEEAVNKAMRATGISDLALQS

VDTLSGGQRQRAWIAMVLAQETAIMLLDEPTTWLDISHQIDLLELLSELNREKGYTLAAVLHDLNQACRY

ATHLIALRDGRIVAEGAPKEIVTADLIERIYGLRCTIIEDPVAHTPLVVPLGRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004147521.1\_1679 [gene=fepG] [locus\_tag=BN49\_RS09795] [protein=iron-enterobactin ABC transporter permease] [protein\_id=WP\_004147521.1] [location=complement(1723001..1723993)] [gbkey=CDS]

MIAPSRRLIASCLLLMAASLLISLLGLAQGPVPLTIDQVFSALFGDAPRNVAMVVNEWRLPRVLMALLIG

AALGVSGAIFQSLTRNPLGSPDVMGFNTGAWSGVLVAMVLFGQNLTAIALAAMAGGVLTSLVVWLLAWRN

GIETFRLIIIGIGVRAMLVAFNTWLLLRASLETALSAGLWNAGSLNGLTWGKTWPSAPLILLMLVGSALL

VRRMRLLEMGDDTACALGVQVERSRLLLMLVAVVLTAASTALAGPISFIALVAPHIARRLSGTARWGLTQ

SALCGALLLALADYGAQRLFMPWQLPVGVLTVSLGGIYLIALLIQESRKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176917.1\_1680 [gene=fepD] [locus\_tag=BN49\_RS09800] [protein=Fe(3+)-siderophore ABC transporter permease] [protein\_id=WP\_004176917.1] [location=complement(1723990..1724997)] [gbkey=CDS]

MSFSTTAVRSVAVPGLLLLLALAAALSLTIGAKSLPIGTVFTAFSGTCQSADCTIVLDARLPRTLAGLLA

GVALGLAGALMQTLTRNPLADPGLLGVNSGASFAIVLGAALFGITSPQEQLLLAFCGALCASLLVAFTGS

QGGGQLSPVRLTLAGVALAAVLEGLSNGIALLNPDVYDQLRFWQAGSLDIRTLQTLKIVLLPVVVAGIAA

LLLSRALNSLSLGNDTATALGSRVARTQLIGLIVITVLCGSATAVVGPIAFIGLMMPHMARWLVGADHRW

SLPVTLLATPALLLFADVIGRLLVPGELRVSVVSAFLGAPVLIWLVRRQPRGGGL

>lcl|NZ\_FO834906.1\_prot\_WP\_004147525.1\_1681 [gene=entS] [locus\_tag=BN49\_RS09805] [protein=enterobactin transporter EntS] [protein\_id=WP\_004147525.1] [location=1725110..1726351] [gbkey=CDS]

MNRQSWLLNLSLLKTHPAFRAVFIARFISILSLGLLGVAIPVQIQMMTHSTWQVGLSVTLTGASMFVGLM

VGGVLADRYERKRLILLARGTCGVGFVGLCLNALLPEPSLAAIYLLGIWDGFFASLGVTALLAATPALVG

RENLMQAGAITMLTVRLGSVISPMIGGLLLATGGVAWNFGLAAAGTFITTLTLLRLPQLPPPPQPREHPL

RSLLAGLTFLCRSPLIGGIALLGGLLTMASAVRVLYPALAGSWQMSAGQIGLLYAAIPLGAALGALTSGQ

LAQTVRPGALMLATTVGSFVAIALFSLMPHWALGALCLALFGWLSAISSLLQYTLIQTQTPEHMLGRING

LWTAQNVTGDAIGAALLGGLGAVMTPAASASASGWALALVGVLLVGLLRELRRFQRPEIVNES

>lcl|NZ\_FO834906.1\_prot\_WP\_046042911.1\_1682 [gene=fepB] [locus\_tag=BN49\_RS09810] [protein=Fe2+-enterobactin ABC transporter substrate-binding protein] [protein\_id=WP\_046042911.1] [location=complement(1726495..1727454)] [gbkey=CDS]

MNFFSFCRRGALTGMLLLLGITSAQAADWPRQVTDSYGTHTLPSQPLRIVSTSVTLTGSLLAIDAPVVAS

GATTPNNHVADSQGFLRQWSEVAKARKLARLYIGEPSAEAVAAQMPDLILVSATGGDSALPLYDQLKTIA

PTLVINYDDKSWQTLLTQLGQITGHEQQASARIADFNKQLVSLKEKMKLPPQPVTALVYTAAAHSANIWT

PESAQGQMLEQLGFSLATLPGGLPASHSQGKRHDIVQLGGENLAAGLNGQSLFLFAGDQKDADAIYANPL

LAHLPAVAGKRVYPLGTETFRLDYYSALLVLQRLSSLFG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042912.1\_1683 [gene=entC] [locus\_tag=BN49\_RS09815] [protein=isochorismate synthase EntC] [protein\_id=WP\_046042912.1] [location=1727643..1728818] [gbkey=CDS]

METSLAEDVKKPTRTLSPDSFFFMSPYRSFTTSGCFRRFSQPAVGGDALNGEFQQQMAAAFAEARAAGIR

KPVMVGAIPFDTCQPSELYIPERWEAFSRPEKQRSARYAAPLEAMEVVERREIPEQDAFLAMVERAAALT

ATPEVDKVVLSRLIDITTRDRVDSGALMERLIAQNPASFNFHVPLSDGGVLLGASPELLLRKEGQHFSSL

PLAGSARRQPDDVLDREAGNRLLASDKDRHEHELVTQAMKSVLGPRSSQLSLPESPQLITTPTLWHLATP

IAGTALAEENAMSLACLLHPTPALSGFPHQAAKRLIAELEPFDRQLFGGIVGWCDDEGNGEWVVTIRCAR

LQQRTLRLFAGAGIVPASSPLGEWRETGVKLTTMLNVFGLN

>lcl|NZ\_FO834906.1\_prot\_WP\_004183353.1\_1684 [gene=entE] [locus\_tag=BN49\_RS09820] [protein=(2,3-dihydroxybenzoyl)adenylate synthase EntE] [protein\_id=WP\_004183353.1] [location=1728828..1730435] [gbkey=CDS]

MIAFTRWPEEFAARYRQKGYWQDLPLTNLITRHAENDAVAIIDGERQISYRQFNQLVDNLACSLQRQGLK

RGETALVQLGNVAEFYMTFFALLRIGVAPVNALFSHQRSELNAYAAQIKPALLIADREHALFADDSFLHA

FIAEHPSLRVALLRNDGGERDLATEINRPADNFIANPTPADEVAFFQLSGGSTGTPKLIPRTHNDYDYSI

RRSNEICGINAETRYLNALPAAHNYAMSSPGSLGVFLAGGRVILAADPSATLCFPLIEKHQINVASLVPP

AVSLWLQAIHEWGSNAQLQSLQLLQVGGARLSATLAARIPAEIGCQLQQVFGMAEGLVNYTRLNDSPERI

INTQGCPMCPDDEVWVADADGNPLPRGEVGRLMTRGPYTFRGYYNSPQHNAEAFDAEGFYCSGDLISIDE

DGYITVQGREKDQINRGGEKIAAEEIENLLLRHEAVIHAALVSIEDNLLGEKSCAYLVVTSPLRAVAVRR

FLREQGVAEFKLPDRVECVAALPLTPVGKVDKKQLRQWLAEGKLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004183356.1\_1685 [gene=entB] [locus\_tag=BN49\_RS09825] [protein=enterobactin biosynthesis bifunctional isochorismatase/aryl carrier protein EntB] [protein\_id=WP\_004183356.1] [location=1730449..1731300] [gbkey=CDS]

MAIPKLQAYALPEASDIPANKVNWAFEPSRAALLIHDMQEYFLNFWGENSAMMEKVVANIAALRDFCKQN

GIPVYYTAQPKEQSDEDRALLNDMWGPGLTRSPEQQQVIAALAPDEDDTVLVKWRYSAFHRSPLEEMLKE

TGRDQLIITGVYAHIGCMTTATDAFMRDIKPFFVADALADFSREEHLMALKYVAGRSGRVVMTEELLPLP

ASKAALRALILPLLDESDEPLDDENLIDYGLDSVRMMALAARWRKVHGDIDFVMLAKNPTIDAWWALLTR

EVH

>lcl|NZ\_FO834906.1\_prot\_WP\_085956482.1\_1686 [gene=entA] [locus\_tag=BN49\_RS09830] [protein=2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase EntA] [protein\_id=WP\_085956482.1] [location=1731309..1732055] [gbkey=CDS]

MDFHGQTVWVTGAGKGIGYATALAFVEAGANVTGFDLAFDGESYPFATETLDVADADQVREACSRLLANT

ERLDVLVNAAGILRMGATDQLSAEDWQQTFAVNVGGAFNLFQQTMAQFRRQRGGAIVTVASDAAHTPRIG

MSAYGASKAALKSLALTVGLELAGSGVRCNLVSPGSTDTDMQRTLWVSDDAEQQRIRGFGEQFKLGIPLG

KIARPQEIANTILFLASSHASHITLQDIVVDGGSTLGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002893892.1\_1687 [gene=entH] [locus\_tag=BN49\_RS09835] [protein=proofreading thioesterase EntH] [protein\_id=WP\_002893892.1] [location=1732056..1732469] [gbkey=CDS]

MAWKRELTLAALNASSENTMVAHLGIIYTRLEEGLLEAEMPVDARTHQPFGLLHGGASAALAETLGSMAG

WLMTEEGQCVVGTELNASHHRAVSSGKVRGECRPLHLGRQSQSWEIVVYDEKGRRCCTCRLGTAVLG

>lcl|NZ\_FO834906.1\_prot\_WP\_012737624.1\_1688 [gene=cstA] [locus\_tag=BN49\_RS09840] [protein=pyruvate/proton symporter CstA] [protein\_id=WP\_012737624.1] [location=1732826..1734931] [gbkey=CDS]

MNNSGKYLIWALLSVIGAFALGYIALNRGEQINALWIVVAAVCVYLIAYRFYGLYIAKTVLGVDPTRMTP

AVRHNDGLDYVPTDKKVLFGHHFAAIAGAGPLVGPVLAAQMGYLPGMIWILAGVVLAGAVQDFMVLFVST

RRDGRSLGELVKEEMGPTAGVLALVACFMIMVIILAVLAMIVVKALTHSPWGTYTVAFTIPLAIFMGIYI

RYLRPGRIGEVSVIGLVMLVFAIISGGWVAESPTWAPWFDYTGVQLTWILVGYGFVAAVLPVWLLLAPRD

YLSTFLKIGTIVGLAIGILIMRPTLTMPALTKFVDGTGPVWTGNLFPFLFITIACGAVSGFHALISSGTT

PKMLANESQACFIGYGGMLMESFVAIMALVAACIIDPGVYFAMNSPMAVLAPAGTTDVVASAAQVVSGWG

FSITPDTLHQIASEVGEQSIISRAGGAPTLAVGMAYILHGSLGGLMDVSFWYHFAILFEALFILTAVDAG

TRAARFMLQDLLGVISPGLKKTSSLPANLLATALCVLAWGYFLHQGVVDPLGGINTLWPLFGIANQMLAG

MALMLCAVVLFKMKRQRYAWVALLPTSWLLICTLTAGWQKSFSPDTKVGFLAIANKFQAMIDSGNIPPQY

TESQLAQLVFNNRLDAGLTIFFMIVVVVLALFSIKTALAALKEDKPTAKETPYQAMPADAQTITAQAKRA

H

>lcl|NZ\_FO834906.1\_prot\_WP\_002893903.1\_1689 [locus\_tag=BN49\_RS09845] [protein=YbdD/YjiX family protein] [protein\_id=WP\_002893903.1] [location=1735036..1735233] [gbkey=CDS]

MFDTLSKAGKYLGQAAKMMIGVPDYDNYVEHMRITHPDQTPMTYEEFFRERQDARYGGKGGAKCC

>lcl|NZ\_FO834906.1\_prot\_WP\_004176911.1\_1690 [locus\_tag=BN49\_RS09850] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004176911.1] [location=complement(1735230..1735634)] [gbkey=CDS]

MTIQYIKDEEGKDQYVVIPYSDYFRMRLALLEYDDEDESDWEDIPYESDIYDDVMLPGEVCDVMHKENVS

LQAAWRILRGMSQQEVAEKLGISQSAVSQLEALDSRPQKRTREKLAAIYGCTQEQISLYLPKEG

>lcl|NZ\_FO834906.1\_prot\_WP\_004147534.1\_1691 [locus\_tag=BN49\_RS09855] [protein=type II toxin-antitoxin system RelE/ParE family toxin] [protein\_id=WP\_004147534.1] [location=complement(1735609..1735911)] [gbkey=CDS]

MKIVWSKTADKQFSKIDTRYKSRIKSRLEKMDDKASPISDIKKLSSPENHYRLRLGDYRVIYTFGDPPGD

TCYVVAVKRRTTTTYLHEEHTEYDYSVHQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002893908.1\_1692 [locus\_tag=BN49\_RS09860] [protein=3-oxoacyl-ACP reductase FabG] [protein\_id=WP\_002893908.1] [location=complement(1736095..1736838)] [gbkey=CDS]

MQIDLTGKKALVTGASRGLGRAIALSLARAGADVVITYEKSVDKAQAVADEIKALGRYGEAVQADSASAQ

AIQDAVTHAARSLGGLDILVNNAGIARGGPLESMTLADIDALINVNIRGVVIATQEALVHMADGGRIINI

GSCLANRVAMPGIAVYAMTKSALNALTRGLARDLGPRGITVNLVHPGPTNSDMNPEDGEQAEAQRQMIAV

GHYGQPEDIAAAVTFLASPAAGQISGTGLDVDGGLNA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530506.1\_1693 [locus\_tag=BN49\_RS09865] [protein=oxidoreductase] [protein\_id=WP\_016530506.1] [location=complement(1736896..1737984)] [gbkey=CDS]

MSNSDIRVVPGPANYFSHPGSLERLSDFFNADQLSRAVWVYGERALAGAEPFLPAAFHLPEAKKIRFTGH

CSERDVAGLVQASGDDRAVVIGVGGGALLDSAKVLARRLGVPLVAIPTIAATCAAWTPLSVWYSDAGQAL

NFELFDDANFLVLVEPRIILNAPAEYLLAGIGDTLAKWYEAVVLAPQPKALPLTVRLGINGALAIRDVLL

ASSETALADQRRGDLTQAFRDVVEAIIAGGGMVGGLGERYTRVAAAHAVHNGLTVLPQTDKFLHGTKVAY

GILVQSALLGQDDVLAQLVQAYQRFNLPTTLAALEVDINNRAELDRVIAHTLRPGESIHYLPVTLTPEVL

RAAFEKVEYFSR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042918.1\_1694 [locus\_tag=BN49\_RS09870] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_046042918.1] [location=1738148..1739650] [gbkey=CDS]

MSANRLEMHNISLAFSGFQALNKVDFTFHGGSVHALTGANGAGKSTLMAVLCGTHAHYEGEVTINNLPVT

IRSPRDAKQLGIHLVQQEVDVALVPGLSIAENIMLDRLAEPGMTFRWSRVRQLAREALAQLDVALDVRRS

IDSCTLAEKQQILLARALSHHCRFLILDEPTAPLDQHESERLFAVVRRLQHQGIGVVFISHRIHELKAIC

DTLTVLRDGRLIESGPMAPLSGEQIVEKMLGHELSDIFPPPRPPHGEEVLLQVDGLHDEALLQDISLRLR

KGEILGIAGLAGAGKTELCKALFGASKSRVQRGELNGQPWRPRDPADSVGRGLALVPEERRKEGIFIEEP

IAMNLAVSADNSFSRWSLFGHRQAWRWAEEVIARLGVRATGPGQTLRRLSGGNQQKVAIGKWLRGDANVL

IFDEPTKGVDVKAKTDLFTLIDGLAREGKGVIYASGEFAELVGLCDRICVLWDGRIVAEIPGAEAREETL

LYYSTGGAAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002894035.1\_1695 [locus\_tag=BN49\_RS09875] [protein=ABC transporter permease] [protein\_id=WP\_002894035.1] [location=1739647..1740645] [gbkey=CDS]

MSKALAVNATVSGRQRFFDFLYKWGMLLTVVLLVAVFGLASDNFLDPFNIINILRSIAIVTVIAIGVSIS

LTIGGFDLSVGSTASLANALVISLFVWHGLGTTEAILITLALCTLVGLFNAFLIVVLRIPDMLATLASLF

VIQGVAMTYSYGGSITENMVLPSGEMAEGTIPAAFGALGQVPTIVIIMLVVTLVAQLALSFTTHGRRMYA

IGGNPEAARLSGLRITRYKVAAYVIASLLAGLGGILLASRIGSSQVNAGGGYLMDAVAAAWIGFSLAGSG

KPNALGTLVGAVILGVLSNGLVMLSVPYYAMDIIKGLVLAGALALTYFQRRT

>lcl|NZ\_FO834906.1\_prot\_WP\_002894036.1\_1696 [locus\_tag=BN49\_RS09880] [protein=sugar ABC transporter substrate-binding protein] [protein\_id=WP\_002894036.1] [location=1740666..1741730] [gbkey=CDS]

MKKIALSLMTLGLLQSTAALATAPTPVPAAIAEHNGPIRIAVIRNLGSDDNTTQFVAGALQEGKKLGFKI

STFLSNGDDAKFQDFVNQAISQKYDGIILSQGRDPYSTALVKKAVDAGIKVAVFDTAVSGEIPGVTVSQQ

DDASLTELSFGQLVKDFNGKANIVKLWVAGFPPMERRQAAYQTLLKQNPGIKELESIGAVSSDVQGDTAN

KVGAILAKYPKGKIDAIWGTWDAFSQGAYKALKENGRTEIKLYSIDISNQDLQLMREAGSPWKVSVAVDP

KLIGATNVRLIANKIAGEPTPATYDFKAAAIPQALLAAQPGAVNVASLGKIIPGWGQTEDFIAPWFATLE

AKNK

>lcl|NZ\_FO834906.1\_prot\_1697 [locus\_tag=BN49\_RS09885] [protein=LVIVD repeat-containing protein] [pseudo=true] [location=1741832..1742994] [gbkey=CDS]

MSALPSPEYSRNMRLIGHSDQGGRPDGVQLMVHRGFAYIGHMVSQGFSVVDVRDPTRPTTVNYIAAPPGT

WNVHLQAHDDLLLVINARDLFADARFADEKVYYTRSVGDTVSDVQDKGWSAGLRIFDISTPAQPREISFL

SLNGIGIHRIWYVGGRWAYVSALIDGFTDYIFLTIDLADPRKPKVAGRWWLPGIPPTAAGATAA\*RCWMS

KTVPSRG\*LVIATGARRSAAERIPRCRCRIVTCWWCWMKRCSTTRRTARS\*SGCLISASQPTR\*ASPPSR

RRTKRIMWRKGRISAHTTCMRTGRGALSAQR\*FLPRIRMPACGLTTFPTRIVRWRPGRWCRLRLRE\*WIS

VPAARG\*SSPVTCLSMRKALSTAPITTAGCR\*LSIWG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151657.1\_1698 [gene=mtnK] [locus\_tag=BN49\_RS09890] [protein=S-methyl-5-thioribose kinase] [protein\_id=WP\_004151657.1] [location=complement(1743208..1744407)] [gbkey=CDS]

MSQYHTFTAHDAVAYAQQFAGIDNPSELVSAQEVGDGNLNLVFKVFDRQGVSRAIVKQALPYVRCVGESW

PLTLDRARLEAQTLVAHYQHSPQHTVKIHHFDPELAVMVMEDLSDHRIWRGELIANVYYPQAARQLGDYL

AQVLFHTSDFYLHPHEKKAQVAQFINPAMCEITEDLFFNDPYQIHERNNYPAELEADVAALRDDAQLKLA

VAALKHRFFAHAEALLHGDIHSGSIFVAEGSLKAIDAEFGYFGPIGFDIGTAIGNLLLNYCGLPGQLGIR

DAAAAREQRLNDIHQLWTTFAERFQALAAEKTRDAALAYPGYASAFLKKVWADAVGFCGSELIRRSVGLS

HVADIDTIQDDAMRHECLRHAITLGRALIVLAERIDSVDELLARVRQYS

>lcl|NZ\_FO834906.1\_prot\_WP\_004147545.1\_1699 [gene=mtnA] [locus\_tag=BN49\_RS09895] [protein=S-methyl-5-thioribose-1-phosphate isomerase] [protein\_id=WP\_004147545.1] [location=1744509..1745537] [gbkey=CDS]

MQTLQTTSLRVSENQLFILDQQALPQEKRWLAADNVALLVDHIHTLRVRGAPLIGLSASLLLALLAQRGL

NRDALQQALETLRAARPTAVNLMNNLDRMKQALALEDYPQALEAEALRLVEEDKQLCDRIAEAGSALVKP

GSRLLTHCNTGGLATAGVGTALGVIALAHRQGKVTNVWVDETRPLLQGGRLTAWELGELGVPYQLIADSM

AASLMAQGQVDAVWVGADRIAANGDVANKIGTYSLAVLAHYHQIPFYVAAPQTTLDRHCPNGAAIPIEQR

AAAEVTGVAGSFGAVQWAPTGAAVYNPAFDVTPAGLISGWVLDSGVVTPAQVAAGAFAPDNG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042920.1\_1700 [locus\_tag=BN49\_RS09900] [protein=histidine phosphatase family protein] [protein\_id=WP\_046042920.1] [location=complement(1745598..1746866)] [gbkey=CDS]

MMPARHQGLLRLFIACALPLLALQSAAAADWQLEKVVELSRHGIRPPTAGNREAIEAATGRPWTEWTTHD

GELTGHGYAAVVNKGRAEGQHYRQLGLLQAGCPTAESIYVRASPLQRTRATAQALVDGAFPGCGVAIHYV

SGDADPLFQTDKFAATQTDPARQLAAVKEKAGDLAQRRQALAPTIQLLKQAVCQADKPCPIFDTPWQVEQ

SKSGKTTISGLSVMANMVETLRLGWSENLPLSQLAWGKITQARQITALLPLLTENYDLSNDVLYTAQKRG

SVLLNAMLDGVKPEADPNVRWLLLVAHDTNIAMVRTLMNFSWQLPGYSRGNIPPGSSLVLERWRNAKSGE

RYLRVYFQAQGLDDLRRLQTPDAQHPMLRQEWHQPGCRQTDVGTLCPLQAAITALGQRIDRSSAPAVAMV

LP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529480.1\_1701 [locus\_tag=BN49\_RS09905] [protein=MFS transporter] [protein\_id=WP\_016529480.1] [location=complement(1746892..1748250)] [gbkey=CDS]

MSGIIAFFRASPPKAGAAFDEHRFRRVRWQTFIATTLAYVTFYVCRLSFTVAKSALVELGITPTELGMIG

STLFFSYAIGKLVNGFIADHANVVRYMSLGLLLSAGMNLMMGMTTNALLLAIFWGINGWAQSMGVGPCAV

SLARWYGVKERGTFYGIWSTAHNIGEAVTYMVIAAVIAGFGWQMGYLSTAALGAAGVVLLVLFMHDSPQS

SGFPSINVIRDEPQEEVEARGSVFKNQLLALRNPALWTLALASAFMYIDRYAVNSWGIFFLEQDKAYSTL

EASGIIGVNAIAGIAGTIIAGMLSDRFFPRNRSVMAGFISLLNTAGFALMLWSPHNYYTDILAMIIFGAT

IGALTCFLGGLIAVDISSRKAAGAALGTIGIASYAGAGLGEFLTGIIIDKTAILENGKTLYDFSTLALFW

VGTGLGSALLCFTTAAIVARRHAVERQTSFSS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529479.1\_1702 [locus\_tag=BN49\_RS09910] [protein=inositol monophosphatase] [protein\_id=WP\_016529479.1] [location=complement(1748361..1749170)] [gbkey=CDS]

MQSQESEALQARYRLACELAKAGAELAFEYYQQREALTVDHKGDDLQDVVSVADKRVETFVKQRIQSAFP

EDGFLGEESGARLPDARVLWVVDPIDGTSCFLNGLHTWCLSLAIVADGEPVIGVVYDPNHRELFHALRGH

GAWLNDAPIRPHPATTVKEGVMGVGTSHRVTPADFLPFLQALLSDGGMFIRNGSGALMSAWAAAGRLIGY

YEPHMNPWDALPGLVLMREAGGASNDFLAQEGIQRGNPLLLASQTLYPQLKKMIPQPLH

>lcl|NZ\_FO834906.1\_prot\_WP\_171819491.1\_1703 [locus\_tag=BN49\_RS09915] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_171819491.1] [location=complement(1749292..1750242)] [gbkey=CDS]

MARLAGVSRSAVSRTFTPGASVSEKTRQKVLSAAEALGYQVNIIARTMITGSSNFIGIVTAGFDNPFRSK

LLAPLVHQLALNGFMPLLMNADDPQQLAPSLKQLLSYHVAGVIITSGAPPLSLAEEYLARKIPVTLINRH

ADLAGCDRVCSDDAQGAKLVADLFSRRGWRQVGFIGENRENFSTRQRYEAFIARTSDMAVSSRFCDGGGY

QAGYQAARELVAENPGMQALFCATDMLALGAQDGLRDAAAPLPAIVGFDDIPQADWQPYQLTTVQQNTAL

LAHHAVDLLMTRIARFSLPSRHREVPVKLIIRHSAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176896.1\_1704 [gene=codA] [locus\_tag=BN49\_RS09920] [protein=cytosine deaminase] [protein\_id=WP\_004176896.1] [location=complement(1750388..1751626)] [gbkey=CDS]

MKIINARLRRQEALFTLDLQDGMIHRITAQAAMQTADAGDIDARGRLAIPPFVEPHIHLDATLTAGEPEW

NRSGTLFEGITRWSQRKASITPEDTRQRAMKTIGMLRDFGVQHVRTHVDVTDPSLAALQALLAVKQEAAD

LIDLQIVAFPQEGIESYPNGRELMTRAIEMGADVVGGIPHYENTRDKGVSSVMFLMDLAQRYGRLVDVHC

DEIDDPQSRFLEVLAEEARVRGMGAQVTASHTCAMGSYDNAYCSKLFRLLKASGINFISCPTESIHLQGR

FDSWPKRRGVTRVAELDRAGINVCFAQDSIQDPWYPLGNGNILRILDAGLHICHMLGYDDLQRCLDFVTD

NSARALCLGDNYGLAEGRPANLLILDAENDYEAVRRQARVLTSIRHGKVILQREVEHIRYPA

>lcl|NZ\_FO834906.1\_prot\_WP\_020803787.1\_1705 [locus\_tag=BN49\_RS09925] [protein=PucR family transcriptional regulator ligand-binding domain-containing protein] [protein\_id=WP\_020803787.1] [location=complement(1751623..1752858)] [gbkey=CDS]

MSLTVSELLALEGLSALRLRAGKQGLQRAVRWYYVAENEHIAEWIMGGELVFITGINHPRDEANLIQLLM

EGKQRGIAGMVILTGEAYIHAIPATLIALADELGMPLIEQPYLLKMVIVTERIGTALVRSENVLQSQRDI

LMQLVTGDYPDLQMLHQRALHQQLDFTRPLRLAALRLEGLSRLFRQFPPEQAEAWLLQAHRSVRQQLQQQ

LNQQGNPFPLLERSNMFLFLLPDEEGEGFQQKKWLQQWLQALADGEESLSLLCGLSAPVRQLQGYPRALS

QARQALDLCDTLRPTQRISDYQQLGFIKLLSAVSDPALLNDFMHDTLGCLIEPGRKAPWLLLETLETLLQ

ENGNVVRAADRLGLHRNTLHQRIQRIEKLTGYPVSHPQFHLNASVALVIWRLSQNHLQDPP

>lcl|NZ\_FO834906.1\_prot\_WP\_046042923.1\_1706 [gene=codB] [locus\_tag=BN49\_RS09930] [protein=cytosine permease] [protein\_id=WP\_046042923.1] [location=complement(1752855..1754114)] [gbkey=CDS]

MSNSNDFPLVEAPASGRKGVFSIAMVLFSFTFFTGTMFAGGKLGVSFSIVNLLWIAVIGNALLALYAASL

GWIAARSGLNTVLMGRFCFGEIGSKLADFILGFAELGWYAWGTATVAISLVKILALPEALTQPLMVLFGI

LFCVTALVGYKGLDALSRLSVPLMFVLLMVSMYLALHHAGGWQAMTRIAPSDTMTWSAAITMVFGTFASG

ATQATNWTRLANSSRTAILASMGSFLIGNGLMIVAGAWCAIVYQQADIVEVLILQGLSVAAVIMLCLNLL

TIQGPTIYNVSAACHLLRSERRRTLTLAAAGVGIVLAIGGMYEMLIPFLVLLGSIIPPIGGVILADYWFA

RGGRYPLLQNARLPRFNWLGLGAYAAGAVVAYLSPWIAPLVGISVSALVYIALALLSKRQPAAVAEQEP

>lcl|NZ\_FO834906.1\_prot\_WP\_002894164.1\_1707 [locus\_tag=BN49\_RS09935] [protein=methylthioribulose 1-phosphate dehydratase] [protein\_id=WP\_002894164.1] [location=1754566..1755174] [gbkey=CDS]

MWQERLAQLVTTCHWIGAKGWAPATGGNMSVRQDDTWCWLSESGRDKGSLTTEDFLQVEIATNQAPSGRK

PSAETGLHTLVYRLFPEANVVLHVHTVNATVLSRIEKSDTLALQGYEMQKTLSGQHSHLDTVPIAIFDND

QDIDALAARIADYAQTRPLRYGFLLRGHGLTCWGKDIQEARRQLEGLEFLFECELMRRRYEP

>lcl|NZ\_FO834906.1\_prot\_WP\_046042926.1\_1708 [locus\_tag=BN49\_RS09940] [protein=carbohydrate kinase] [protein\_id=WP\_046042926.1] [location=1755187..1756683] [gbkey=CDS]

MDFYLGIDIGTSRVKAVLFDQHFTACASAAENTSPRLSANGYAEQDMTQLWHSVLAILRQIARHPALQAG

RLRAIGLAGQGEGVWLSDEQGEPVGPGILWSDTRSHELMSDLLRRPGFDRRYFADTGTHLQPCNTSLQLY

WLKQYQPARLAAARYLFFAKDWIRFRLTGVAALELTDASSSLLNQQTGSWSSVVMNEMGLNELLPLFPPL

LAPDAPAGTLSDAVAALTGLPAATPVAAGALDVCSAALGCGAVNEGDIYTILGTTCCTGIVCRGPQTVNE

ATRFVTHTEAGQVISLFPMQAGTPNIDWLQQHISLDADLGRLEQAIAAVEPGSGGVFWQPYLNGERAPFY

SPDARAGFFGISPHTTRAELQRAVFEGLAFAIVDALQGYPQGGELYLTGGGAASATWLQIIADCTGRTVV

SSAFNELSARGAAILAARSVAALAETPPLAQTRYQPRPQAHARYAALYPVYRLLREQMLPVWQARQAALQ

PFSQDLQP

>lcl|NZ\_FO834906.1\_prot\_WP\_004191366.1\_1709 [locus\_tag=BN49\_RS09945] [protein=2-hydroxyacid dehydrogenase] [protein\_id=WP\_004191366.1] [location=1756680..1757708] [gbkey=CDS]

MKIVFTAEHAGDLSAFHQLGELLVEGWALGKPKLSAGQLIELAHDAEVLVTSYDEVTDAVMAACPRLQVI

ACTRANPVNIDTQAAQARGIRVLYTPGRNADAAAELTLGLMLSLARHIPQSHAALKRGEFTQADNAAAAT

QQGLRRDVVWDVSPESPYEVFKGTELRNKTLGLVGYGNIGRRVARIARAFGMAVLVVDPFVAAEDINEPG

LQKTTLEALFREADIVSLHLSSGPHSDGLVNAALLNSMKPGALLINTSRAAVVDEAALIDALRHGPLGGA

ALDVYHREPLWRDHPFVIEFDNVIITPHIAGATRESIAKHTAMIAADLQRYVAGEPLLYQWR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531620.1\_1710 [locus\_tag=BN49\_RS09950] [protein=sugar kinase] [protein\_id=WP\_016531620.1] [location=complement(1757751..1758692)] [gbkey=CDS]

MATFDAVFVGLTILDIARRPVVAIPPRGGVAFIEQIRLNPAGTAAGANINAAKLGIRTAAVACLGEDEKA

DFILASYARLGIDCSLIQRTALKETSATILPIRPNGERPALHCRGASDALFVSEAEFDAVLDCRFLHHGG

TGLLAAMDQGQSARLLQAAKARGVTTSFDLIAPNEETLELLRPLLPSVDYFMPSLEEAAFLSGETQPEAI

GRFFLALGVGTCILKDGENGSWLIGRDGGPQHIAPWPVEAVDTTGCGDSYCGGFIAALARGLSVKAACDV

ASAVAALVATGMGSDAGVVDWEQTQAFMAAHRP

>lcl|NZ\_FO834906.1\_prot\_WP\_004147554.1\_1711 [locus\_tag=BN49\_RS09955] [protein=ABC transporter permease] [protein\_id=WP\_004147554.1] [location=complement(1758704..1759708)] [gbkey=CDS]

MSQITLKTSASAEQTASSPLAWLSRAGFGVITLLAIALFGWANPVFLTVDNWANLLQGSAILLIVAMAMT

LIVSAGAIDLSVGVALDFGAAFALVALKTWHLPWQAAVGCALLGGVLIGLLNAFLILICRIRPFLATLGT

WFIASSAERIYTDGGGAIAYRRMAPEYHDLAVGNLGGIPTPVAIVLALWLAAWLVTERTLWGKYVRAIGQ

NSEAARIAGIRDRLTMLGVLVTASALCAVGGVILSANLRQFTPLAGQSYLMDAIAAVFIGTAFTRLGRVS

ILGTLGGVLFLAIIDNGLNLMGLNYLVKDALVGVILVVALALSFWQARLRQTHR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531617.1\_1712 [locus\_tag=BN49\_RS09960] [protein=ABC transporter permease] [protein\_id=WP\_016531617.1] [location=complement(1759705..1760694)] [gbkey=CDS]

MSTAIQRRGRPGLATLIEKFPLILFLALLVWLSVQSSYFLSWQNISLMLVQSVPLAILCFGLVCVIAVGG

DDVVSGGIDLSLPATAVLGVALLSLGLAEWHTPYLLLLALLAAVCLLCGAINGLLVLAAGLPPLLATLST

SVAFTGLTDLLTGQRRIAVSDPLMVAFRDNSVLGLPWPLVYLLGVFILFQFLLHHSRFGQHVQAVGGNRD

MAQMSGLNVRRLTLLVWLLAGIAAGLAILPLLSQGSGSSSGTATPLLLETVLATFIGAAFSRRRVVTIWG

ALLGAILVNALSNGLGLLGVNIFWMGAIKGGLILVVLAASAVRHKGGEA

>lcl|NZ\_FO834906.1\_prot\_WP\_023158362.1\_1713 [locus\_tag=BN49\_RS09965] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_023158362.1] [location=complement(1760691..1762193)] [gbkey=CDS]

MEQIGKRFASVTALNAVTLRLNPGEIHGLIGENGAGKSTLIKILAGVYQADSGSATLDGHPLPLGNPAAI

EAAGIRVIHQELNLIPHFTVAESVFLGQEYRTRWGALDRRRMKAATAQFFQQNWQLAIDPERLVRDLSLA

ERKLVQIARALIDGAARLVVFDEPTAPLEAQEASLVSSAILRLRDQGIAILYISHYLNEIATLCDRGTVL

RNGEVVGYPDRDLLQNTEALIAMMVGREIDQLYTPRQRPAADNGATPLLSVRQLSDGRQLQDLSFDIQPG

EIVGVAGLLGAGRDVLVDLLYGLRPAERGTIHLEGRPRRIRTPKQAIRAGMALVPRDRRHQGLILPFTTA

DNINLASLPETATFGWERRGIAEQKARDWIEQLAIRPGRPGLPVRYMSGGNQQKAILARWLGTDARLFIL

DEPTLGVDIGARRDIYQRTRQLADKGRAVLVSSSDAPELLGLCDRILVLWRGALAANLPTRGLTLDALLV

AINGGQEPSP

>lcl|NZ\_FO834906.1\_prot\_WP\_002894353.1\_1714 [locus\_tag=BN49\_RS09970] [protein=sugar ABC transporter substrate-binding protein] [protein\_id=WP\_002894353.1] [location=complement(1762238..1763218)] [gbkey=CDS]

MSQKRKLLPAALGLLSLASLSVAAADALSLQGKTIGVAVVGTQHFWDREAFKGATEEVEKLGGKVIGVDG

GRDNQVHANNHDILLSRKVDAVISILGDSAVEPKFKALRDAGIPVFTVDHVSQYSVNNTTSDNYTLGSTI

GRYMADELGGKGNVAVFNAFSSALRICGIRYDQWKYVLKDYPDIHIIQPELAEQFANSPEDARKKTLELL

SQYPKGKLDAIHVACWDQPAIGIVQALEETGRDKDVKVTAIDAGPETLEIMAEPGSPFVANVAQQPHLIG

QTSADNVARYFAGQKLPVQTFIPVVPVKGPQEAKAVYKQLGYGELQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016531616.1\_1715 [locus\_tag=BN49\_RS09975] [protein=molybdopterin-dependent oxidoreductase] [protein\_id=WP\_016531616.1] [location=1763627..1765936] [gbkey=CDS]

MKKQHNYTVMHWGTWQVESSEGEIVAVKPVPWDKNPSRIGQSLPDAVTSQTRIRRPAVRAGYLQHGPASR

EGRGKEPFVEVSWEVALDLLARELRSVKARCGNEAIYGGSYGWASAGRFHHAQSQLHRFLKGFGGYTAST

NTYSSAAGERILPHILGPLSPLHRQHTHFSELARECQLFVAIGGLPLRNAQVNGGGANDHMLQYWLDKMQ

ANGTRFINISPVRNDLSAVPDAEWLAIRPGTDTALLLALSYVLIAESLYDQAFVASHTVGFAPYRAYLLG

EHDGVAKTPAWAAAITGLDAQRIADLAREMARHRTMVNISWSIQRARQGEQAYWATVALTALLGQLGTPG

GGLGFGYACTNLAGAVRKAFSGPRLPAGENAVDSVIPVARLSDMLLHPGETYEFDGQQRRYPDIRLVYWA

GGNAFHHHQDINRLCEAWRRPETVVVHEQYWTAQAKFSDIVLPATTSLEREDIGSGGHDGFMIAMSAQIP

PVGEARDDYAIFCDLAGRLGFGEAFSEGRDAGQWLRHLYEESRPRAQEEGIALPSFDDFWQQGVLEYSAP

ERPQIFLADFRADPQRYPLSTPSGKIELFSATVAGFGYRECPGHPWWDEQEAARQRQEAARWPLHLLSSQ

PRARLHSQYDHGSVSRATKIQGREPLWMHPSDAQARDIREGSVVKVYNDRGAILAGVHLSEQILPGVVQM

STGAWYDPLDPNEKGTLDKHGNPNVLTEDRGSSRLGQGCSAQSCWVEIAPWREELPPITAFDPPKFIEV

>lcl|NZ\_FO834906.1\_prot\_WP\_002894357.1\_1716 [locus\_tag=BN49\_RS09980] [protein=1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase] [protein\_id=WP\_002894357.1] [location=complement(1766044..1766586)] [gbkey=CDS]

MSALTLFSVTDPQTPVWHSTDAKAIQDQLNAKGVRFERWQADRDLGANPSPETVIAAYQHAIDKLVAEKG

YQSWDVISLRADNPQKEALREKFLNEHTHGEDEVRFFVEGAGLFCLHIGDEVFQVLCEKNDLISVPAHTP

HWFDMGSEPNFTAIRIFDNPEGWIAQFTGDDIASAYPRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004893454.1\_1717 [gene=mtnC] [locus\_tag=BN49\_RS09985] [protein=acireductone synthase] [protein\_id=WP\_004893454.1] [location=complement(1766583..1767272)] [gbkey=CDS]

MIRAIVTDIEGTTSDIRFVHNVLFPYARERLAGFVTAQQHAEPVKTILDNLRRETDAPAASTADLITTLF

AFMDEDRKSTALKALQGIIWRDGYLNGDFTGHLYPDVLPALEKWKAQGIDLYVYSSGSVAAQKLLFGYSD

EGDITHLFTGYFDTLVGAKREVQSYRNIAEHLGHAPGTILFLSDIHQELDAAEAAGLRTIQLVRGDRDPA

SHHPQVQRFDDIHPEQIPA

>lcl|NZ\_FO834906.1\_prot\_WP\_171819492.1\_1718 [locus\_tag=BN49\_RS09990] [protein=pyridoxal phosphate-dependent aminotransferase] [protein\_id=WP\_171819492.1] [location=1767414..1768559] [gbkey=CDS]

MIPESKLPALGTTIFTQMSALAQQHQAINLSQGFPDFDGPRYLQERLAYHVAQGANQYAPMTGVPALREA

IAGKTAELYGYQPDVNSEITVTAGATEALYAAITALVRRGDEVICFDPSYDSYAPAVALAGGELRRIALQ

PPHFRVDWRQFAAALSEKTRLVILNTPHNPSATVWQCEDFAALWQAIAEREIYVLSDEVYEHICFAEGGH

ASVLAHPQLRERAVAVSSFGKTFHMTGWKVGYCVAPAAISAELRKVHQYLTFSVNTPAQLAIADMLREAP

EHYRELPAFYRERRDLFIEALRSSRLEILPCEGTYFLLADYSAISDLDDVSFCRWLTTEVGVAAIPLSVF

CADPFPHKLIRLCFAKQPATLLAAATRLCQL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531614.1\_1719 [locus\_tag=BN49\_RS09995] [protein=ParB/RepB/Spo0J family partition protein] [protein\_id=WP\_016531614.1] [location=complement(1768560..1769186)] [gbkey=CDS]

MQQQLTQALEAYLQKLDDEARIEAINAFRQVLHHYSPFRSQPVDCVLWVKQELISPNDYNPNNVAPPEKR

LLQTSLEADGFTQPVVVIQQRPQAYTIVDGFHRHELACSKAALKKTLKGYLPVTCLTSDAASRDGLMAAT

IRHNRARGRHQIHAMSEIVRELTRLGWTPQKIGKELGMDADEVLRLKQISGLTEMFAGRQFSQAWTIK

>lcl|NZ\_FO834906.1\_prot\_WP\_002894369.1\_1720 [locus\_tag=BN49\_RS10000] [protein=DUF3440 domain-containing protein] [protein\_id=WP\_002894369.1] [location=complement(1769171..1770394)] [gbkey=CDS]

MSFIKYPLPESVLQATEQRIQWVMDNFSRICVSFSGGKDSTVMLHLTAQAARLQGKKICVLFIDWEAQFS

CTIAHCEKLRALYADVIETFYWVALPLTTQNALTQYKPQWQCWEPGTEWVRQPPPWAITHPGYFSFYQPG

MSFEAFVSHFAEWFSQRRPAAVLVGIRADESLNRFMTISSQRKQRFADDKPWTTSAPGGHAWYIYPLYDW

KTADIWTWFAKSGEPYNPLYDLMYQAGVPLRYMRICEPFGPEQRQGLWLYHVLEPERWAAMCQRVSGAHS

GGVYAGHDNQFYGHRKIDKPDHLTWKSYALFLLDSMPETTAEHYRNKIAVYLRWYQKKGMEDIPDTQPAD

IGTKDIPSWRRVCKVLLNNDYWCRQLSFSPTKSSHYQRYRKRMEKHRQQWGILCNNN

>lcl|NZ\_FO834906.1\_prot\_WP\_004212615.1\_1721 [locus\_tag=BN49\_RS10005] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004212615.1] [location=complement(1770505..1771437)] [gbkey=CDS]

MANLYDLKKFDLNLLVIFECIYQHLSISKAAAMLFITPSAVSQSLQRLRQQLNDPLFVRVGKGMTPTTAC

VNLHYHLQQNLEQLEKTINLNNRSELRKRIVIYGPPLFCSVNSHVMINQLCHQANLQIEHHNLTTTESAE

ELLAYRQADLVFTRMPITNRATICQPYQTVQTLAVCRAGHPRRETLTSVESLAQEFFTHYITNDPVIQRV

QQSSIAWLNPRNIAFRSDSFMTILNMINKTDLIGFLPSYLYDFISPTMQLHAINIDNLFPDITIYINYHH

ASSQNHFLTELITILMNDREASRPQFNHSE

>lcl|NZ\_FO834906.1\_prot\_WP\_009485194.1\_1722 [gene=dsbG] [locus\_tag=BN49\_RS10010] [protein=thiol:disulfide interchange protein DsbG] [protein\_id=WP\_009485194.1] [location=complement(1771618..1772367)] [gbkey=CDS]

MLKRLLLLSLLPLCSHAEELPAPVKAIEKQGITIIKPFEAPGGMKGWLGKYQDMGVAIYLTPDGKHAISG

YMYDENGSNLSEQLFQKELYTPAGQEMWKKMASAHWLQDGRKDAPIVLYVFADPFCPYCKQFWQQSRPWV

EAGKVQIRTLLVGVIKPESPATAAAILASNDPAKTWHDYEQSNGKMALTIPKVIPPEKMKMLNVNQQLMD

DLGANVTPAIYYMNKDNMLQQVVGLPDKEKLHIMMGEKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002894394.1\_1723 [gene=ahpC] [locus\_tag=BN49\_RS10015] [protein=alkyl hydroperoxide reductase subunit C] [protein\_id=WP\_002894394.1] [location=1772779..1773342] [gbkey=CDS]

MSLINTKIKPFKNQAFKNGEFIEVTEKDTEGRWSVFFFYPADFTFVCPTELGDVADHYEELQKLGVDVYS

VSTDTHFTHKAWHSSSETIAKIKYAMIGDPTGALTRNFDNMREDEGLADRATFVVDPQGIIQAIEVTAEG

IGRDASDLLRKIKAAQYVASHPGEVCPAKWKEGEATLAPSLDLVGKI

>lcl|NZ\_FO834906.1\_prot\_WP\_004142378.1\_1724 [gene=ahpF] [locus\_tag=BN49\_RS10020] [protein=alkyl hydroperoxide reductase subunit F] [protein\_id=WP\_004142378.1] [location=1773530..1775095] [gbkey=CDS]

MLDTNMKTQLKAYLEKLTKPVELIATLDDSAKSAEIKELLAEIAELSDKVTFKEDNTLAVRKPSFLITNP

GSDQGPRFAGSPLGHEFTSLVLALLWTGGHPSKEAQSLLEQIRDIDGDFEFETYYSLSCHNCPDVVQALN

LMAVLNPRIKHTAIDGGTFQNEITERNVMGVPAVFMNGQEFGQGRMTLTEIVAKVDTGAEKRAAEELNQR

DAYDVLIVGSGPSGAAAAVYSARKGIRTGLMGERFGGQVLDTVDIENYISVPKTEGQKLAGALKAHVNDY

NVDVIDSQSATKLTPAATEGGLHQIETASGAVLKARSVIIATGAKWRNMNVPGEEQYRTKGVTYCPHCDG

PLFKGKRVAVIGGGNSGVEAAIDLAGVVEHVTLLEFAPEMKADQVLQDKVRSLKNVDIILNAQTTEVKGD

GSKVTGLQYRDRVSGDEHHVALAGIFVQIGLLPNTTWLEGAVERNRMGEIIIDAKCETNVKGVFAAGDCT

TVPYKQIIIAAGEGAKASLSAFDYLIRTKTA

>lcl|NZ\_FO834906.1\_prot\_WP\_002894401.1\_1725 [gene=uspG] [locus\_tag=BN49\_RS10025] [protein=universal stress protein UspG] [protein\_id=WP\_002894401.1] [location=complement(1775172..1775600)] [gbkey=CDS]

MYKTIIMPVDVFEMALSDKAVRHAEFLAQQDGVIHLLHVLPGSASFTMSRFTADLRRFEEHLQHEAETRL

QTMVSHFSIDPSRIKLHVRFGSVRDMVNELASEINADVVVIGSRNPSISTHLLGSNASSVIRHAHIPVMV

VR

>lcl|NZ\_FO834906.1\_prot\_WP\_002894404.1\_1726 [gene=rnk] [locus\_tag=BN49\_RS10030] [protein=nucleoside diphosphate kinase regulator] [protein\_id=WP\_002894404.1] [location=complement(1775787..1776197)] [gbkey=CDS]

MTRPAIIINELDAERIDRLLEQPAFANSPVADALNEELDRAQMLAPEAMPHDVVTMNSRVKFRDLTSGEE

RVRTLVFPSQVTDSASQLSVLAPVGAALLGLKVGSTIHWELPGGASTHLEVLELLYQPEAAGEFHR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531613.1\_1727 [gene=rna] [locus\_tag=BN49\_RS10035] [protein=ribonuclease I] [protein\_id=WP\_016531613.1] [location=complement(1776376..1777173)] [gbkey=CDS]

MFRKDFAAIALVLTATQAGAEPLTATRYADFDRYVLALSWQTGFCQSMYDRNRNEPEECRLQQDTANKAD

FLTVHGLWPGLPKSIAARGVDERRWMRYGCATRPAPNMPEVKANRKCQAAETGLSLEMANKLNNVMPGSG

GTSCLERYEYAKHGVCFGFDPDSYFGAMVRLNGEIKRSPVGDFLAKHYGQTVSRADFDAAVARAWGPQSV

KAFKLTCNGNPAYLTEMQISLNAATINAPLATSAFLPQPHPGNCGAQFILDKVGH

>lcl|NZ\_FO834906.1\_prot\_WP\_004142371.1\_1728 [gene=dcuC] [locus\_tag=BN49\_RS10040] [protein=anaerobic C4-dicarboxylate transporter DcuC] [protein\_id=WP\_004142371.1] [location=complement(1777266..1778639)] [gbkey=CDS]

MLTFIEILIGIVVIVGVARYIIKGYSATGVLFVGGLILLIVSALLGHKVLPGNTASTGYSATDIIEYIKI

LLMSRGGDLGMMIMMLCGFATYMTHIGANDMVVKLASKPLRYINSPYLLMIAAYFVACLMSLAVSSATGL

GVLLMATLFPVMVNVGISRGAAAAICASPAAIILSPTSGDVVLAAKAAEMPLIDFAFKTTLPISIAAIIC

MAIAHFFWQRYLDKKEHISHEMLDVNDITTTAPALYAILPFTPIIGVLIFDGKWGPELHIITILVGCMLL

AAILEFLRGFNTKNVFSGLEVAYRGMADAFAGVVMLLVAAGVFAQGLSTIGFINGLISIATSFGSASIIL

MLVLVILTMLAAMTTGSGNAPFYAFVEMIPKLAHSSGINPAYLSIPMLQASNLGRTISPVSGVVVAVAGM

AKISPFEVVKRTSVPVLVGLLVVIVATEILVPGSALH

>lcl|NZ\_FO834906.1\_prot\_WP\_004183399.1\_1729 [gene=pagP] [locus\_tag=BN49\_RS10045] [protein=lipid IV(A) palmitoyltransferase PagP] [protein\_id=WP\_004183399.1] [location=1778978..1779496] [gbkey=CDS]

MSGNASASFSSTLSEGYHTLSNNVAQTWNEPEHYDLYVPAITWHARFAYDKEKTDKYNERPWGAGFGVSR

WDEKGNWHGLYLMAFKDSFNKWEPIGGYGWEKTWRPLTDQNFHLGLGYTLGVTARDNWNYIPIPVILPLA

SIGYGPATFQMTYIPGTYNNGNVYFAWARFQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002439184.1\_1730 [gene=cspE] [locus\_tag=BN49\_RS10050] [protein=transcription antiterminator/RNA stability regulator CspE] [protein\_id=WP\_002439184.1] [location=1779691..1779900] [gbkey=CDS]

MSKIKGNVKWFNESKGFGFITPEDGSKDVFVHFSAIQSNGFKTLAEGQRVEFEITNGAKGPSAANVIAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002894459.1\_1731 [gene=crcB] [locus\_tag=BN49\_RS10055] [protein=fluoride efflux transporter CrcB] [protein\_id=WP\_002894459.1] [location=complement(1779968..1780351)] [gbkey=CDS]

MFQLLCAVFIGGGTGSVLRWWLGMKLNPVHHAIPIGTLTANLLGAFVIGAGLAWFNRLTGIDPMWKLLIT

TGFCGGLTTFSTFSAEVVFLLQQGRVSWALLNVAVNLLGSFAMTAVAFWLFSQAASR

>lcl|NZ\_FO834906.1\_prot\_WP\_002894461.1\_1732 [locus\_tag=BN49\_RS10060] [protein=deaminated glutathione amidase] [protein\_id=WP\_002894461.1] [location=1780441..1781229] [gbkey=CDS]

MRVAAGQFAVTPVWRTNAQTCVAMMQQAEREGAALLVLPEALLARDDNDPDLSVKSAQPLDGAFLQPLLA

ESRRNSLTTVLTLHVPSGEGRATNTLVVLREGAVIAHYHKLHLYDAFAMQESRRVDPGQQIPPVIEVAGL

RVGLMTCYDLRFPELALSLALNGAQLLVLPAAWVKGPQKEHHWATLLAARALDTTCYIVAAGECGTRNIG

LSRIVDPLGTTLAGAGSEPQLIFADLSADDLARVRERLPVLRNRRFAPPQLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002894464.1\_1733 [gene=tatE] [locus\_tag=BN49\_RS10065] [protein=twin-arginine translocase subunit TatE] [protein\_id=WP\_002894464.1] [location=1781472..1781678] [gbkey=CDS]

MGEISITKLLVVAALIILVFGTKKLRTLGGDLGSAIKGFKKAMNEDDDSAKKTTAEEEAPAQKLSHKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002894467.1\_1734 [gene=lipA] [locus\_tag=BN49\_RS10070] [protein=lipoyl synthase] [protein\_id=WP\_002894467.1] [location=complement(1781869..1782834)] [gbkey=CDS]

MSKPIVMERGVKYRDADKMALIPVKNVATEREALLRKPEWMKIKLPADSSRIQGIKAAMRKNGLHSVCEE

ASCPNLAECFNHGTATFMILGAICTRRCPFCDVAHGRPVAPDANEPQKLAQTIADMGLRYVVVTSVDRDD

LRDGGAQHFADCISAIREKNPSIKIETLVPDFRGRMDRALDILTVTPPDVFNHNLENVPRLYRQVRPGAD

YNWSLKLLERFKEAHPEIPTKSGLMVGLGETNDEIIEVMRDLRRHGVTMLTLGQYLQPSRHHLPVQRYVS

PEEFEEMKAEAMAMGFTHAACGPFVRSSYHADLQAKGMEVK

>lcl|NZ\_FO834906.1\_prot\_1735 [locus\_tag=BN49\_RS10075] [protein=YbeF family transcriptional regulator] [pseudo=true] [location=complement(1783015..1783974)] [gbkey=CDS]

MPENTPPSESPDRQDERYDRQMFRILRNIDLNLLTIFEAVYVHKGIVNAAKILNITPSAISQSINKLRAL

FPDPLFIRKGQGVTPTAYATHLHQYISRGMEAFLSALDITGSPHQQRVITIATTPAMGALLMPGLASALK

PTFPQILLHNIAIVDAARQLDQR\*VDLLIDTHLHSGQAISHHVLYQDRVQMYCRAGHPALDGPQDETTLA

EYEFALLLPEGQRYPTLHRRLQEEMGERRCGFSTFNLMTQAAMIAGSDMLGLTTERLFAMVSRLWPLQTL

DFPSLGGEQIDVALHFNKLSGKEPLLKEIIETVIRSFKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002894472.1\_1736 [gene=lipB] [locus\_tag=BN49\_RS10080] [protein=lipoyl(octanoyl) transferase LipB] [protein\_id=WP\_002894472.1] [location=complement(1784105..1784749)] [gbkey=CDS]

MQHNKILIRQLGLQPYEPVSQAMHEFTDARDEDTLDEIWLVEHHPVFTQGQAGKAEHVLVPGDIPVIQSD

RGGQVTYHGPGQQVMYVLLDLKRRKLGVRELVTLLEQTVVNTLAEYSIESHPRADAPGVYVGERKICSLG

LRIRKGCSFHGLALNIAMDLTPFLRINPCGYAGMEMTQMRQWQPAASPETVAPRLVANLLALLNHPPHEY

LPRD

>lcl|NZ\_FO834906.1\_prot\_WP\_002894474.1\_1737 [gene=ybeD] [locus\_tag=BN49\_RS10085] [protein=DUF493 family protein YbeD] [protein\_id=WP\_002894474.1] [location=complement(1784854..1785117)] [gbkey=CDS]

MKTKLNELLEFPTPFTYKVMGQALPELVDQVVEVVQRHAPGDYSPSVKPSSKGNYHSVSITINATHIEQV

ETLYEELGNIDIVRMVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002894539.1\_1738 [gene=dacA] [locus\_tag=BN49\_RS10090] [protein=D-alanyl-D-alanine carboxypeptidase DacA] [protein\_id=WP\_002894539.1] [location=complement(1785230..1786429)] [gbkey=CDS]

MKTSFTARLLITALSVAALSSAARADDLNIKTMIPGAPQIDAESWILIDYNSGKVLAENNADSRRDPASL

TKMMTSYVIGQAMKAGKFKESDLVTVGNDAWATGNPVFKGSSLMFLKPGMQVPVSQLIRGINLQSGNDAC

VAMADYVAGSQDAFVSLMNNYVNALGLKNTHFQTVHGLDADGQYSSARDMALIGQALIRDVPNEYSIYRE

KEFTFNGIRQLNRNGLLWDNSLNVDGIKTGHTDKAGYNLVASATEGQMRLISAVMGGRTFKGRESESKKL

LTWGFRFFETVNPIKAGKEFASEPAWFGDSDRASLGVDKDVYLTIPRGRMKDLKASYVLNNTELHAPLQK

NQVVGTINFQLDGKTIDQRPLVVLQEIPEGNFFGKIIDYIKLMFHHWFG

>lcl|NZ\_FO834906.1\_prot\_WP\_004183403.1\_1739 [gene=rlpA] [locus\_tag=BN49\_RS10095] [protein=endolytic peptidoglycan transglycosylase RlpA] [protein\_id=WP\_004183403.1] [location=complement(1786568..1787716)] [gbkey=CDS]

MRKQWLGICIAAGLLAACSSDDVQQKTVSTPQPAVCNGPTVEISGADPQYETPNATANQDYERDGKSYKI

VQDPANFTQAGFAAIYDAEPNSNLTASGEAFDPTQLTAAHPTLPIPSYARITNLANGRMIVVRINDRGPY

GNDRVISLSRASADRLNTSNNTKVRIDPIIVAPDGSLSGPGMACTTVAKQTYALPARPNLDGGDAAGMSQ

PAPTDVRPISNSTLTPADSVGAPVNSGGFLGAPTPLNNGVLESSEPAAAAATAPAAGATPTAPVTAPGSI

QGNVAPAATTAAAAGAVAASSSATSSASGNFVVQVGAVSDQTRAQQYQQRLSQQFSVPGRVMQNGAVWRI

QLGPFADKAQASAVQQRLQSEAQLQSFITRAN

>lcl|NZ\_FO834906.1\_prot\_WP\_002894613.1\_1740 [gene=mrdB] [locus\_tag=BN49\_RS10100] [protein=peptidoglycan glycosyltransferase MrdB] [protein\_id=WP\_002894613.1] [location=complement(1787728..1788840)] [gbkey=CDS]

MTDNPNKKSLWDKIHLDPTMLLILLALLTYSALVIWSASGQDVGMMERKIGQIAMGVVIMIVMAQIPPRV

YEGWAPYLYIFCIILLVAVDAFGAISKGAQRWLDLGIVRFQPSEIAKIAVPLMVARFINRDVCPPSLKNT

GIALVLIFLPTLLVAAQPDLGTSILIALSGLFVLFLSGLSWRLIGIAVVLVAAFIPILWFFLMHDYQRQR

VMMLLDPETDPLGAGYHIIQSKIAIGSGGLRGKGWLHGTQSQLEFLPERHTDFIFAVLAEELGLIGVLIL

LALYILLIMRGLWIAAQAQTTFGRVMAGGLMLILFVYVFVNIGMVSGILPVVGVPLPLVSYGGSALIVLM

AGFGIVMSIHTHRKMLSKSV

>lcl|NZ\_FO834906.1\_prot\_WP\_002894617.1\_1741 [gene=mrdA] [locus\_tag=BN49\_RS10105] [protein=peptidoglycan DD-transpeptidase MrdA] [protein\_id=WP\_002894617.1] [location=complement(1788840..1790741)] [gbkey=CDS]

MKLQNSFRDYTAESSLFVRRALVAFLGILLLTGVLIANLYNVQIVRFDDYQTRSNENRIKLVPIPPSRGI

IYDRNGTPLALNRTIYQLEMMPEKVDNVQQTLDALRDVVDLTDDDIAGFKKERARSHRFTSIPVKVNLSE

VQVARFAVNQYRFPGVEVKGYKRRYYPYNSALTHVIGYVSKINDKDVDRLDKEGKLANYASTHDIGKLGI

ERYYEDVLHGQTGYEEVEVNNRGRVIRQLKEVPPQAGRDIYLTLDLKLQQYIETLLAGSRAAVVVTDPRT

GAILALVSTPSYDPNLFVDGISSKDYSALLNDPNTPLVNRATQGVYPPASTVKPYVAVSALSAGVITRNT

SLFDPGWWQLPGSEKRYRDWKKWGHGHLNVTKALEESADTYFYQVAYDMGIDRLSEWMSKFGYGHYTGID

LSEERSGNMPTREWKLKRFKKPWYQGDTIPVGIGQGYWTATPIQMNKALMILINDGVVKVPHLLQSTVED

GKPVPWVQPHEPPVGDIHSGYWEIAKDGMYGVANRGNGTAHKYFASAPYKIAAKSGTAQVFGLKANETYN

AHRISERLRDHKLMTAFAPYNNPQVAVAMILENGGAGPAVGTIMRQILDHIMLGDNNTTLPSENPAVTAG

EDQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002894620.1\_1742 [gene=rlmH] [locus\_tag=BN49\_RS10110] [protein=23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH] [protein\_id=WP\_002894620.1] [location=complement(1790769..1791236)] [gbkey=CDS]

MKLQLVAVGTKMPDWVQTGFSEYLRRFPKDMPFELVEIPAGKRGKNADIKRILEKEGEMMLAAAGKNRIV

TLDIPGKPWDTPQLARELERWKQDGRDVSLLVGGPEGLSPACKAAAEQSWSLSTLTLPHPLVRVLVAESL

YRAWSITTNHPYHRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002894623.1\_1743 [gene=rsfS] [locus\_tag=BN49\_RS10115] [protein=ribosome silencing factor] [protein\_id=WP\_002894623.1] [location=complement(1791240..1791557)] [gbkey=CDS]

MQGKALQDFVIDKIDDLKGQDIVAIDVHGKSSITDCMIICTGTSTRHVMSIADHVVQESRAAGMLPLGVE

GEAAADWIVVDLGDVMVHVMQEESRRLYELEKLWS

>lcl|NZ\_FO834906.1\_prot\_WP\_019705380.1\_1744 [locus\_tag=BN49\_RS10120] [protein=adenosylcobalamin/alpha-ribazole phosphatase] [protein\_id=WP\_019705380.1] [location=complement(1791780..1792409)] [gbkey=CDS]

MKLWLVRHGETEANVAGLYSGHAPTPLTPRGVAQARALGERLRLAPFDKVFCSELARTGTTADLLLGDRA

IPRERHPALNEMFFGDWEMRHHRDLQREDAENYAAWCADWQHAAPTNGESFQNFARRVSEFIPTLTDCRH

LDHLLIVGHQGVLSLLTALLLQMPPAAMWHFPIAHGAWSLLEIRDDFTTLRVLNSQAVWQPQEEFPPDH

>lcl|NZ\_FO834906.1\_prot\_WP\_004176879.1\_1745 [gene=nadD] [locus\_tag=BN49\_RS10125] [protein=nicotinate-nucleotide adenylyltransferase] [protein\_id=WP\_004176879.1] [location=complement(1792482..1793132)] [gbkey=CDS]

MVDMTQLQAIYGGTFDPVHYGHLKPVEILANQIGLSKVIIMPNNVPPHRPQPEATSAQRVHMLKLAIADK

PLFTLDERELRRDTPSWTAQTLQEWRQEQGPRKPLAFIIGQDSLLTFPTWHNYETILDNVHLIVCRRPGY

PLTMAQEADQRWLDRHLTHDVESLHNRPSGVIYLAETPWFDISATIIRQRLERGESCAEMLPAAVLDYIR

EQGLYC

>lcl|NZ\_FO834906.1\_prot\_WP\_002894692.1\_1746 [gene=holA] [locus\_tag=BN49\_RS10130] [protein=DNA polymerase III subunit delta] [protein\_id=WP\_002894692.1] [location=complement(1793125..1794156)] [gbkey=CDS]

MIRLYPEQLRAQLTEGLRAAYLLLGNDPLLLQESQDAIREAAAAQGFTEHHTFSIDNSTDWQAIFALSQA

MSLFASRQTLLLILPENGPNAAINEQLATLVGLLHDDLLLIVRGNKLTKAQENAAWLTALAQRAVQVSCQ

TPEYAQLPRWLAARAKQHQLQLDDAASQLLCYCYEGNLLALAQALERLALLWPDGKLTLPRVEQAVNDAA

HFTPYHWVDALLAGKSKRVLHVLQQLRLEGCEPAILLRTLQRELLLLVTLKRQATHTPLRSLFDKHRVWQ

NRRQLLSDALTRLSGEQLRQAVTLLTRAELTFKQDYGHDVWPELESLSLLLCHKALADVFIDG

>lcl|NZ\_FO834906.1\_prot\_WP\_009308182.1\_1747 [gene=lptE] [locus\_tag=BN49\_RS10135] [protein=LPS assembly lipoprotein LptE] [protein\_id=WP\_009308182.1] [location=complement(1794156..1794746)] [gbkey=CDS]

MRYLVTMLLSLAVLVTAGCGWHLRSTTKVPATMKTMIFQSSDPNGPLSRAVRNQLRLNGVELIDASTLRK

DVPSLRLDGSSIQKDTASVFQDGRTAEYQMVMTVHASVLIPGHDIYPITTKVYRSFFDNPQAALAKDAEQ

DMIIQEMYDKAAEQLIRKLPSVQVADVEATQQEEKPVASSAAPSSSGNRVSTTLGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004147581.1\_1748 [gene=leuS] [locus\_tag=BN49\_RS10140] [protein=leucine--tRNA ligase] [protein\_id=WP\_004147581.1] [location=complement(1794761..1797343)] [gbkey=CDS]

MQEQYRPEEIESKVQLHWDENRTFEVTEDESKEKYYCLSMLPYPSGRLHMGHVRNYTIGDVIARYQRMLG

KNVLQPIGWDAFGLPAEGAAVKNNTAPAPWTYDNIAYMKNQLKMLGFGYDWSRELATCTPEYYRWEQKFF

TELYKKGLVYKKTSAVNWCPNDQTVLANEQVIDGCCWRCDTKVERKEIPQWFIKITAYADELLNDLDKLD

HWPDTVKTMQRNWIGRSEGVEISFDVNDYADKLTVYTTRPDTFMGCTYLAVAAGHPLAQQAAANNPALAT

FIDECRNTKVAEADMATMEKKGVDTGFKAIHPLTGEEIPVWAANFVLMEYGTGAVMAVPGHDQRDYEFAS

KYGLNIKPVILAADGSEPDLSEQALTEKGVLFNSGEFSGLDYEAGFNAIADKLAAMGVGERKVNYRLRDW

GVSRQRYWGAPIPMVTLEDGTVLPTPEDQLPVILPEDVVMDGITSPIKADPEWAKTTVNGQPALRETDTF

DTFMESSWYYARYTCPQYQEGMLDSKAANYWLPVDIYIGGIEHAIMHLLYFRFFHKLMRDAGMVNSDEPA

KQLLCQGMVLADAFYYVGENGERNWVSPVDAIVERDEKGRIVKAKDAAGHELVYTGMSKMSKSKNNGIDP

QVMVERYGADTVRLFMMFASPADMTLEWQESGVEGANRFLKRVWKLVYEHTTKGEVAALNVAALSEDQKA

LRRDIHKTIAKVTDDIGRRQTFNTAIAAIMELMNKLAKAPQEDEQDRALMQEALLAVVRMLNPFTPHASF

TLWRELNGEGDIDNAPWPVADESAMVEDSTLVVVQVNGKVRGKITVAVDATEEQVRERAGQEHLVAKYLD

GKTVRKVIYVPGKLLNLVVG

>lcl|NZ\_FO834906.1\_prot\_WP\_002894699.1\_1749 [locus\_tag=BN49\_RS10145] [protein=zinc ribbon-containing protein] [protein\_id=WP\_002894699.1] [location=1797570..1798052] [gbkey=CDS]

MNKVAQYYRELVSSLSERLRHGERDIDALVTQAREKIVRAGDLTQSEIESVIAAVKRDLEEFARSYEESH

EDESDSVFMRVIKESLWQELADITDKTQLEWREVFQDLNHHGVYHSGEVVGLGNLVCEKCHYHLAVYTPD

VLPRCPKCGHDQFQRRPFEP

>lcl|NZ\_FO834906.1\_prot\_WP\_042940394.1\_1750 [locus\_tag=BN49\_RS10150] [protein=filamentous hemagglutinin N-terminal domain-containing protein] [protein\_id=WP\_042940394.1] [location=complement(1798098..1799891)] [gbkey=CDS]

MFKFKASYVALAAVLTSSVVYADPTSYTHSSGATVIDIEKPNAAGVSHNLYRDFNVGTNGTILNNSGDDV

SHSTFGNIARNNNLTAGSASVILNEVTSKNASSLKGFIEVNGQKADVVIANPNGITCSGCSFVNTNKAIL

TTGKVDMTDDGAIGSYTVTGGTLTIGENGMNAANGYAVLLADAIKINGKVQANNALVSAGNFTMDNSSGS

VTSAGKKATLIQMRVNPQYSIDVSSLGGIEANSISMVGNNIGFGVRNKGSIISNGTLMLTSNGNLLNKGS

ITGKGLLSQVSTVTGITNDGSIAGAYYLMLSSGDYIVNTGSLSGGQLIATANGNITNGDSGTMTGTSGLS

LTSGGKIRNEEKASLLSNNQIAATAIGDFLNEGKISAKHTSLTFVGDSFKNTGNINSTGQTTIQSLTQDG

SANTGEIYNLGNITGENINLQTNGTLAQSSSGRIEATNAITAHSYWLNQNGYMNAADITTDHGVVNNYGN

ITAKNISITTYSDITNEGQISSTGDLTLNTKNKGAIYNYSTLSAGGNMTLTATKVVNGGKSCGILGLAKC

GVGTLTADKLVLNSSQKYVSDMGGKQYFKSTEVNTVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528989.1\_1751 [locus\_tag=BN49\_RS10155] [protein=ShlB/FhaC/HecB family hemolysin secretion/activation protein] [protein\_id=WP\_016528989.1] [location=complement(1799957..1801627)] [gbkey=CDS]

MLIRSRTLTGLLFITLAGTSAAEAAPLTSSTHQTEQDKARQEALAPQQQDFQSSQQRVAPQGIPFPEETH

CKLINRVDIDSDNQALTRKLLAKTARQAQGRCLGSESIRLLAYTLQNELIAQGYITSLIDVPSQSLEHGI

LRFTLHYGKVGAIDYADGSDTTRLWNSLPTSSGTILRLSDLEQGMANLQRLPGATAHMKLLPGQHEGESD

IQIARSLAKKWQLGAWLDDAGSKASGRYQAGGALYLYDLTTLNDILYLSGGGDIEFNQHNDGNHNGSLYY

SIPFGYWTLSAYGAYSQYRQQFNGNWSTMDYKSKNRYYSATLSRLLSHTRQQKTTADLRIAKSTSHYYFG

GSELLVMRKQNPSWEFTLNHQHYFNKKIVDASIGIQRSLPWLSSTATPEEQAGLYSPLSRIVHGNLQAMM

KFDATGDKFTWAPRLSAQFSPDKLASDNKFNIGSRWSVRGFDGENSLSGNQGWYWRNDFIWDLATHERQF

YLGADIGRLIGADLYQKGKVLSGAVSGLRGQLWSTQYDLFISTPLSKPDKFHSDALNMGFSLQWRY

>lcl|NZ\_FO834906.1\_prot\_WP\_002894706.1\_1752 [locus\_tag=BN49\_RS10165] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_002894706.1] [location=complement(1802009..1802734)] [gbkey=CDS]

MITLKNVSKWYGHFQVLTDCSTEVKKGEVVVVCGPSGSGKSTLIKTVNGLEPVQQGQIIVDGTVVNDKKT

NLAKLRSHVGMVFQHFELFPHLSIIDNLTLAQVKVLNRDKASARKKGLKLLERVGLAAHAEKYPAQLSGG

QQQRVAIARALCMDPIAMLFDEPTSALDPEMINEVLDVMVELANEGMTMMVVTHEMGFARKVANRVIFMD

EGKIVEDADKEAFFANPQSERAKDFLAKILH

>lcl|NZ\_FO834906.1\_prot\_WP\_002894707.1\_1753 [gene=gltK] [locus\_tag=BN49\_RS10170] [protein=glutamate/aspartate ABC transporter permease GltK] [protein\_id=WP\_002894707.1] [location=complement(1802734..1803408)] [gbkey=CDS]

MYDFDWSSIVPSMPYLLAGLVITLKITVIAIVVGIVWGTLLAVMRLSSFLPLAWFAKSYVNVFRSIPLVM

VLLWFYLIVPGFLQNVLGLSPKTDIRLISAMVAFSMFEAAYYSEIIRAGIQSISRGQSSAALALGMTHWQ

SMRLVILPQAFRAMVPLLLTQGIVLFQDTSLVYVLSLADFFRTASTIGERDGTQVEMILFAGGVYFVISL

SASLLVSWLKKRTV

>lcl|NZ\_FO834906.1\_prot\_WP\_002894709.1\_1754 [locus\_tag=BN49\_RS10175] [protein=amino acid ABC transporter permease] [protein\_id=WP\_002894709.1] [location=complement(1803408..1804148)] [gbkey=CDS]

MSIDWNWGIFLQQAPFGNTTYLGWLWSGFQITVALSISAWIIAFLVGSLFGILRTVPNRFLSGIGTCYVE

LFRNVPLIVQFFTWYLVVPEFLPENIGMWFKSELDPNIQFFVSSMLCLGLFTAARVCEQVRAAIQSLPRG

QKNAGLAMGLTLPQTYRYVLLPNAYRVIVPPMTSEMMNLVKNSAIASTIGLADMAAQAGKLLDYSAHAWE

SFTAITLAYVFINAVIMLIMYVVERKVRLPGNMGGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002894712.1\_1755 [locus\_tag=BN49\_RS10180] [protein=amino acid ABC transporter substrate-binding protein] [protein\_id=WP\_002894712.1] [location=complement(1804313..1805224)] [gbkey=CDS]

MQLRKLATAMLVMGMTAGLAQAEDAAPAAGQNTLDKIAKNGVIVVGHRESSVPFSYYDNQQKVVGYSQDY

SNAIVDAIKKKLNKPDLQVKLIPVTSQNRIPLLQNGTFDFECGSTTNNLERQKQAAFSDTIFVVGTRLLV

KKGGPIKDFPDLKDKAVVVTSGTTSEILLHKLNDEKKMNMRIISAKDHGDSFRTLESGRAVAFMMDDALL

AGERAKAKKPDNWEIVGTPQSKEAYGCMLRKDDPTFKALVDETVAQAQTSGEAEKWFDKWFKNPIPPKNL

NLNFELSDDMKALFKSPNDKALN

>lcl|NZ\_FO834906.1\_prot\_WP\_002894716.1\_1756 [gene=lnt] [locus\_tag=BN49\_RS10185] [protein=apolipoprotein N-acyltransferase] [protein\_id=WP\_002894716.1] [location=complement(1805579..1807117)] [gbkey=CDS]

MVFASLLERQRIRLLLALLFGASGTLAFSPYDFWPAAIVSLIGLQALTLNRRPLQSAGIGYFWGLGLFGT

GINWVYVSIAQFGGMPGPVNVFLVVLLAAYLSLYTGLFAGLLARLWPKTNWIRMAIAAPVVWQITEFLRG

WVLTGFPWLQFGYSQIDGPLKGLAPVMGVEAINFLLMVVSGLLALALVQRNWKPLAIAALLFALPFPLRY

IQWYQLLPARATQVSLVQGDIPQAMKWDEKQLVNTLKTYLALTQPHIGHSQLIIWPESAIPDLEINQQQF

LSMMDDLLRAKDSSLITGIVDARLNKQNRYDTYNTIITLGKDNPYRYDSTNRYNKNHLVPFGEFVPLESI

LRPLAPFFDLPMSSFSRGPYVQPQLMAHNLKLTAAICYEIILGEQVRDNFRPDTDFLLTISNDAWFGKSI

GPWQHFQMARMRALELARPLLRSTNNGITAVIGPRGEIQKMIPQFTREVLTTTVTPASGLTPYARTGNWP

LWALTALFGFAALLMSLRQRRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004197606.1\_1757 [gene=corC] [locus\_tag=BN49\_RS10190] [protein=CNNM family magnesium/cobalt transport protein CorC] [protein\_id=WP\_004197606.1] [location=complement(1807243..1808121)] [gbkey=CDS]

MSDDNSHSSDTVNSKKGFFSLLLSQLFHGEPKNRDELLALIRDSGQNDLIDEDTRDMLEGVMDIADQRVR

DIMIPRSQMITLKRNQTLDECLDVIIESAHSRFPVISEDKDHIEGILMAKDLLPFMRSDAEAFSMEKVLR

PAVVVPESKRVDRMLKEFRSQRYHMAIVIDEFGGVSGLVTIEDILELIVGEIEDEYDEEEDIDFRQLSRH

TWTVRALASIEDFNDAFDTHFSDEEVDTIGGLVMQAFGHLPARGESIDIDGYQFKVAMADSRRIIQVHVK

LPDDAPQPKLEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002894722.1\_1758 [gene=ybeY] [locus\_tag=BN49\_RS10195] [protein=rRNA maturation RNase YbeY] [protein\_id=WP\_002894722.1] [location=complement(1808269..1808742)] [gbkey=CDS]

MSQVILDLQLACEETSGLPDEALFQRWVDAVIPPFQEESELTIRLVDVAESHELNLTYRGKDKPTNVLSF

PFEAPPGIEMPLLGDLIICRQVVEQEASEQGKPLEAHWAHMVVHGSLHLLGYDHIEDDEAEEMEGLETEI

MLALGYEDPYISEKIAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004176871.1\_1759 [locus\_tag=BN49\_RS10200] [protein=PhoH family protein] [protein\_id=WP\_004176871.1] [location=complement(1808739..1809785)] [gbkey=CDS]

MNIDTREITLEPADNARLLALCGPFDDNIKQLERRLGIEINRRDNHFKLTGRALCVHAAADILRSLYVDT

APMRGQIQDIEPEQIHLAIKEARVLEQSAESVPEYGKAVNIKTKRGVIKPRTPNQAQYIANILDHDITFG

VGPAGTGKTYLAVAAAVDALERQEIRRILLTRPAVEAGEKLGFLPGDLSQKVDPYLRPLYDALFEMLGFE

KVEKLIERNVIEVAPLAYMRGRTLNDAFIILDESQNTTIEQMKMFLTRIGFNSKAVITGDITQIDLPRST

KSGLRHAIEVLAEVDEISFNFFHSEDVVRHPVVARIVNAYEAWEAADQKRKAELAAERKREAQEQEQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002894730.1\_1760 [gene=miaB] [locus\_tag=BN49\_RS10205] [protein=tRNA (N6-isopentenyl adenosine(37)-C2)-methylthiotransferase MiaB] [protein\_id=WP\_002894730.1] [location=complement(1809939..1811363)] [gbkey=CDS]

MTKKLHIKTWGCQMNEYDSSKMADLLDATHGYQLTEVAEEADVLLLNTCSIREKAQEKVFHQLGRWKLLK

EKNPDLIIGVGGCVASQEGDHIRQRAHYVDIIFGPQTLHRLPEMINSVRGNRSPVVDISFPEIEKFDRLP

EPRAEGPTAFVSIMEGCNKYCTYCVVPYTRGEEVSRPCDDILFEIAQLAAQGVREVNLLGQNVNAWRGEN

YDGTTGSFADLLRLVAAIDGIDRIRFTTSHPIEFTDDIIDVYRDTPELVSFLHLPVQSGSDRVLNLMGRT

HTALEYKAIIRKLREARPDIQISSDFIVGFPGETTEDFEKTMKLIADVNFDMSYSFIFSARPGTPAADMV

DDVPEADKKQRLYILQERINQQAMAWSRRMLGTVQRILVEGTSRKNIMELSGRTENNRVVNFEGTPDLVG

KFVDVEIVDVYTNSLRGKIVRTEAEMGLRIAESPESVIARTRKENDLGVGIYQP

>lcl|NZ\_FO834906.1\_prot\_WP\_040088679.1\_1761 [gene=ubiF] [locus\_tag=BN49\_RS10210] [protein=3-demethoxyubiquinol 3-hydroxylase] [protein\_id=WP\_040088679.1] [location=1811543..1812718] [gbkey=CDS]

MTIHVTDVAIVGGGMVGGALALGLAQQGFTVTVLEKAAPPAFDPASAPDVRISAISAASVGLLKSLGVWD

AIRAMRVHAYRRLETWEWESAHVAFDAAELKLPELGYMVENKVLQWGLWQALAAHEAVTLRVGSELKTMQ

RGETQTALHLREGETIHARLVIGADGANSQVREMAGIGVHAWQYQQSCMLISVECADDPGDSTWQQFTPS

GPRAFLPLFDHWASLVWYDAPARIRQLQSMTMAQLQQEIASHFPARLGQVTPQAAGAFPLTRRHALQYVQ

PGLALVGDAAHTIHPLAGQGVNLGYRDVDALLEILAEARGRGEDWASLPVLKRYQARRRADNFIMQSGMD

LFYAGFSNDLAPVRMLRNIGLMAAERAGMLKRQALKYALGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002894734.1\_1762 [gene=asnB] [locus\_tag=BN49\_RS10250] [protein=asparagine synthase B] [protein\_id=WP\_002894734.1] [location=complement(1813826..1815490)] [gbkey=CDS]

MCSIFGVLDIKTDAGELRKKALELSRLMRHRGPDWSGVYASDKAILAHERLSIVDVNAGAQPLYNAEKTH

ALAVNGEIYNHQALRAEYGDRYQFQTGSDCEVILALYQEKGPEFLDDLQGMFAFALYDSEKDAYLIGRDH

IGIIPLYMGHDEHGNFYVASEMKALVPVCRTIKEFPAGSYLWSKDGEIRQYYQRDWFDYDAVKDNVTDKN

ELRQALEESVKSHLMSDVPYGVLLSGGLDSSVISAITKKFAARRVEDQERSEAWWPQLHSFAVGLEGSPD

LKAAQEVANHLGTVHHEIHFTVQEGLDAIRDVIYHIETYDVTTIRASTPMYLMSRKIKAMGIKMVLSGEG

SDEVFGGYLYFHKAPNAKELHEETVRKLQALHMFDCARANKAMSAWGVEARVPFLDKKFLDVAMRINPQD

KMCGNGKMEKHILRECFESYLPASVAWRQKEQFSDGVGYSWIDTLKEVAAKQISDQQLETASFRFPYNTP

TSKEGYLYREIFEELFPLPSAAECVPGGPSVACSSAKAIEWDEAFKTMNDPSGRAVGVHQSAYK

>lcl|NZ\_FO834906.1\_prot\_WP\_002894738.1\_1763 [locus\_tag=BN49\_RS10255] [protein=HAD-IIA family hydrolase] [protein\_id=WP\_002894738.1] [location=complement(1815769..1816521)] [gbkey=CDS]

MTIQNIICDIDGVLMHDNVAVPGAAEFIKRILDKGMPLVMLTNYPSQTGQDLANRFATAGIDVPDSAFYT

SAMATADFLRRQEGKKAYVVGEGALIHELYKAGFTITDVNPDFVIVGETRSFNWEMMHKAAFFVANGARF

IATNPDTHGRGFYPACGALCAGIEKISGRKPFYVGKPSPWIIRSALNKMQAHSEQTVIVGDNLRTDILAG

FQAGLETILVLSGVSTLDDIDSMPFRPSWIYPSVAEIDIF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529781.1\_1764 [locus\_tag=BN49\_RS10260] [protein=ROK family transcriptional regulator] [protein\_id=WP\_016529781.1] [location=complement(1816638..1817858)] [gbkey=CDS]

MTAGGQAQIGNVDLVKQLNSAAVYRLIDQHGPISRIQIAEQSQLAPASVTKITRQLIERGLIKEVDQQAS

TGGRRAISIIAETRNFNAIGVRLGRYDATLTLYDLSSKTLEEEHFPLPERTQETLEHALLNIIATFIENC

QRKIRELIAISVILPGLVDPESGVIRYMPHIAVENWGLVGALEKRFNVTCFVGHDIRSLALAEHYFGASQ

DCEDSILVRVHRGTGAGIISNGRIFIGRNGNVGEIGHIQVDPLGERCHCGNFGCLETVAANAAIEQRVRH

LLEQGYQSRLTPDDCTIKTICNAANKGDALACEVIEYVGRHLGKTIAIAINLFNPQKIVVAGEIVEAEKV

LLPAIEGCINAQALKAFRKNLPVVRSTLDHRSAIGAFALVKRAMLNGTLLQRLLES

>lcl|NZ\_FO834906.1\_prot\_WP\_004223668.1\_1765 [gene=nagA] [locus\_tag=BN49\_RS10265] [protein=N-acetylglucosamine-6-phosphate deacetylase] [protein\_id=WP\_004223668.1] [location=complement(1817867..1819015)] [gbkey=CDS]

MYALTQGRVYTGHEILDDHAVVIADGFIERLCPLADLPSDIEQRSVNGAIIAPGFIDVQLNGCGGVQFND

SPEAVTVETLEIMQKANERSGCTSFLPTLITSSDDLMKQGVRVMREYLQKHPNQALGLHLEGPWLNIVKK

GTHNPDYVRKPDAALVDFLCDNADVITKVTLAPERVEPEVIRKLVAAGIVVSAGHSNATLKEAKVGFRAG

ITFATHLYNAMPYITGREPGLAGAIFDEPDVYCGIIVDGMHVDYANVRNAKRLKGDKLCLVTDATAPAGA

NIDQFIFAGKTIYYRNGLCVDENGTLSGSSLTMIEGVRNLVEHCGVALDEVLRMATLYPARAIGVDKQLG

SIAPGMVANLTAFTRDYKITKTIVNGNEVVTE

>lcl|NZ\_FO834906.1\_prot\_WP\_002894749.1\_1766 [gene=nagB] [locus\_tag=BN49\_RS10270] [protein=glucosamine-6-phosphate deaminase] [protein\_id=WP\_002894749.1] [location=complement(1819125..1819925)] [gbkey=CDS]

MRLIPLVTAEQVGKWAARHIVNRINAFKPTADRPFVLGLPTGGTPLTAYKALVEMHKAGQVSFKHVVTFN

MDEYVGLPKEHPESYHSFMHRNFFDHVDIPAENINLLNGNAPDIDAECRRYEEKIRSYGKIHLFMGGVGN

DGHIAFNEPASSLASRTRIKTLTHETRVANSRFFDGDVDLVPKYALTVGVGTLLDAEEVMILVLGHQKAL

ALQAAVEGNVNHMWTITCLQLHPKAVIVCDEPSTMELKVKTLKYFNELEAENIKGL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529782.1\_1767 [gene=nagE] [locus\_tag=BN49\_RS10275] [protein=PTS N-acetyl glucosamine transporter subunit IIABC] [protein\_id=WP\_016529782.1] [location=1820240..1822195] [gbkey=CDS]

MNILGFFQRLGRALQLPIAVLPVAALLLRFGQPDLLNVPFIAQAGGAIFDNLALIFAIGVASSWSKDNAG

SAALAGAVGYFVMTKAMVTINPEINMGVLAGIITGLVAGAVYNRWAGIKLPDFLSFFGGKRFVPIATGFF

CLILAAIFGYVWPPVQHAIHSGGEWIVSAGALGSGIFGFINRLLIPTGLHQVLNTIAWFQIGEFTNAAGA

VFHGDINRFYAGDGTAGMFMSGFFPIMMFGLPGAALAMYLAAPKARRPMVGGMLLSVAITAFLTGVTEPL

EFLFMFLAPLLYLLHAVLTGISLFIATALGIHAGFSFSAGAIDYVLMYSLPAASKNVWMLLVMGVVFFFV

YFLLFSAVIRMFNLKTPGREDKAADVVTEEANSNTEEGLTQLATSYIAAVGGTDNLKAIDACITRLRLTV

GDSAKVNDAACKRLGASGVVKLNKQTIQVIVGAKAESIGDEMKKVVTRGPVAAAAATPAGNVATAAPAAK

PQAVANAKTVESLVSPITGDVVALEQVPDEAFASKAVGDGIAVKPTSNIVVAPAAGTVVKIFNTNHAFCL

ETNNGAEIVVHMGIDTVALEGKGFKRLVEEGTDVKAGEPILEMDLDFLNANARSMISPVVCSNSDDYSAL

VILASGKVVAGQTPLYEIKGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529783.1\_1768 [gene=glnS] [locus\_tag=BN49\_RS10280] [protein=glutamine--tRNA ligase] [protein\_id=WP\_016529783.1] [location=1822374..1824041] [gbkey=CDS]

MSEAEARPTNFIRQIIDEDLATGKHTTVHTRFPPEPNGYLHIGHAKSICLNFGIAQDYQGQCNLRFDDTN

PVKEDIEYVESIKNDVQWLGFHWSGDVCYSSDYFDQLHQYAVELINKGLAYVDELSPDEIREYRGTLKAP

GKNSPYRDRSVEENLALFEKMRSGGFEEGKACLRAKIDMASPFIVMRDPVLYRIKFAEHHQTGNKWCIYP

MYDFTHCISDALEGITHSLCTLEFQDNRRLYDWVLDNISIPVHPRQYEFSRLNLEYTVMSKRKLNQLVTE

KHVEGWDDPRMPTISGLRRRGYTAESIREFCKRIGVTKQDNTIEMASLESCIREDLNENAPRAMAVIDPV

KLVIENYPQGESEMVVMPNHPNKPEMGSREVPFSAEIWIDRADFREEANKQYKRLVLGKEVRLRNAYVIK

AERVEKDAEGNITTIFCTYDADTLSKDPADGRKVKGVIHWVSAAHALPVEIRLYDRLFSVPNPGAAEDFL

AVINPESLVIKQGYAEPSLAQAEAGKAYQFEREGYFCLDSRYATATSLVFNRTVGLRDTWAKAGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004176868.1\_1769 [locus\_tag=BN49\_RS10285] [protein=hypothetical protein] [protein\_id=WP\_004176868.1] [location=complement(1824096..1824404)] [gbkey=CDS]

MWGGKKDRETTVDRLFFVARIINVFREAKLKIMTKRTYFMSFCYSLISDDFVMEVIAKSGKNAIIESDYI

GFLYVTGNIRSAIYYHAETELIRIAKMKSLIS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529784.1\_1770 [gene=chiP] [locus\_tag=BN49\_RS10290] [protein=chitoporin] [protein\_id=WP\_016529784.1] [location=1824478..1825881] [gbkey=CDS]

MRTFSGKRSTLALAIAAVTAMSGWVVAPQASAAGFIDDSTLTGGIYYWQRERDRKDVTDGDKYKTNLSHS

TWNANLDFQSGYAADMFGLDIAAFTAIEMAENGDSGHPNEIAFSSRNKAYDEDYSGDKSGISLYKAAAKF

KYGPAWARAGYIQPTGQTLLAPHWSFMPGTYQGAEAGANFDYGTAGALSFSYMWTNEYKAPWHIEMDDFY

QNDKKTKVDYLHSVGAKYDFKNDLVLEAAFGQAQGYIDQYFAKASYKFDVAGAPLSTSYQFYGTRDKVSN

GGVNDIYDGTAWLQALTFGYKVADVLDLRLEGTWVKADGQQGYFLQRMTPTYASSNGRLDIWWDNRSDFN

ANGEKAVFFGAMYDMKNWDMPGWAFGASYVYAWDAKPGRMSSPDAYYDPDYRLKESAYSLDAMYTVQEGW

AKGTLFKLHFTQYDNHSDIPSWSGGYGNIFQDERDVKFMVIAPFTIF

>lcl|NZ\_FO834906.1\_prot\_WP\_002894759.1\_1771 [locus\_tag=BN49\_RS10295] [protein=ChiQ/YbfN family lipoprotein] [protein\_id=WP\_002894759.1] [location=1825929..1826261] [gbkey=CDS]

MKKMLLIAMMAAGLVACTTSPAPKEDTKLKDAYSACINTAEGNPDKIEACQSVLNVLKKDKQHQQFANQE

SVRVLDYQQCIQATRTGNDQAVKARCDQIWKEIRSNNTTH

>lcl|NZ\_FO834906.1\_prot\_1772 [locus\_tag=BN49\_RS28855] [protein=hypothetical protein] [pseudo=true] [partial=5',3'] [location=complement(<1826319..>1826735)] [gbkey=CDS]

GAISDRIGRRPVLMGITVLALLTTWPVMHWLTVAPDFTRMTLVLLWFSFFFGMYNGAMVAALTEVMPVHV

RTVGFSLAFSLATAIFGDLTPAISTALVELTGDKSAPGWWLMCAALCGFIATALLFVRLSRGYQPAESQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529785.1\_1773 [gene=fur] [locus\_tag=BN49\_RS10300] [protein=ferric iron uptake transcriptional regulator] [protein\_id=WP\_016529785.1] [location=complement(1826878..1827330)] [gbkey=CDS]

MTDNNTALKKAGLKVTLPRLKILEVLQEPDNHHVSAEDLYKRLIDMGEEIGLATVYRVLNQFDDAGIVTR

HNFEGGKSVFELTQQHHHDHLICLDCGKVIEFSDDSIELRQREIASRHGIRLTNHSLYLYGHCAEGDCRE

DEHAHDVVEK

>lcl|NZ\_FO834906.1\_prot\_WP\_002894765.1\_1774 [gene=fldA] [locus\_tag=BN49\_RS10305] [protein=flavodoxin FldA] [protein\_id=WP\_002894765.1] [location=complement(1827622..1828152)] [gbkey=CDS]

MAIIGIFFGSDTGNTENIAKMIQKQLGKDVADVHDIAKSSKEDLEAHDILLLGIPTWYYGEAQCDWDDFF

PTLEEIDFNGKLVALFGCGDQEDYAEYFCDALGTIRDIIEPRGATIVGHWPTAGYHFEASKGLADDDHFV

GLAIDEDRQPELTNERVEKWVKQVAEELHLEEIKNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002894767.1\_1775 [gene=ybfE] [locus\_tag=BN49\_RS10310] [protein=LexA regulated protein] [protein\_id=WP\_002894767.1] [location=complement(1828304..1828597)] [gbkey=CDS]

MAKEQTDRTTLDLFANERRPGRPKTNPLSRDEQLRINKRNQLKRDKVRGLKRVELKLNADAVDALNELAE

ARNMSRSDLIEEMLMTQLTALRSQGKV

>lcl|NZ\_FO834906.1\_prot\_WP\_032102936.1\_1776 [gene=ybfF] [locus\_tag=BN49\_RS10315] [protein=esterase] [protein\_id=WP\_032102936.1] [location=complement(1828731..1829504)] [gbkey=CDS]

MKLNSRAQSAQNPHNHSPIVLVHGLFGSLDNLGILARDLIADHDIVQVDMRNHGLSPRSPEMTYPAMAQD

LLDTLDAHQIERATFIGHSMGGKAVMALTALAPERISGLVAIDIAPVDYHVRRHDEIFAAIRAVSESAAS

TRQQAAQVMREHLQEEGVIQFLLKSFVDGDWRFNVPVLWDQYLHIVGWETIPAWPHPTQFIPGGNSPYVT

DAYRDALLAQFPQARAHVIAGAGHWVHAEKPEAVLRAIRRYLTSIAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002894771.1\_1777 [gene=seqA] [locus\_tag=BN49\_RS10325] [protein=replication initiation negative regulator SeqA] [protein\_id=WP\_002894771.1] [location=1829688..1830236] [gbkey=CDS]

MKTIEVDDELYRYIASHTLHIGESASDILRRMLKFSAVSQPATPVSKAAPTLAPAPVAEVKPANPVKDKV

RAMREMLLSDEYAEQKRAVNRFMLVLTTLYSLDSKAFAEATESLHGRTRVYFAEDARTLLKSGNQTKPKQ

VPGTPWWVITNTNTGRKCSMIEHIMQSMQFPAELIEKVCGTI

>lcl|NZ\_FO834906.1\_prot\_WP\_004183423.1\_1778 [gene=pgm] [locus\_tag=BN49\_RS10330] [protein=phosphoglucomutase (alpha-D-glucose-1,6-bisphosphate-dependent)] [protein\_id=WP\_004183423.1] [location=1830269..1831909] [gbkey=CDS]

MAIDKRAGQPAQQSDLINVAQLTAQYYVLKPEVGNAEHAVKFGTSGHRGSAARHNFNEPHILAIAQAIAE

DRAKNGITGPCYVGKDTHALSEPAFISVLEVLTANGVDVIVQENNGFTPTPAVSNAILVHNKKGGPLADG

IVITPSHNPPEDGGIKYNPPNGGPADTNVTKVVENRANELLAAGLQGVKRISLDAALASGHVKEQDLVQP

FIEGLADIVDMAAIQKAGLTLGVDPLGGSGIEYWKRIGEHYKLNLTIVNDQVDQTFRFMHLDKDGAIRMD

CSSECAMAGLLALRDKFDLAFANDPDYDRHGIVTPAGLMNPNHYLAVAINYLFQHRPQWGKEVAVGKTLV

SSAMIDRVVNDLGRKLVEVPVGFKWFVDGLFDGSFGFGGEESAGASFLRFDGTPWSTDKDGIIMCLLAAE

ITAVTGKNPQEHYNELAERFGAPSYNRLQASATSAQKAALSKLSPEMVSADTLAGDPITARLTAAPGNGA

AIGGLKVMTDNGWFAARPSGTEDAYKIYCESFLGEEHRKQIEKEAVEIVSEVLKNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004179052.1\_1779 [locus\_tag=BN49\_RS10335] [protein=hypothetical protein] [protein\_id=WP\_004179052.1] [location=1831964..1832401] [gbkey=CDS]

MKIQRKSLFLFWAWMDLFFVLQFLWWNIAHRRLPFYDDLLAYLQLLHTWGSAAVWLYPLNVLLIISIPLS

MIFFFRQSRYALWLAWGQAPLRLLFMQPSLSLGLWLIQAAGVRHVAILAGFLLLSEGLKIASLWYCRGGI

QGIKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002894776.1\_1780 [gene=kdpE] [locus\_tag=BN49\_RS10340] [protein=two-component system response regulator KdpE] [protein\_id=WP\_002894776.1] [location=complement(1832383..1833060)] [gbkey=CDS]

MINVLIIEDEHAIRRFLRTALEADGMRVFEAETLQRGLIEAATRKPDLAILDLGLPDGDGIDFIRDLRQW

SQMPIIVLSARSEEHDKIAALDAGADDYLSKPFGIGELQARLRVALRRHGAAQADEPVVRFADLEVNIPA

RRILRGSEEIHLTPIEFRLLAALLNNPGKVLTQRQLLNQVWGPNAVEHSHYLRIYMGHLRQKLEADPARP

QHLLTETGIGYRFMP

>lcl|NZ\_FO834906.1\_prot\_WP\_032102933.1\_1781 [gene=kdpD] [locus\_tag=BN49\_RS10345] [protein=two-component system sensor histidine kinase KdpD] [protein\_id=WP\_032102933.1] [location=complement(1833057..1835744)] [gbkey=CDS]

MSDEPLRPDPDRLLQHTAAPHRGKLKVFFGACAGVGKTWAMLAEAQRLRAQGLDILIGVAETHGRKETAA

MLQGLSTLPPRRLAHRGRYVYEFDLDAALARRPALILVDELAHSNAPGSRHPKRWQDVDELLEAGIDVFT

TVNVQHLESLNDVVSGITGVQVRETVPDPFFDAADDVVLVDLPPDDLRQRLNEGKVYIGGQAERAIENFF

RKGNLIALRELALRRTADRVDEQMRAWRDRQGQEKVWHTRDAILLCIGHNTGSEKLVRAAARLAARLGSI

WHAVYVETPSLHRLPEGRRRAILAALRLAQELGAETATLSDPSEEKAVLHYAREHNLGKIVIGRQSKRRW

WDRSGFADRLARHAPDLDLVVIALDEKPSPLPARGNDSRTALEKWRLQLQGCAVAVALCAIITLVAMQWL

MAFEAANLVMLYLLGVVLIALVYGRWPSVLATVINVISFDLFFVAPRGTLAVSDVQYLLTFGVMLTVGLL

IGNLTAGVRYQARVARYRERRTRHLYEMSKALAVGRSQQDIATTSERFIASTFQARSQLLLPDAQGKLLP

LTHQPGLTPWDDAIARWSFDKGQPAGAGTDTLPGVPYQILPLKSAARTWGLLVVEPENLRQLMIPEQQRL

LETFTLLVASALERLTLTASEEQARLTSERESLRNSLLAALSHDLRTPLTVLFGQAEILTLDLASEGSKH

APQANEIRQHVLNTTRLVNNLLDMARIQSGGFNLHKEWLTLEEVVGSALRMLEPSLGGQHIQLDLPDPLQ

LVHVDGPLFERVLINLLENAHKYAGARASIGIRAEADARQLSLEVWDNGPGIPAGQEQTIFDKFARGNKE

SAIPGVGLGLAICQAIVDVHGGTISASNRPEGGASFRVTLPGETPPELEELPEEL

>lcl|NZ\_FO834906.1\_prot\_WP\_016532167.1\_1782 [gene=kdpC] [locus\_tag=BN49\_RS10350] [protein=potassium-transporting ATPase subunit KdpC] [protein\_id=WP\_016532167.1] [location=complement(1835745..1836320)] [gbkey=CDS]

MSLIRPALVLFILLTLLTGGVYPLLTTSLGQWWFNPQANGSLIRLNGEVRGSALIGQNFTAAGYFQGRPS

ATAETADNPMASGGSNLAASNPELDKAVSERVQALRAANPDADPRVPVELVTTSASGLDNNLTPAAALWQ

VPRVAQARQLSVEQVTQLVNQATQTPLLSFLGQPVVNILQLNMALDALKDK

>lcl|NZ\_FO834906.1\_prot\_WP\_032102931.1\_1783 [gene=kdpB] [locus\_tag=BN49\_RS10355] [protein=potassium-transporting ATPase subunit KdpB] [protein\_id=WP\_032102931.1] [location=complement(1836331..1838379)] [gbkey=CDS]

MSRKQLALLEPTLVRQALLDAVKKLSPMVQWRNPVMFIVWVGSLLTTLLAIAMAGGALTGSATFTAAVSI

WLWFTVLFANFAEAMAEGRSKAQANSLKGVKKTAFARKLRAPQHDAPVDHVPAEDLRKGDVVLVEAGDII

PCDGEVIEGGASVDESAITGESAPVIRESGGDFASVTGGTRILSDWLVIRCSVNPGETFLDRMIAMVEGA

QRRKTPNEIALTILLIALTLVFLLATATIWPFSAWSGNAVSVTVLVALLVCLIPTTIGGLLSAIGVAGMS

RMLGANVIATSGRAVEAAGDVDVLLLDKTGTITLGNRQASAFLPARGVEERTLADAAQLSSLADETPEGR

SIVVLAKQRFNLRERDLQSLHATFVPFTAQTRMSGINIDQRMIRKGSVDAIRRHVEANGGHFPANVDKQV

EEVARQGATPLVVAEGEKVLGIIALKDIVKGGIKERFAQLRKMGIKTVMITGDNRLTAAAIAAEAGVDDF

LAEATPEAKLALIRQYQSEGRLVAMTGDGTNDAPALAQADVAVAMNSGTQAAKEAGNMVDLDSNPTKLIE

VVHIGKQMLMTRGSLTTFSIANDVAKYFAIIPAAFAAVYPQLAMLNVMGLHSPSSAILSAVIFNALIIVF

LIPLALKGVSYRPLSASAMLRRNLWIYGLGGLLVPFIGIKAIDLLLTLSGLV

>lcl|NZ\_FO834906.1\_prot\_WP\_004142245.1\_1784 [gene=kdpA] [locus\_tag=BN49\_RS10360] [protein=potassium-transporting ATPase subunit KdpA] [protein\_id=WP\_004142245.1] [location=complement(1838400..1840079)] [gbkey=CDS]

MAAQGFLLLASYLLVLLVLARPLGMCLARMVNDIPLPGLAGVERVLWRVAGIRAEEMGWLQYLLALLLFN

ALGGLALFALLMLQGVLPFNPQHLPGLSWDLALNTAISFVSNTNWQAYAGESTMSYLSQMVGLTVQNFLS

AATGIAVVFALTRAFARQKMSTLGNAWVDLTRITLWLLLPLSLLVALFFIQQGVPQNLQAYQPFTTLEGV

HQLLPMGPVASQEAIKLLGTNGGGFFNANSAHPFENPTALTNLVQMLAIFLIPAALCFAFGEVVSDRRQG

RAILWAMTLIFILCVAVVMWAETRGNPHLLTLGADSSLNMEGKESRFGILASSLFAVITTAASCGAVNAM

HDSFTALGGMVPMWLMQIGEVVFGGVGSGLYGMLLFVMLAVFIAGLMVGRTPEYLGKKIDVREMKMIALA

ILVTPTLVLLGTALAMMTDAGRAGMFNPGPHGFSEVLYAVTSAANNNGSAFAGLGAATPFWNLLLAFCML

VGRFAVIIPVMAIAGSLVAKKIQPASPGTLATHDALFIGLLIGTVLLVGALTFIPALALGPLAEHFSLL

>lcl|NZ\_FO834906.1\_prot\_WP\_020323459.1\_1785 [gene=kdpF] [locus\_tag=BN49\_RS30080] [protein=K(+)-transporting ATPase subunit F] [protein\_id=WP\_020323459.1] [location=complement(1840079..1840168)] [gbkey=CDS]

MTAGVLTGVGLVFLLLAYLVYALIHAEAF

>lcl|NZ\_FO834906.1\_prot\_WP\_004142243.1\_1786 [locus\_tag=BN49\_RS10365] [protein=DUF2517 family protein] [protein\_id=WP\_004142243.1] [location=1840475..1840684] [gbkey=CDS]

MMALYKAYPAHIILLRRAFAVVAGVAALPVMLFWKDRARYYSWLHRVWSKTSEQPVWMAQAEKAAHDFY

>lcl|NZ\_FO834906.1\_prot\_WP\_020316935.1\_1787 [gene=phrB] [locus\_tag=BN49\_RS10370] [protein=deoxyribodipyrimidine photo-lyase] [protein\_id=WP\_020316935.1] [location=1840868..1842310] [gbkey=CDS]

MATHLVWLRTDLRIHDNLALAAACRDPQAQVLALYIATPGQWREHHLAPRQAAFIASHLQSLHAALAERG

IPLWVEEADDFTASVERLADFCQQHQVSHLFYNYQYEFNERQRDAAVENTLRDVICQGFDDSVLLPPGSV

LTGGGEMYKVFTPFKNAFIRRLRDGLPACVAAPKPRQAPARQAPPLPELNYPQTPFDGLLFAADEKTALA

RLRAFCQQAAADYEGQRDFPAVEGTSRLSPCLAIGVLSPRQCLHRLLTEHPAALDGGAGATWLNELIWRE

FYRHLMVYYPKLCKGRPFTAWTDKVAWRAEEASLQAWQRGETGFPIVDAAMRQLNATGWMHNRLRMIVAS

FLTKDLRLDWRAGERYFMSQLIDGDLAANNGGWQWAASTGTDAAPYFRIFNPTTQGEKFDKQGVFIRRWL

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>lcl|NZ\_FO834906.1\_prot\_WP\_016532353.1\_1788 [locus\_tag=BN49\_RS10375] [protein=MFS transporter] [protein\_id=WP\_016532353.1] [location=complement(1842282..1843760)] [gbkey=CDS]

MQTTSSQPRAIYYVVALQIWEYFSFYGMRALLILYLTNQLKYDDNHAYALFSAYCSLVYVTPILGGYLAD

KLLGNRMAVMLGAMLMAIGHLVLGASETAPVFLYLSLAIIVCGYGLFKSNVSCLLGELYEPADPRRDGGF

SLMYAAGNIGSIIAPIACGYVQEEYSWAMGFALAAIGMVAGLVIFLCGNRHFQHTAGVNRQALCARRFLL

PNWGWLLVLLVTAPLLIAVLFWQEWSVYALIVATAIGLAVLARIYLRAETDKQRKDLRLIVVLTAFSLLF

WAFAQQGGSSISLYIDRFVNRHIMSYEVPTAMFQSINAFAVMLCGMVLAWLVKESVNGNRTVRIWGKFAL

GLGLMSAGFCILTLSARWSAAYGQSSMPLMVLGLAVMGFAELFIDPVAMSQITRIEIPGVTGVLTGIYML

LSGAIANYLAGVIADQTSQASFDAAGAVNYSIDAYITVFSQITWGALACVGVVLVIWLYHSLKVRTRRLA

VE

>lcl|NZ\_FO834906.1\_prot\_WP\_004176858.1\_1789 [locus\_tag=BN49\_RS10380] [protein=type 2 GTP cyclohydrolase I] [protein\_id=WP\_004176858.1] [location=1844028..1844771] [gbkey=CDS]

MKNSELEQLINDKLNSAAISDFAPNGLQVEGRETVHKIVTGVTACQALLDEAVRLQADAVIVHHGYFWKN

ESPVIRGMKRRRLKTLLANDINLYGWHLPLDAHPELGNNAQLAHLLGINVLGEIEPLVPWGELSMPVSGL

ELASWIEARLGRKPLWCGDTGPDTVSRVAWCTGGGQSFIDAAARFGVDAFITGEVSEQTIHSAREQGLHF

YAAGHHATERGGIRALSEWLTETTDLDVTFIDIPNPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176857.1\_1790 [gene=pxpB] [locus\_tag=BN49\_RS10385] [protein=5-oxoprolinase subunit PxpB] [protein\_id=WP\_004176857.1] [location=1844786..1845442] [gbkey=CDS]

MQRARCYLLGETAVVLELEPPVTLESQKRIWGLTQRLTDREEVVEVIPGMNNITVVLRRPQEMAWEAIDK

LQRWWEESDALEPESREISIPVIYGGEAGPDLGDVARHSGLSEKQVVELHSSVEYMVWFLGFQPGFPYFG

GLPEQLAMPRRAEPRVLVPAGSVGIGGSQTGIYPLATPGGWQLLGRTPLALFDPKREEPVLLRSGDRVRF

VPQKEGVC

>lcl|NZ\_FO834906.1\_prot\_WP\_016532356.1\_1791 [locus\_tag=BN49\_RS10390] [protein=biotin-dependent carboxyltransferase family protein] [protein\_id=WP\_016532356.1] [location=1845436..1846368] [gbkey=CDS]

MLKFIRAGMYTSVQDGGREGQRQWGISRCGALDKPAMTIANLLVGNAPEAAALEITLGQIDVQFTRHCWF

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GRRLQDGDQVKIGKSSRRFSASRGVKQLPIGNIIRALPGPEYHEFDSVSQESFWRSPWKLSPQSNRMGYR

LQGQPLKRTTDREMLSHGLLPGVVQVPHNGQPIVLMNDAQTTGGYPRIACIIEADMYQLAQIPLGQPIHF

APCSLEEALKARADQQRYLEQLAWRLSDEN

>lcl|NZ\_FO834906.1\_prot\_WP\_032438623.1\_1792 [gene=pxpA] [locus\_tag=BN49\_RS10395] [protein=5-oxoprolinase subunit PxpA] [protein\_id=WP\_032438623.1] [location=1846358..1847101] [gbkey=CDS]

MKIDLNADLGEGCASDSALLQLVSSANIACGFHAGDAVLMQQCVREALKNGVAIGAHPSFPDRENFGRTA

MQLPPETVYAQVLYQIGALAAIVHAQGGELRHVKPHGMLYNQAAKEPPLADAIARAVRDADADLVLVGLA

GSELIRAGQHYQLTTRQEVFADRGYQADGSLVPRSQPGALIESEEQALAQTLEMVQHNRVRSLSGEWTHV

KAETVCLHGDGAHALDFARRLRAAFAGRNIDVSADLE

>lcl|NZ\_FO834906.1\_prot\_WP\_002894928.1\_1793 [locus\_tag=BN49\_RS10400] [protein=DUF969 domain-containing protein] [protein\_id=WP\_002894928.1] [location=1847183..1847908] [gbkey=CDS]

MQEAISLWPLIGIAVIVVGFVLRFNPVLVVIISGIVTGVAAHMPIATILEKLGEGFLNTRNLPFILLLPL

AVIGLLERHGLKERAQAWIAKIHSATAGRLLIVYLFVREATAALGLTSLGGHPQMVRPLLAPMAEGAAEK

RFGPLPGNVRYRLRAMSAATDNVGLFFGEDIFVAFGAIIFMHNFMLESGGIQTEPLHIALWGIPTAICAF

LIHAARLWRLDRHLQRELDRINAGQAKGGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004223689.1\_1794 [locus\_tag=BN49\_RS10405] [protein=DUF979 domain-containing protein] [protein\_id=WP\_004223689.1] [location=1847905..1848900] [gbkey=CDS]

MNFQQTYLYWLAGAVLLVVAIMSWRDKSNPRRLTTGLFWGLYGLVFLLGDWTYQLVGDKRTVNIAVGGVV

VILALIAGFGGVRLGSYHQRTQEEKTASAKRLGNKLFFPALAIPVVTVIGVLLFNNLPSWQVALFGPGNH

ATLITLFSMTVGTLIGLAMAIRMTHETVAQPMQEARRLLDSVGWAFILPQILAVLGLLFTAAGVGTSISW

LTEHYLAVDNRFIAVAVYAIGMAVLTMVMGNAFAAFPIVTAGVGIPILVLQHGGNPAVMAAIGMFSGYCG

TLMTPMAANFNIVPAALLELPDKNAVIKAQIPTGILLLIVNVFLLYFLMFL

>lcl|NZ\_FO834906.1\_prot\_WP\_016528902.1\_1795 [gene=pcp] [locus\_tag=BN49\_RS10410] [protein=pyroglutamyl-peptidase I] [protein\_id=WP\_016528902.1] [location=1848910..1849554] [gbkey=CDS]

MAGVLITGFEPFGGETVNPSWEVVKQLDGMIIRGQQVVAKQLPCVFGEALKVLKAALETYQPRLTIAVGQ

AGGRVDITVERVAINVDDARIPDNKGQQPIDEPIVANGPAAYFSTLPIKAIVSALRQQGIPASVSQTAGT

FVCNHVMYGLLHQLQGKSGQKGGFIHIPYLPEQAAAHPGQASMSVATVRTALETAIAVALEQDDDVKIGG

GATH

>lcl|NZ\_FO834906.1\_prot\_WP\_002894935.1\_1796 [gene=nei] [locus\_tag=BN49\_RS10415] [protein=endonuclease VIII] [protein\_id=WP\_002894935.1] [location=1849570..1850361] [gbkey=CDS]

MPEGPEIRRAADKLEAAIKGEPLTNVWFAFPQLQPYQTQLIGQRVTHIATRGKALLTHFSGGLTLYSHNQ

LYGVWRVVDAGVEPQSNRVLRVRLQTASKAILLYSASDIDILTAEQVANHPFLLRVGPDVLDMTLTAEQV

KARLLSAKFRNRQFSGLLLDQAFLAGLGNYLRVEILWQVGLSGKRKAAELSDSQLDALAHALLDIPRLSY

RTRGLVDDNKHHGALFRFKVFHRDGERCERCGGIIEKTTLSSRPFYWCPGCQH

>lcl|NZ\_FO834906.1\_prot\_WP\_002894943.1\_1797 [gene=gltA] [locus\_tag=BN49\_RS10425] [protein=citrate synthase] [protein\_id=WP\_002894943.1] [location=complement(1850452..1851735)] [gbkey=CDS]

MSDAKAKITLGGDTAIELDVLKGTLGQDVIDIRSLGSKGVFTFDPGFTSTASCESKITFIDGDEGILLHR

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ALAAFYHDSLDVNNPRHREIAAYRLLSKMPTMAAMCYKYSIGQPFVYPRNDLSYAGNFLRMMFATPCEEY

EVNPVLERAMDRILILHADHEQNASTSTVRTAGSSGANPFACIAAGIASLWGPAHGGANEAALKMLEEIS

SVEHIPEFVRRAKDKNDSFRLMGFGHRVYKNYDPRATVMRETCHEVLKELGTKDDLLQVAMELEHIALND

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FQSDIKR

>lcl|NZ\_FO834906.1\_prot\_WP\_042940334.1\_1798 [gene=sdhC] [locus\_tag=BN49\_RS10430] [protein=succinate dehydrogenase cytochrome b556 subunit] [protein\_id=WP\_042940334.1] [location=1852376..1852780] [gbkey=CDS]

MWALFMVRNVKKQRPVNLDLQTIRFPITAIASILHRVSGVITFVAVGILLWLLGTSLSSPEGFLTAASIM

DSFFVKFIMWRILTALAYHVVVGIRHLMMDFGYLDETLEAGKRSAKISFVITVVLSLLAGVLVW

>lcl|NZ\_FO834906.1\_prot\_WP\_002894949.1\_1799 [gene=sdhD] [locus\_tag=BN49\_RS10435] [protein=succinate dehydrogenase membrane anchor subunit] [protein\_id=WP\_002894949.1] [location=1852774..1853121] [gbkey=CDS]

MVSNASALGRNGVHDFILVRATAIVLTLYIIYMVGFFATTGEISWEVWTGFFASGFTKVFTLLALVSILI

HAWIGMWQVLTDYVKPLALRLVLQLAIVVALVAYVLYGFVVVWGV

>lcl|NZ\_FO834906.1\_prot\_WP\_004179067.1\_1800 [gene=sdhA] [locus\_tag=BN49\_RS10440] [protein=succinate dehydrogenase flavoprotein subunit] [protein\_id=WP\_004179067.1] [location=1853121..1854887] [gbkey=CDS]

MKLPVREFDAVVIGAGGAGMRAALQISQSGQTCALLSKVFPTRSHTVSAQGGITVALGNSHEDNWEWHMY

DTVKGSDYIGDQDAIEYMCKTGPEAILELEHMGLPFSRLDDGRIYQRPFGGQSKNFGGEQAARTAAAADR

TGHALLHTLYQQNLKNHTTIFSEWYALDLVKNQDGAVVGCTALCIETGEVVYFKARATVLATGGAGRIYQ

STTNAHINTGDGVGMAIRAGVPVQDMEMWQFHPTGIAGAGVLVTEGCRGEGGYLLNKHGERFMERYAPNA

KDLAGRDVVARSIMIEIREGRGCDGPWGPHAKLKLDHLGKEVLESRLPGILELSRTFAHVDPVKEPIPVI

PTCHYMMGGIPTKVTGQALTVNEKGEDVVIPGLFAVGEIACVSVHGANRLGGNSLLDLVVFGRAAGLHLQ

ESIAEQGTLRDASESDIEGSLDRLNRWNNTRSGEDPVAIRKALQECMQHNFSVFREGDAMHKGLEQLKVI

RERLKNARLDDTSSEFNTQRVECLELDNLMETAYATAVSANFRTESRGAHSRFDFPDRDDENWLCHSLYL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002894954.1\_1801 [gene=sdhB] [locus\_tag=BN49\_RS10445] [protein=succinate dehydrogenase iron-sulfur subunit SdhB] [protein\_id=WP\_002894954.1] [location=1854903..1855619] [gbkey=CDS]

MKLEFSIYRYNPDVDDAPHMQDYTLEAEEGRDMMLLDALIQLKEKDPSLSFRRSCREGVCGSDGLNMNGK

NGLACITPISALNQPGKKIVIRPLPGLPVIRDLVVDMGQFYAQYEKIKPYLLNNGQNPPAREHLQMPEQR

EKLDGLYECILCACCSTSCPSFWWNPDKFIGPAGLLAAYRFLIDSRDTETSERLDGLSDAFSVFRCHSIM

NCVSVCPKGLNPTRAIGHIKSMLLQRSA

>lcl|NZ\_FO834906.1\_prot\_WP\_012068464.1\_1802 [gene=sucA] [locus\_tag=BN49\_RS10450] [protein=2-oxoglutarate dehydrogenase E1 component] [protein\_id=WP\_012068464.1] [location=1856001..1858808] [gbkey=CDS]

MQNGAMKAWLDSSYLSGSNQSWIEQLYEDFLTDPDSVDANWRSMFQQLPGTGVKPDQFHSKTRDYFRRLA

KDASRYTSSISDPDTNVKQVKVLQLINAYRFRGHQHANLDPLGLWKQERVADLDPAYHDLTEADFQESYN

VGSFAIGKDTMKLGELIAALKQTYCGSIGAEYMHITSTEEKRWIQQRIESVAGKASFTPEEKKRFLSELT

AAEGLERYLGAKFPGAKRFSLEGGDALIPMLKEMIRHAGKSGTREVVLGMAHRGRLNVLVNVLGKKPQDL

FDEFAGKHKEHLGTGDVKYHMGFSSDMETEGGLVHLALAFNPSHLEIVSPVVIGSVRARLDRLDEPSSNK

VLPITIHGDAAVTGQGVVQETLNMSKARGYEVGGTVRIVINNQVGFTTSNPLDARSTPYCTDIGKMVQAP

IFHVNADDPEAVAFVTRLALDFRNTFKRDVFIDLVCYRRHGHNEADEPSATQPLMYQKIKKHPTPRKIYA

DKLEQEKVATLEDATEQVNLYRDALDAGECVVQEWRPMNMHSFTWSPYLNHEWDESYPDKVEPKRLQELA

KRISTVPEGIEMQSRVAKIYADRQAMAAGEKLFDWGGAENLAYATLVDEGIPVRLSGEDSGRGTFFHRHA

VIHNQTNGSTYTPLQHVHNGQGQFRVWDSVLSEEAVLAFEYGYATAEPRTLTIWEAQFGDFANGAQVVID

QFISSGEQKWGRMCGLVMLLPHGYEGQGPEHSSARLERYLQLCAEQNMQVCVPSTPAQVYHMLRRQALRG

MRRPLVVMSPKSLLRHPLAVSSMDELANGTFLPAIGEIDQLDPQAVKRVVLCSGKVYYDLLEQRRKNEQK

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SPAVGYMSVHQKQQQDLVNDALNVD

>lcl|NZ\_FO834906.1\_prot\_WP\_004142209.1\_1803 [gene=odhB] [locus\_tag=BN49\_RS10455] [protein=2-oxoglutarate dehydrogenase complex dihydrolipoyllysine-residue succinyltransferase] [protein\_id=WP\_004142209.1] [location=1858823..1860049] [gbkey=CDS]

MSSVDILVPDLPESVADATVATWHKKPGDAVVRDEVLVEIETDKVVLEVPASADGILDAVLEDEGATVLS

RQILGRLREGNSAGKESSEKADAKASTPAQRQQASLEEQNNDALSPAIRRLLAEHNLDPAAIKGTGVGGR

LTREDVEKHLAKAPAPAEAKAPAAAPAAAPAPQLGHRSEKRVPMTRLRKRVAERLLEAKNSTAMLTTFNE

VNMKPIMDLRKQYGEAFEKRHGIRLGFMSFYVKAVVEALKRYPEVNASIDGDDVVYHNYFDVSMAVSTPR

GLVTPVLRDVDLLGMADIEKNIKELAVKGRDGKLTVDDLTGGNFTITNGGVFGSLMSTPIINPPQSAILG

MHAIKDRPMAVNGKVEILPMMYLALSYDHRLIDGRESVGFLVAIKELLEDPTRLLLDV

>lcl|NZ\_FO834906.1\_prot\_WP\_002895039.1\_1804 [gene=sucC] [locus\_tag=BN49\_RS10460] [protein=ADP-forming succinate--CoA ligase subunit beta] [protein\_id=WP\_002895039.1] [location=1860153..1861319] [gbkey=CDS]

MNLHEYQAKQLFARYGLPAPVGYACTTPREAEEAASKIGAGPWVVKCQVHAGGRGKAGGVKVVKSKEEIR

AFAEHWLGKRLVTYQTDANGQPVNQILVEAATDIDKELYLGAVVDRSSRRVVFMASTEGGVEIEKVAEET

PHLIHKIAIDPLAGPMPYQGRELAFKLGLEGKQVQQFTKIFMGLATIFLERDLALIEINPLVITKQGDLI

CLDGKLGADGNALFRQPDLREMRDQSQEDPREAQAAQWELNYVALDGNIGCMVNGAGLAMGTMDIVKLHG

GEPANFLDVGGGATKERVTEAFKIILSDDNVKAVLVNIFGGIVRCDLIADGIIGAVAEVGVNVPVVVRLE

GNNAELGAKKLADSGLNIIAAKSLTDAAQQVVAAVEGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002895043.1\_1805 [gene=sucD] [locus\_tag=BN49\_RS10465] [protein=succinate--CoA ligase subunit alpha] [protein\_id=WP\_002895043.1] [location=1861319..1862188] [gbkey=CDS]

MSVLINKDTKVICQGFTGSQGTFHSEQAIAYGTQMVGGVTPGKGGTTHLGLPVFNTVREAVEATGATATV

IYVPAPFCKDSILEAIDAGIKLIITITEGIPTLDMLTVKVKLDEAGVRMIGPNCPGVITPGECKIGIMPG

HIHKPGKVGIVSRSGTLTYEAVKQTTDYGFGQSTCVGIGGDPIPGSNFIDILKMFEEDPQTEAIVMIGEI

GGSAEEEAAAYIKDHVTKPVVGYIAGVTAPKGKRMGHAGAIIAGGKGTADEKFAALEAAGVKTVRSLADI

GEALKAIIK

>lcl|NZ\_FO834906.1\_prot\_WP\_002895047.1\_1806 [gene=cydA] [locus\_tag=BN49\_RS10475] [protein=cytochrome ubiquinol oxidase subunit I] [protein\_id=WP\_002895047.1] [location=1863014..1864582] [gbkey=CDS]

MLDIVELSRLQFALTAMYHFLFVPLTLGMAFLLAIMETVYVLSGKQIYKDMTKFWGKLFGINFALGVATG

LTMEFQFGTNWSYYSHYVGDIFGAPLAIEGLMAFFLESTFVGLFFFGWDRLGKVQHMAVTWLVALGSNLS

ALWILVANGWMQNPIASDFNFETMRMEMVSFSELVLNPVAQVKFVHTVASGYVTGAMFILAISSWYMLKG

RDFAFAKRSFAIAASFGMAAILSVIVLGDESGYEMGDVQKTKLAAIEAEWETQPAPAAFTLFGIPDQNAQ

TNHFAIQIPYALGIIATRSVDKPVIGLKDLMVQHEERIRNGMKAYALLEQLRAGSTDQAVRDQFNNVKKD

LGYGLLLKRYTPNVADATEEQIAKATKDSIPSVAPLYFAFRIMVACGILMLLIIGASFWSVIRNRIGEKK

WLLRAAFYGLPLPWIAVESGWFVAEYGRQPWAIGEVLPTAVANSSLTAGDLIFSMLLICGLYTLFLVAEL

FLMFKFARKGPSSLKTGRYHFEQSSAAIQSAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002895049.1\_1807 [gene=cydB] [locus\_tag=BN49\_RS10480] [protein=cytochrome d ubiquinol oxidase subunit II] [protein\_id=WP\_002895049.1] [location=1864598..1865737] [gbkey=CDS]

MIDYEVLRFIWWLLIGILLIGFAVADGFDMGVGMLTRFLGRNDTERRIMINAIAPHWDGNQVWLITAGGA

LFAAWPMVYAAAFSGFYVAMILVLASLFFRPVGFDYRSKIEDTRWRNMWDWGIFIGSFVPPLVIGVAFGN

LLQGVPFHVDEYLRLFYTGNFFQLLNPFGLLAGIVSVAMILTQGATYLQMRTVGELHLRTRTVSMVAALV

TLVCFALAGVWVYYGIDGYVVKSVIDHTGPSNPLTKEVVREAGAWMVNFNNMPALWAVPALGVVLPLLTV

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ILAYTSWCYWKMFGRITREDIEKNTHSLY

>lcl|NZ\_FO834906.1\_prot\_WP\_002895051.1\_1808 [gene=cydX] [locus\_tag=BN49\_RS10485] [protein=cytochrome bd-I oxidase subunit CydX] [protein\_id=WP\_002895051.1] [location=1865753..1865869] [gbkey=CDS]

MWYFAWILGTLLACAFGVITALALEHVEATKAGKKEEI

>lcl|NZ\_FO834906.1\_prot\_WP\_002895053.1\_1809 [gene=ybgE] [locus\_tag=BN49\_RS10490] [protein=cyd operon protein YbgE] [protein\_id=WP\_002895053.1] [location=1865869..1866159] [gbkey=CDS]

MKFIATLYAIMDKRPLRALSLLMALLLAGCIFWDPSRFAAKTSELEIWHGFLLMWAVCSGVIHGVGFRPR

AVHWQGIFCPLIADIVLALGLFFFFF

>lcl|NZ\_FO834906.1\_prot\_WP\_002895056.1\_1810 [gene=ybgC] [locus\_tag=BN49\_RS10495] [protein=tol-pal system-associated acyl-CoA thioesterase] [protein\_id=WP\_002895056.1] [location=1866309..1866713] [gbkey=CDS]

MNTTLFRWPVRVYYEDTDAGGVVYHASYVAFYERARTEMLRHHHFSQQVLLAERVAFVVRKMTLEYFAPA

RLDDMLEVQTEITSMRGTSLVFTQRIVNAENTVLNEAEVLIVCVDPLLMKPRALPKSIVAEFKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004152221.1\_1811 [gene=tolQ] [locus\_tag=BN49\_RS10500] [protein=Tol-Pal system protein TolQ] [protein\_id=WP\_004152221.1] [location=1866710..1867402] [gbkey=CDS]

MTDMNILDLFLKASLLVKLIMLILIGFSIASWAIIIQRTRILNSAAREAEAFEDKFWSGIELSRLYQESQ

GRRDNLTGSEQIFYSGFKEFARLHRANSHAPEAIVEGASRAMRISMNRELETLETHIPFLGTVGSISPYI

GLFGTVWGIMHAFIALGAVKQATLQMVAPGIAEALIATAIGLFAAIPAVMAYNRLNQRVNKLELNYDNFM

EEFTAILHRQAFTTSESNKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002895061.1\_1812 [gene=tolR] [locus\_tag=BN49\_RS10505] [protein=colicin uptake protein TolR] [protein\_id=WP\_002895061.1] [location=1867406..1867834] [gbkey=CDS]

MARARGRGRRELKSEINIVPLLDVLLVLLLIFMATAPIITQSVEVDLPDATESQAVKSNDDPPVIVEVSG

VGQYSVKVGQETLSQLPPEQVIAEAKRRLEANEKTVFLIGGAKDVPYDEIIKALNLLHSAGVKSVGLMTK

PI

>lcl|NZ\_FO834906.1\_prot\_WP\_004179068.1\_1813 [gene=tolA] [locus\_tag=BN49\_RS10510] [protein=cell envelope integrity protein TolA] [protein\_id=WP\_004179068.1] [location=1867934..1869259] [gbkey=CDS]

MSKATEQNDKLKRAIIISVALHIILIALLIWSSFDEHLDASAGGGGGSSIDAVMVDPGAVVNNYNRQQQQ

QASARRAAEQREKQAQQQAEELREKQAAEQERLKQLEQERLQAQEAAKEAKEQQKQAEEAAAKAAAAAKA

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EAQKKAEAAAAKKAQQEAEKKAQQEAAKQAAAEKAAAEKAAEKAAAQKAAAEKAAAEKAAAAEKAAAAKA

AAAEKAAADKAAKAAAAKAAAAKKAAAAKEADGVDNLLGDLSSGKNAPKTGGGAKGNNASAAGSGNTKNS

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529962.1\_1814 [gene=tolB] [locus\_tag=BN49\_RS10515] [protein=Tol-Pal system beta propeller repeat protein TolB] [protein\_id=WP\_016529962.1] [location=1869389..1870681] [gbkey=CDS]

MKQALRVAFGFLMLWAAVLHAEVRIEITQGVDSARPIGVVPPQWAGQGAAPEDVGGIVAADLRNSGKFNP

LDRSRLPQQPTSAQEVQPAAWSALGIDAVVVGQVTQNPDGSYQVAYQLVDTGGAPGTTLAQGSFKVTKQY

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GSKLAYVTFESGRSALVVQTLANASVRQIASFPQHNGAPAFSPDGSKLAFALSKTGSLNLYVMDLGSGQI

RQVTNGRSNNTEPSWFPDSQNLAFTSDQAGRPQVYKVNINGGTPQRITWEGSQNQDADVSADGKTMVMVS

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VKSPAWSPYL

>lcl|NZ\_FO834906.1\_prot\_WP\_002895068.1\_1815 [gene=pal] [locus\_tag=BN49\_RS10520] [protein=peptidoglycan-associated lipoprotein Pal] [protein\_id=WP\_002895068.1] [location=1870716..1871240] [gbkey=CDS]

MQLNKVLKGLMIALPVMAIAACSSNKNASNDQSGEGMLGAGTGMDANGNGGNMSSEEQARLQMQQLQQNN

IVYFDLDKYDIRSDFAAMLDAHANFLRSNPSYKVTVEGHADERGTPEYNIALGERRANAVKMYLQGKGVS

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>lcl|NZ\_FO834906.1\_prot\_WP\_002895071.1\_1816 [gene=cpoB] [locus\_tag=BN49\_RS10525] [protein=cell division protein CpoB] [protein\_id=WP\_002895071.1] [location=1871250..1872044] [gbkey=CDS]

MSSNFRHHLLSLSLLVGIAAPWAAFAQAPISSVGSGSVEDRVTQLERISNAHSQLLTQLQQQLSDNQTDI

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>lcl|NZ\_FO834906.1\_prot\_WP\_020324031.1\_1817 [locus\_tag=BN49\_RS30350] [protein=hypothetical protein] [protein\_id=WP\_020324031.1] [location=complement(1873112..1873261)] [gbkey=CDS]

MVFYMLNKIADYELKVVMNFVHQTLFPGTVLRICPNDRFVPYAGTVSAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531320.1\_1818 [gene=nadA] [locus\_tag=BN49\_RS10560] [protein=quinolinate synthase NadA] [protein\_id=WP\_016531320.1] [location=1873331..1874374] [gbkey=CDS]

MSVMFDPETAIYPFPAKPQPLTVDEKQFYREKIKRLLRERDAVMVAHYYTDPEIQQLAEETGGCIADSLE

MARFGARHSASTLLVAGVRFMGETAKILSPEKTILMPTLNAECSLDLGCPIEEFNAFCDAHPDRTVVVYA

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EAPTAGEGATCRSCAHCPWMAMNGLKAIAEGLEQGGAEHEIHVDEALRTGALIPLNRMLDFAATLRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151689.1\_1819 [gene=pnuC] [locus\_tag=BN49\_RS10565] [protein=nicotinamide riboside transporter PnuC] [protein\_id=WP\_004151689.1] [location=1874410..1875129] [gbkey=CDS]

MDFFSTQNILVHIPIGAGGYDLSWIEAVGTIAGLLCIWLASLEKISNYAFGLVNVTLFAIIFFQIQLYAS

LLLQLFFFAANVYGWYAWSRQSSNHEAELQIRWLPRSKALGWLAACVVAIGLLTLFINPFFAFLTRIAVS

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>lcl|NZ\_FO834906.1\_prot\_WP\_004147641.1\_1820 [gene=zitB] [locus\_tag=BN49\_RS10570] [protein=CDF family zinc transporter ZitB] [protein\_id=WP\_004147641.1] [location=complement(1875126..1876070)] [gbkey=CDS]

MAHSHSHSSVQAPDNSNARRLLWAFIVTAGFMLIEAVGGAISGSLALLADAGHMLTDSAALLFALLAVRF

ASRPPNARHTFGWLRLTTLAAFLNAIALVVITMLIVWEAIQRFQHPQPVAGVTMMVIAVAGLLANVLAFW

ILHRGSEERNLNVRAAALHVLGDLLGSVGAIVAAVVILTTGWTPVDPILSVLVSCLVLRSAWRLLKESLN

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EIAHATVQMEYQPCSGPECHLNTMHAGHDHHHHH

>lcl|NZ\_FO834906.1\_prot\_WP\_002895084.1\_1821 [locus\_tag=BN49\_RS10575] [protein=YbgS-like family protein] [protein\_id=WP\_002895084.1] [location=complement(1876188..1876553)] [gbkey=CDS]

MNMKKLTTLLLTATLGLASGAALAADTGAQSNNGQANSSADAGQVAPDARENVAPNNVDNSQINSGSGGT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529483.1\_1822 [gene=aroG] [locus\_tag=BN49\_RS10580] [protein=3-deoxy-7-phosphoheptulonate synthase AroG] [protein\_id=WP\_016529483.1] [location=1876868..1877920] [gbkey=CDS]

MNYQNDDLRIKEINELLPPVALLEKFPATENAANTVAHARKAIHQILKGDDDRLLVVIGPCSIHDPAAAK

EYAARLLTLREALKGELEIVMRVYFEKPRTTVGWKGLINDPHMDNSFRINDGLRIARKLLLDINDSGLPA

AGEFLDMITPQYVADLMSWGAIGARTTESQVHRELASGLSCPVGFKNGTDGTIKVAIDAIIAAGAPHCFL

SVTKWGHSAIVNTSGNGDCHIILRGGKEPNYSAKHVAEVKIGLAKAGLPAQVMIDFSHANSSKQFKKQME

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>lcl|NZ\_FO834906.1\_prot\_WP\_002895089.1\_1823 [gene=gpmA] [locus\_tag=BN49\_RS10585] [protein=2,3-diphosphoglycerate-dependent phosphoglycerate mutase] [protein\_id=WP\_002895089.1] [location=complement(1877994..1878746)] [gbkey=CDS]

MAVTKLVLVRHGESQWNNENRFTGWYDVDLSEKGVSEAKAAGKLLKAEGFSFDFAYTSVLKRAIHTLWNV

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GVPLVYEFDENFKPIKHYYLGNAEEIAAKAAAVANQGKAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004142169.1\_1824 [gene=galM] [locus\_tag=BN49\_RS10590] [protein=galactose-1-epimerase] [protein\_id=WP\_004142169.1] [location=complement(1879038..1880081)] [gbkey=CDS]

MLTQTTALAPDGQPWQQVTLRNKSGMTVTVADWGATLLSAEVPLADGSLRRPLLGCAKLEDYARQAAFLG

ASVGRYANRIGHSRFPLDGQVVNVTPSNDAGHQLHGGPEGFDKRRWRIVRADEQEVLFALTSPDGDQGFP

GTLQATAHYRLTDDNRIAITYRATVDQPCPVNMTNHVYFNLDGEQGDVRQHQLQILAQRYLPVESDGIPG

GELKDVANTSFDFRQPKTIAADFLADADQQKVKGYDHAFLLDAKGDASQPAAQVWSQDGKLQMTVYTSAP

ALQFYSGNYLGGTPSQTTEPYADWQGLALESEFLPDSPNHPQWPQPDCVLRPGQEYVSLTEYQFIAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179071.1\_1825 [gene=galK] [locus\_tag=BN49\_RS10595] [protein=galactokinase] [protein\_id=WP\_004179071.1] [location=complement(1880075..1881223)] [gbkey=CDS]

MSLKEKTQTLFADAFGYPASHVIQAPGRVNLIGEHTDYNDGFVLPCAIDYQTVISCAPRDDRTVRVIAAD

YDNQTDEFSLDAPIISHDTQQWSNYVRGVVKHLQQRNSHFGGADLVISGNVPQGAGLSSSASLEVAVGTV

FQQLYHLPLDGAQIALNGQEAENQFVGCNCGIMDQLISALGKKDHALLIDCRSLGTKAVSMPKGVAVVII

NSNFKRTLVGSEYNTRREQCETGARFFQQPALRDVTLEQFNAVAHELDPVVAKRVRHVLTENARTVEAAS

ALEKGDLKRMGELMAESHASMRDDFEITVPQIDTLVEIVKAAIGDKGGVRMTGGGFGGCVVALIPEDLVD

TVQQAVANEYEAKTGIKETFYVCKPSQGAGQC

>lcl|NZ\_FO834906.1\_prot\_WP\_002895147.1\_1826 [gene=galT] [locus\_tag=BN49\_RS10600] [protein=galactose-1-phosphate uridylyltransferase] [protein\_id=WP\_002895147.1] [location=complement(1881226..1882272)] [gbkey=CDS]

MSVFNPVDHPHRRYNPLTGQWILVSPHRAKRPWQGAQETPAKQTLPAHDPDCFLCPGNTRVTGDTNPNYT

GTYVFTNDFAALMTDTPDAPESDDPLMRCQSARGTSRVICFSPDHSKTLPELSLEALEDVVKTWQEQTAD

LGKSYPWVQVFENKGAAMGCSNPHPHGQVWANSFLPNEAEREDRLQKEYYAAQGQPMLLDYVQRELADGS

RTVVDTEHWLAVVPYWAAWPFETLLLPKAHVQRITDLTDAQRSDLALALKKLTSRYDNLFQCSFPYSMGW

HGAPFNDEDHNHWQLHAHFYPPLLRSATVRKFMVGYEMLAETQRDLTAEQAAERLRAVSDVHFRESGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002895150.1\_1827 [gene=galE] [locus\_tag=BN49\_RS10605] [protein=UDP-glucose 4-epimerase GalE] [protein\_id=WP\_002895150.1] [location=complement(1882282..1883298)] [gbkey=CDS]

MKVLVTGGSGYIGSHTCVQLLQQGHEVVILDNLCNSKRSVLPVIERLGGKEATFIEGDIRNEALMTEILH

DHAIEAVIHFAGLKAVGESVAKPLEYYDNNVTGTLKLVSAMRAAGVKNFIFSSSATVYGDQPKIPYVESF

PTGTPQSPYGKSKLMVEQILTDLQKAQPEWSIALLRYFNPVGAHPSGDMGEDPQGIPNNLMPYIAQVAVG

RRESLAIFGNDYPTEDGTGVRDYIHVMDLADGHVAAMEKLADKAGVHIYNLGAGVGSSVLDVVNAFSKAC

GKPINYHFAPRRDGDLPAYWADAAKADRELNWRVTRNLDEMAQDTWHWQSRHPQGYPD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530610.1\_1828 [gene=modF] [locus\_tag=BN49\_RS10610] [protein=molybdate ABC transporter ATP-binding protein ModF] [protein\_id=WP\_016530610.1] [location=complement(1883508..1884980)] [gbkey=CDS]

MSSLHISQGTFRLSDTKTLKIDHLSVAAGESWAFVGSNGSGKSALARALAGDLPLLSGQRESHFSRVTRL

SFEQLQKLVSDEWQRNNTDLLSPGEEDTGRTTAEIIQDEVKDPARCARLAEQFGISALLDRRFKYLSTGE

TRKTLLCQALMTDPQLLILDEPFDGLDVNSRQQLAALLADLHSAGITLVLVLNRFDEIPEFVQFAGVLAD

CTLSETGEKSSLLQQALVAQLAHSEKLDGITLPEPDVPPARHALADSAPRIVLNDGVVSYNDRPVINHLS

WTVNPGEHWQIVGPNGAGKSTLLSLVTGDHPQGYSNDLTLFGRRRGSGETIWDIKKHIGYVSSSLHLDYR

VSTNVRNVILSGYFDSIGIYQAVSDKQHKLVQQWLDILGIDKRTADAPFHSLSWGQQRLALIVRALVKHP

TLLILDEPLQGLDPLNRQLVRRFVDVLIGEGATQLLFVSHHAEDAPDCITHRLAFVPSGDGYTYQLGPVA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530611.1\_1829 [gene=modE] [locus\_tag=BN49\_RS10615] [protein=molybdenum-dependent transcriptional regulator] [protein\_id=WP\_016530611.1] [location=complement(1885048..1885836)] [gbkey=CDS]

MQAEILLTLKLQQRLFADPRRIALLKQIDQTGSISQGAKHAGISYKSAWDAINEMNQLSEQPLVDRATGG

KGGGGAVLTRYGQRLIQLYDLLAQIQQKAFDVLSDDDALPLDSLLAAISRFSLQTSARNQWFGTITGRDR

QQVQQHVEVLLADGKTRLNVAITAQSAEKQGLDEGQEVLVLLKAPWVGITLDPAAARQADNQLSGRISHI

ECGSGQCEVLMTLADGQTLCATLPQAQAAGLAEGTEAIAYFNADRIILATLC

>lcl|NZ\_FO834906.1\_prot\_WP\_016530612.1\_1830 [locus\_tag=BN49\_RS10620] [protein=AcrZ family multidrug efflux pump-associated protein] [protein\_id=WP\_016530612.1] [location=1885989..1886138] [gbkey=CDS]

MLELLKSLVFAVIMVPVVMAIILGLIYGLGEVFNLFSGVGHKDRSQQNH

>lcl|NZ\_FO834906.1\_prot\_WP\_004176834.1\_1831 [gene=modA] [locus\_tag=BN49\_RS10625] [protein=molybdate ABC transporter substrate-binding protein] [protein\_id=WP\_004176834.1] [location=1886281..1887054] [gbkey=CDS]

MAGSWLRGVVGVSLTLCVAGQALAAEGKVTVFAAASLTNAMQDIAQAYKKEKNVEVVSSFASSSTLARQI

EAGAPADLFISADQKWMDYAADKKAIDPATRATLLGNSLVVVAPKASAQGAITIDEKTDWTSLLKGGRLA

VGDPQHVPAGIYAKEALQKLGAWETLSPKLAPAEDVRGALALVERNEAPLGIVYGSDAVASKGVKVVGTF

PEASHQKVEYPLAIVDGHRNAAVSAFYDYLKGPEASAIFKRYGFTTR

>lcl|NZ\_FO834906.1\_prot\_WP\_002895159.1\_1832 [gene=modB] [locus\_tag=BN49\_RS10630] [protein=molybdate ABC transporter permease subunit] [protein\_id=WP\_002895159.1] [location=1887054..1887743] [gbkey=CDS]

MFLSEPEWQAVLLSLKVSSLAVALSLPFGIFFSWLLVRRTFPGKALLDSILHLPLVLPPVVVGYLLLVAM

GRRGFIGSWLYDWFGISFAFSWRGAVLAAAVMSFPLMVRAIRLALEGVDVKLEQAARTLGASRWRVFLTI

TLPLTLPGIIVGTVLAFARSLGEFGATITFVSNIPGETRTLPSAMYTLIQTPGGEGAAARLCLIAIGLAL

VSLLISEWLARVSRQRMGG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529863.1\_1833 [gene=modC] [locus\_tag=BN49\_RS10635] [protein=molybdenum ABC transporter ATP-binding protein ModC] [protein\_id=WP\_016529863.1] [location=1887746..1888804] [gbkey=CDS]

MLELDFTQTLGSHCLQIRETLPASGITAVFGVSGAGKTSLINAISGLTRPQAGRIVLNGRVLNDTAQRIC

LAPEQRRIGYVFQDARLFPHYKVRGNLQYGMAKSMVSQFDKLVDLLGIAPLLDRLPGRLSGGEKQRVAIG

RALLTAPELLLLDEPLASLDIPRKRELLPYLQRLAQEIHIPMLYVSHSLDEIQHLADRVLVLEAGKVKAF

GPLEEVWSSSVMHPWLPAEQQSTILSATVAAQHPQYAMTALALGDQLLWVNRLERPAGDTARISIQASDV

SLTLAQPSGTSIRNILRAEVVQYLEVNGQIEVQLRVSGRLLWARISPWARDDLAIAPGQQVFAQIKSVSI

AA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529864.1\_1834 [locus\_tag=BN49\_RS10640] [protein=pyridoxal phosphatase] [protein\_id=WP\_016529864.1] [location=complement(1888805..1889623)] [gbkey=CDS]

MTTRVIALDLDGTLLTSKKTILPASLEALARAREAGYQVIVVTGRHHVAIHPFYQALALDTPAICCNGTY

LYDYHAKKVLAADPMPVEQAVSLTAMLAKQQIHGLAYVDDAMLYEHPTGHVIRTRNWAQALPEDQRPVFA

QVDSLAQAVREVNAVWKFALTDDDIPRLQRFAQQVGETLGLECEWSWHDQVDIAHAGNSKGKRLAQWVAD

QGLSMQDVVAFGDNYNDLSMLEAAGTGVAMGNAVDEVKARANIVIGDNESTSIAEFIYRQLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004183458.1\_1835 [gene=pgl] [locus\_tag=BN49\_RS10645] [protein=6-phosphogluconolactonase] [protein\_id=WP\_004183458.1] [location=1889852..1890847] [gbkey=CDS]

MKQTVYTASPESQQIHVWSLEADGKLTLVQVVDAPGQVQPMVVSPNKEFLYVGVRPEFRVLAYRITPDNG

ALTFAGEAALPGSPTHISTDHHGRFVFSASYNQGCVSVTPLHDGLPGETITVVEGLEGCHSANISPDNRT

LWVPALKQDRICLFTLSDDGFLSAQEPAEVTTVEGAGPRHMVFHPNQQYGYCVNELNSSIDVWELKDPKG

NIECVQTLDMMPPDFSGVRWAADIHITPDGRHLYACDRTASIITVFSVSEDGSVLAVEGYQPTETQPRGF

NLDHSGKYLIAAGQKSHHIAVYDIVGEQGLLQEKGRYAVGQGPMWVVVNAH

>lcl|NZ\_FO834906.1\_prot\_WP\_002895168.1\_1836 [locus\_tag=BN49\_RS10650] [protein=biofilm development regulator YmgB/AriR family protein] [protein\_id=WP\_002895168.1] [location=complement(1890958..1891224)] [gbkey=CDS]

MHQQPDIYARLQDTALSDYFRNAGDKLVDESAVMSLAINSILQSEGHLNNKAIILWLIQALETTDDVVTA

DVIRKTLEIVVGYTMDDI

>lcl|NZ\_FO834906.1\_prot\_WP\_004147654.1\_1837 [locus\_tag=BN49\_RS10655] [protein=hypothetical protein] [protein\_id=WP\_004147654.1] [location=complement(1891276..1891581)] [gbkey=CDS]

MNNSETEEITDEIIGEAVLALLKTNRPITTPTLLVRLRLMQATEPDRQRRKIIAAVIEEICAKLIRQRKY

APLQVKKINGRWETRGSLAPDSMPSEAKKIH

>lcl|NZ\_FO834906.1\_prot\_WP\_004151693.1\_1838 [locus\_tag=BN49\_RS10660] [protein=regulatory protein YcgZ] [protein\_id=WP\_004151693.1] [location=complement(1891708..1891953)] [gbkey=CDS]

MQQNGYIPDTANAIAQYFNKASLPSQQETLGQIVMDILNEGRHLNRKALCTKLLSRLDRARAPEEESHYQ

TLIGLLFAGQE

>lcl|NZ\_FO834906.1\_prot\_1839 [locus\_tag=BN49\_RS30355] [protein=BLUF domain-containing protein] [pseudo=true] [partial=3'] [location=1892283..>1892492] [gbkey=CDS]

MLTTIIYRSHICDNVSFKSIEAMVARANERNGQADVTGILLFNGTHFFQLIEGPEEKVQDIYQHICQDPR

>lcl|NZ\_FO834906.1\_prot\_WP\_171819468.1\_1840 [locus\_tag=BN49\_RS28885] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_171819468.1] [location=complement(join(1892503..1893416,1893416..1893731))] [gbkey=CDS]

MIDVLRPEKRRRRTTQEKIAIVQHSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFISRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_1841 [locus\_tag=BN49\_RS10675] [protein=EAL domain-containing protein] [pseudo=true] [partial=5'] [location=<1893823..1894830] [gbkey=CDS]

PRHYNLVELLCDYAPSRRFGKVGMELFDLREHDREEVLQAVMDRGTSKYQLTYDDRALQFFRTFVEATEK

ANYFEIPSADSWVFIPDKETFYPDTPIIDNTEGCSFAFQPIVDPFACEIISWEALLRTPDGQSPGAYFAG

LTGDDIYLADLHSKRVALSLAGKLGLRNKALSINLLPMTMVKAPNAVAFLLDEISRNDLIPEQIIVEFTE

REVISRMDDFTDAVRKLKGAGINLAIDHFGAGFAGLSLLAQYQPDRIKIDHELIRNIHQDGPRQSIVQAI

IKCCTSLEIAVSAVGVERAEEWMWLESAGISQFQGNLFASARLGGLPAVAWPEKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176830.1\_1842 [locus\_tag=BN49\_RS10680] [protein=MerR family transcriptional regulator] [protein\_id=WP\_004176830.1] [location=1894986..1895720] [gbkey=CDS]

MAFYSIGEVAERCGINPVTLRAWQRRYGLLKPQRSEGGHRQFDEEDILRIEEIKRWIERGVSVGKVKALL

EDNLPAARDESAHLQEEMMSILRYMQPARIRAKLMALSHQHPVDTLIDSLLVPVRQRLKLDQNTSLVISS

MLDGLLIDCVALFLAEARKKNGKETLLVGWSNEDRTRLWLEAWRLSQRGWHVNVLAEPLESPRPELFPGQ

HIFVWTGRAATPLQEELLSHWQEQGFSIHFHGQN

>lcl|NZ\_FO834906.1\_prot\_WP\_004151695.1\_1843 [locus\_tag=BN49\_RS10685] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004151695.1] [location=complement(1895762..1896316)] [gbkey=CDS]

MSHHNTCYRSEHYDLWFDNGFLLYGMSLILNSLPASYFRKKHVFFTSDNYFAVLQHNYNRRDTLFILLTE

GNDLNFLSELPMLRLPANSTPEELKIFLHQPTRYYKTHPAPGASVQFTEREKKVIQLISNGEAVASIGRS

LNLHIKTIYQIRLNLIKKLGCSGRTDFFNISRSETFKSWSQIHL

>lcl|NZ\_FO834906.1\_prot\_WP\_002895280.1\_1844 [locus\_tag=BN49\_RS10690] [protein=biofilm development regulator YmgB/AriR family protein] [protein\_id=WP\_002895280.1] [location=complement(1896398..1896610)] [gbkey=CDS]

MHIKNTIPAEFVFNSALMKNIENTLIKQHRTVNNERMITEIQHRLQTESNEILSDLYLQALDMLYSKPHH

>lcl|NZ\_FO834906.1\_prot\_WP\_004229842.1\_1845 [locus\_tag=BN49\_RS30950] [protein=hypothetical protein] [protein\_id=WP\_004229842.1] [location=1896996..1897142] [gbkey=CDS]

MAGEMHEIAPTREGVNSNAVVDRWLSSASDSEHSGKYDEALSAFCTVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002895283.1\_1846 [locus\_tag=BN49\_RS10700] [protein=hypothetical protein] [protein\_id=WP\_002895283.1] [location=1897347..1897853] [gbkey=CDS]

MRGKSVMLLAGLASLAQANELNLYSVNTGSYVYHLTNNHGQYTENFENHFFSVERKFSADSKYSLLLGTM

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YNFTDYFAVESGIIIPSVFVISIQWSFR

>lcl|NZ\_FO834906.1\_prot\_WP\_002895284.1\_1847 [locus\_tag=BN49\_RS10705] [protein=acyltransferase family protein] [protein\_id=WP\_002895284.1] [location=complement(1897870..1898793)] [gbkey=CDS]

MTAVTFFTIYNTWDRFDYDYHWILGLLTFISTIATPLFFVVAGYLDAQTRHDANWQIGKIKSVVIVFLFW

VTVYYVWEPYQRGYLIQPWFIFALIVIYTFHPLIAWLSQRRGLFFAVLLTLLCCSYGYDLLSVIYPDRHL

FSLPPQYRLWTWLLFYLTGQLFNDPKVAEWIRNPQVIKGSIIALPFVYLFTWFYERHFFFALFKADRNAF

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IALTFVLSVLISLAALSSTLLRKVITL

>lcl|NZ\_FO834906.1\_prot\_WP\_046042940.1\_1848 [locus\_tag=BN49\_RS10710] [protein=efflux RND transporter permease subunit] [protein\_id=WP\_046042940.1] [location=complement(1898832..1901897)] [gbkey=CDS]

MDISRQFINNPTRVWLAILLLGVGGLFALLNIGRLEDPAFTIKTAVIVTHYPGASAQQVEEEVTLPLENA

IQQLPSLDNVSSISSNGLSQITVNIASQYHSSELPQIWDELRRRVGDASRLFPPGVVPPFVNDDFGDVFG

FFFAISGDSFTNPELVRYAEQLRRELVLVPGVGKVAIGGVIPQQINVDISLAKMAARGITLNQLAAILAR

LNVVSSAGEIRVGSESIRLHPTGEFQSIDELGDLLVSPHGASATTRLRDIATLSRGLTDSPASIYHANGR

QAVTMGVSFIPGVNVIDVGHALEARLQQMAADKPAGIDIAIFYDQAAEVAHSVNGFITNFLMALAIVVGV

LLVFMGVRSGIIIALSLALNVLGTLLIMYIWGIELQRISLGALIIALSMLVDNAIVIVEGVLIARQQGSP

LLGAINYVIRRSALPLLGATIIAILAFAPIGLSQDSTGEYCKSLFQVLLISLMLSWFSALTITPVLIKWW

LFKNAPSAAAAEEKADPYRGSFYRGYQQALRILLQQKTLTLVLMGALLAGAIWGFTFVRQNFFPSSNTPI

FFVDLWLPYGTDINATEKMTRDIERSIAGQPGVVTTVSTIGQGSMRFILTYSGQRQYSNYAQIMVRMDDQ

RGIAPVTRHVEDWIARNYPQVNASTKRIMFGPSGDSAIEVRIKGPDPDTLRALASQVGDILAADPATDSV

RNDWQNRSKVIRPQYSPALGRELGVDKQDIDNALEMNFSGSRAGLYREGADLLPVIVRPPEAERQDANHL

NNVLVWSQSRQQYIPLSNVINGFALEWEDPLILRRDRTRVLTVQTDPSPLSGQTSGDILARVKPRIDALP

LPHGYRIEWGGDAENSSEAQQGLFTTLPLGYLVMFIITVLMFSSLKNAVAIWLTVPLALIGVTPGFLLTG

IPFGFMALIGLLSLSGMLIRNGIVLVEEIEQEKQEKDQRQAIIDAATSRLRPILLTAFTTVLGLAPLLRD

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>lcl|NZ\_FO834906.1\_prot\_WP\_046042944.1\_1849 [locus\_tag=BN49\_RS10715] [protein=efflux RND transporter periplasmic adaptor subunit] [protein\_id=WP\_046042944.1] [location=complement(1901898..1902983)] [gbkey=CDS]

MNRYFSLIPVVIIFTTACDQKAPTVESAPRMVKVAQVTAVGNTQQRTFPARIESGDSTELSFKRGGQVES

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ALKIAREELAQMSLIAPFSGIAAGVHIRNHQVVAAGQPVITLTRTDLLDVVFSIPENLFTSLDIRNTAYR

PVVRINTLPGREFTAEYKEHTGSSDNSTLTWQIVLTMPRPDDFPVVGGVSGTVTVNLGNLPASAGRETLI

VPAEAVFNPDNRPKNEPVVWVVKGDNAHRYLEERKVTVGEVTSQGVAITDGLREGEQVVAAGVSELHAGQ

PVRVWTRERGL

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MYKNIVVPVDVFDAGLADKALSHAKFLAQHSAGQIHLIHVIPAFSPVLTRGFISDARKMEDHLLNTAKEK

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VVR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179084.1\_1851 [locus\_tag=BN49\_RS10725] [protein=cation-transporting P-type ATPase] [protein\_id=WP\_004179084.1] [location=1904000..1906687] [gbkey=CDS]

MNTDKPGAPYYQRSVEETLASVQSSPEGISGTEAATRLQQYGENALPQKPGKPAWLRFIAHFNDVLIYVL

LAAALLKAVMGHWIDMAVILAVAVVNALIGFIQESNAEKSLQSIRNMLSSEAVAIRQGNHETIPTTSLVP

GDIVVIRAGDRIPADLRVIEAHNLRVEEAILTGESTVVEKTTEPLSGDLPLGDRSNLLFSGTTVSSGAGK

GIVVATGGDTELGHINQMMAGIEKHRTPLLVQMDKLGKAIFILILVMMAALFVFSLLFRDMPVSELMLSL

ISLAVASVPEGLPAIISIILSLGVQAMARQKAIIRKLPTVETLGAMTVICSDKTGTLTMNEMTVKAVITA

DSVYRVEGDSYEPVGKIHAIDDPTPVTIAPGSLFERYLRTIDLCNDSQLIKEESGLWKITGGPTEGALKV

LAAKVTLPPLTSELRSKIPFDSQYKYMSTLYRLGEEEVVLVTGAPDVLFRLCQYQQSDSGLQPLDLPYWE

GKIEEYAREGLRMVAAAWKPAAAGQTELTHQDLQQGVILLGVAGMMDPPRPEAITAIADCLQAGIRVKMI

TGDHPQTAMSIGKMLGIGNAGNAITGRELEVMDDAQLSVAAQQFDIFARTSPEDKFRLVQALQSKKEIVG

MTGDGVNDAPALKQADVGVAMGIKGTEVTKEAADMVLTDDNFATIASAVREGRRVYDNLKKTILFVMPTN

LAQGLLIVIALLAGNVLPLTPVLILWMNMATSATLSFGLAFEAGEKNIMRRPPRDPKIHVMDGFAIWRVA

FVGSMIAVSAFILEAWLQPRGYSPEFIRTVLLQTLVTAQWFYMLNCRVSDGFSLTKGLLANKGIWIVSGV

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MNTYSVSRLALALAFGVTLSACSSTPADQQPSTQTAPGTTARPILNAEEAKIFTPAAYFQSLAPNAAAWT

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QNLTIANNLGDSVDAGTHQAVALRSDGDQVQINKVNILGRQNTFFVTNSGVQNRLQDNRQTRTLVTNSYI

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VVAEPKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004153329.1\_1853 [gene=hutI] [locus\_tag=BN49\_RS10735] [protein=imidazolonepropionase] [protein\_id=WP\_004153329.1] [location=1908399..1909718] [gbkey=CDS]

MVFSHKKITFPCAIVDFTGVMKINVYTTHDKLSAMTEATSELVIWRNGRLATLNPDHAQPYGLLERHALL

VRDGRIAAIVAEDDVPSGRSIDLEGRLVTPGLIDCHTHLVFGGSRAQEWEQRLNGVSYQTISASGGGINS

TVRATRDSSEAELLALAQPRLERLLREGVTTLEIKSGYGLDLPNERKMLRVARQLADHNGVELSATLLSA

HATPPEYQGDADGYITLVCETILPTLWQEGLFESVDVFCENVGFSPQQTERVFQAAQALGIPVKGHVEQL

SSLGGAQLVSRYHGLSADHIEYLTEEGVAAMRESGTVAALLPGAFYFLNETRKPPVELLRKYQVPMAVAT

DFNPGTSPFASLHLAMNMACVKFGLTPEEAWAGVTRHAARALGRQASHGQLAPGFVANFAIWDAEHPVEM

VYEPGRSPLWHRVVQGELQ

>lcl|NZ\_FO834906.1\_prot\_WP\_020804490.1\_1854 [gene=hutG] [locus\_tag=BN49\_RS10740] [protein=formimidoylglutamase] [protein\_id=WP\_020804490.1] [location=1909715..1910671] [gbkey=CDS]

MMLWQATPASLWQGRDDSAEAPNALRLFQTIARAERFAPQEMPGDIALLGFACDEGVRRNKGRTGAADGP

ATLRRALANMASHQGHDRCVDMGTISVDGEQLEAAHQALREAVADCQRAGKRTLVLGGGHETAFGHGAGV

LDAFPGEKVGIINLDAHLDLRFADCASSGTPFRQLALECDAQQRGFHYTCIGVSRAANTQALWDEAARRQ

VAIVEDLEVLTAFETRVLPELERNIAQFDRLYLTIDLDVLPAREMPAVSAPAALGVPLGTLLRIVEPLCR

SGKLQAVDLVEFNPLFDIDGQGARAAARVAWQIAHWWR

>lcl|NZ\_FO834906.1\_prot\_WP\_016528899.1\_1855 [locus\_tag=BN49\_RS10745] [protein=histidine utilization repressor] [protein\_id=WP\_016528899.1] [location=1910733..1911458] [gbkey=CDS]

MFAQQPRSAPAPFYEKVKRAISEKIHSGVWRPHDRIPSEAELVAQFGFSRMTINRALRELTDEGLLVRLQ

GVGTFVAEPKGQSALFEVRSIAAEIVARHHQHRCEVLLLEETRADHIQATALSVPEGTRIFHSLMVHYEN

EVPVQIEDRCVNAAVVPDYLHQDYTATTPHDYLSLIAPLTEGEHIVEAVQATAEECALLHIHAHDPCLLI

RRRTWSTTHIVSHARLLFPGSRYRLQGRFGS

>lcl|NZ\_FO834906.1\_prot\_WP\_016528900.1\_1856 [gene=hutU] [locus\_tag=BN49\_RS31410] [protein=urocanate hydratase] [protein\_id=WP\_016528900.1] [location=1911601..1913289] [gbkey=CDS]

MSQSKYRQLDVRAPRGTTLTAKSWLTEAPLRMLMNNLDPDVAENPHELVVYGGIGRAARNWECYDAIVKA

LKNLESDETLLVQSGKPVGVFKTHENSPRVLIANSNLVPHWATWEHFNELDAKGLAMYGQMTAGSWIYIG

SQGIVQGTYETFVEAGRQHYQGSLKGRWVLTAGLGGMGGAQPLAATLAGACSLNIECQQSRIDFRLRTRY

VDEQATSLDDALARIKKYTAEGRAISIALCGNAAEIVPELVKRGVRPDMVTDQTSAHDPLHGYLPKGWSW

EEYQQKAESDPQGTILAAKRSMADHVQAMLAFHEMGVPTFDYGNNIRQMAQEVGVSNAFDFPGFVPAYIR

PLFCRGIGPFRWVALSGDPQDIYKTDAKVKEIIKDDQHLHHWLDMARERISFQGLPARICWVGLEWRQKL

GLAFNEMVRSGEVSAPIVIGRDHLDSGSVASPNRETEAMRDGSDAVSDWPLLNALLNTASGATWVSLHHG

GGVGMGFSQHSGMVIVCDGTDEAAARIARVLHNDSATGVMRHADAGYEIAIECAAEQGLNLPMVAATQGN

AK

>lcl|NZ\_FO834906.1\_prot\_WP\_012737677.1\_1857 [gene=hutH] [locus\_tag=BN49\_RS10755] [protein=histidine ammonia-lyase] [protein\_id=WP\_012737677.1] [location=1913286..1914812] [gbkey=CDS]

MKSLTLIPGQLSLSQLRDVYSHPVNITLDSGAFAAIDESVACVNAILAEGRTAYGINTGFGLLAQTRIST

EDLENLQRSLVLSHAAGVGEPLDDDLARLIMVLKINSLSRGFSGIRLSVIQALIGLVNAGVTPWIPAKGS

VGASGDLAPLAHMSLTLLGEGKARVRGGDWLPATEALRQVGLEPITLAAKEGLALLNGTQASTAFALRGL

FEAEDLFASAVVCGALTTEAALGSRRPFDARIHEVRGQRGQIDAAALYRHLLTDDSAISQSHHNCSKVQD

PYSLRCQPQVMGACLTQIRQAAEVLLAEANAVSDNPLVFAAENDVISGGNFHAEPVAMAADNIALAIAEI

GSLSERRIALMMDSHMSQLPPFLVKNGGVNSGFMIAQVTAAALASENKALSHPHSVDSLPTSANQEDHVS

MAPAAGRRLWAMAENTRGVLAVEWLAAAQGLDMREGLTTSPLLEEARHLLRERVPHYTQDRYFAPDIDNA

IALLAARHLTRLLPAVLH

>lcl|NZ\_FO834906.1\_prot\_WP\_004142109.1\_1858 [locus\_tag=BN49\_RS10760] [protein=amino acid permease] [protein\_id=WP\_004142109.1] [location=1914911..1916293] [gbkey=CDS]

MQQQHKPHLLRGLNARHIRFIALGSAIGTGLFYGSASAIKAAGPAVLLAYLIGGAAVFIVMRALGEMAVR

NPVSGSFGSYARQYLGPLAGFITGWTYTFEMVIVALADVTAFGIYMGLWYPDVPRWIWILSIIFFIGAMN

LCNVRVFGEMEFWLSLVKVVAIIAMMLAGAGIIFFGFGHSFPATGLENLWSHGGFAPNGWQGVIASLGIV

MFAFGGVEIIGVTAAEAKDPKKVIPQAINTIPLRIILFYVCTLAVLMAIFPWNSFGEQGSPFVLIFDGLG

IPAAATILNIIVISASISAINSDIFGAGRMMYGMSKEGLAPKSFQRIASNGVPWMTVVVMGGALLAAVVL

NYLIPEQVFVLIASLAAFATVWVWLMILLSHFAMRRGLSAEERSQIAFPIPFWPVAPLLTLLFMGLVIAV

LGMFAETRMALIAGLVWLGLLTVVWYARVRKTALQVVTEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002895575.1\_1859 [locus\_tag=BN49\_RS10770] [protein=kinase inhibitor] [protein\_id=WP\_002895575.1] [location=complement(1917072..1917548)] [gbkey=CDS]

MKLISHDLQDGGKLPNRHVFNGMGYDGDNISPHLMWDDVPAGTKSFVVTCYDPDAPTGSGWWHWVVANLP

ADTRVLPQGAGSGQAELPEEAVQTRTDFGKAGYGGAAPPKGETHRYIFTVHALDVEKIEVDAEASGAMVG

FNVHFHSLASASITALFS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176805.1\_1860 [gene=bioA] [locus\_tag=BN49\_RS10775] [protein=adenosylmethionine--8-amino-7-oxononanoate transaminase] [protein\_id=WP\_004176805.1] [location=complement(1917619..1918908)] [gbkey=CDS]

MTLDDLAFDRRHIWHPYTSMTSPLPVYPVVSAHGCELSLAGGEQLVDGMSSWWAAIHGYNHPRLNAALKG

QIDQMSHVMFGGITHPPAVALCRQLVAMTPASLECVFLADSGSVAVEVAMKMALQYWQAKGEPRRRFLTF

RNGYHGDTFGAMSVCDPQNSMHSLWQGYLPDNLFAPAPQSRFDGEWDEMDMVPFARLMAAHRHEIAAVIL

EPIVQGAGGMRMYHPEWLKRVRKMCDREGILLIADEIATGFGRTGKLFACEHAGITADILCLGKALTGGT

MTLSAAITTRTVAETISNGEAGCFMHGPTFMGNPLACAVASESLRLLESGEWQPQVAAIEAQLQAELAPA

RGSALVADVRVLGAIGVVETRRPVNMAALQRFFVEQGVWIRPFGRLIYLMPPYIITPEQLTRLTRAVNQA

VQDETFFSE

>lcl|NZ\_FO834906.1\_prot\_WP\_002895580.1\_1861 [gene=bioB] [locus\_tag=BN49\_RS10780] [protein=biotin synthase BioB] [protein\_id=WP\_002895580.1] [location=1919122..1920162] [gbkey=CDS]

MAHQPRWTMSQVTELFNKPLIDLLFEAQQIHRQHFDPRQVQVSTLLSIKTGACPEDCKYCPQSARYKTGL

EAERLMEVEQVLESARQAKNAGSTRFCMGAAWKNPNDRDMPYLEQMVKGVKALGLESCMTLGTLTDSQAQ

RLAEAGLDYYNHNLDTSPEFYGNIITTRTYQERLDTLDKVRDAGIKVCSGGIVGLGESVKDRAGLLLQLA

NLPTPPESVPINMLVKVKGTPLADNDDVDAFDFIRTIAIARIMMPTSYVRLSAGREQMNEQTQAMCFMAG

ANSIFYGCKLLTTPNPEEDKDLQLFRKLGINPQQTAVLEGDNEQQQRLEQALLTPDTEEYYNAAAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004176804.1\_1862 [gene=bioF] [locus\_tag=BN49\_RS10785] [protein=8-amino-7-oxononanoate synthase] [protein\_id=WP\_004176804.1] [location=1920159..1921316] [gbkey=CDS]

MSWQQRIDRALDERRAAEAFRRRLPVTHGAGRWLEREGERWLNFSSNDYLGLSQHPAIIAAWQQGATRYG

VGAGGSGHVSGYSEAHRALEEALADWLGYPRALLFISGFAANQALIAALVEKDDRIVADRLSHASLLEAA

SLSPAQLRRFTHNDPQQLAQLLAKPLAGEQLAVTEGIFSMDGDSAPLAAIHAATQAAGAVLLVDDAHGVG

VVGDEGRGSCAAQAVRPELLVVTFGKAFGVSGAAVLCDEAMADYLLQFARHLIYSTAMPPAQAVALSAAL

GIIRSDEGQQRRDILAARIRQFREGMGEVSLGLTDSVSAIQPLIVGDNARALNLACRLRDAGCWATAIRP

PTVPVGSARLRLTLTAAHHAEDINRLLEVLHGHSE

>lcl|NZ\_FO834906.1\_prot\_WP\_039110527.1\_1863 [gene=bioC] [locus\_tag=BN49\_RS10790] [protein=malonyl-ACP O-methyltransferase BioC] [protein\_id=WP\_039110527.1] [location=1921300..1922055] [gbkey=CDS]

MATVNKQAVAAAFGRAASGYTQHDELQRRCADLLLRQLARCDFAQVLDAGCGPGSMSRYWREAGSVVTAL

DLSAGMLAQAQRNDAAQHYLLGDIEALPLPDACVDLAWSNLAVQWCDDLRAAIGELYRVARPGGRVAFST

LLADSLPELNQAWQAIDDRPHANRFLSEAAVRAALSGLRATGEVHQISLPFADALSAMRSLKGIGATHLH

QGRTAAPLGRGKLRELQLAWPQRQGICPLTYSLFTGVIERD

>lcl|NZ\_FO834906.1\_prot\_WP\_002895648.1\_1864 [gene=bioD] [locus\_tag=BN49\_RS10795] [protein=dethiobiotin synthase] [protein\_id=WP\_002895648.1] [location=1922048..1922770] [gbkey=CDS]

MTKRFFVTGTDTEVGKTIASSALLQAANLLGFHTAGYKPVASGSELTGDGLRNEDALALQRHSRVALRYD

QVNPYTFAEPTSPHIISADEGRPIAAARLSSGLRELEGLADWVLVEGAGGWFTPLSDSLTFADWAQAEQL

PVILVVGVKLGCINHAMLTAQAVRQAGLPLAGWIANDVQPPGKRHAEYLATLKNRLAAPFLGEIPWLADI

AQRDDLGQYLDLRALDPALSTAPAAAHPAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004152853.1\_1865 [locus\_tag=BN49\_RS10800] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_004152853.1] [location=complement(1922712..1923434)] [gbkey=CDS]

MLNLQAVNHFYGNQHSLWNVDLVLRPGECIGVLGREGMGKTTLVNCIAGHLPVASGRMTWHDIGAPPQDL

TPLSAQSRSAIGIGYVPQDKRIFSQLSVEENLHIALAAGKPGANASGGEIYEHFPELYALRQRKGASLSD

DDQYQLALARALIVQPRLLILDEPSRGRGPRCLQKLADLLLRLNRDIGLTVLLAEQHLPFIRRVADRFCV

LHRGRNVAEGDIMALDEPLLAQWITPDPAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002895652.1\_1866 [locus\_tag=BN49\_RS10805] [protein=hypothetical protein] [protein\_id=WP\_002895652.1] [location=complement(1923521..1923733)] [gbkey=CDS]

MDNCPQPKTTAARRLSPFAVNRVAKNFYRTIFDNYPLKAARFLLLFAPPFSVGHRKSAAPALTRPDGIGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002895655.1\_1867 [gene=uvrB] [locus\_tag=BN49\_RS10810] [protein=excinuclease ABC subunit UvrB] [protein\_id=WP\_002895655.1] [location=1924145..1926166] [gbkey=CDS]

MSKSFVLHSAFRPSGDQPEAIRRLEEGLEDGLAHQTLLGVTGSGKTFTIANVIADLQRPTMVLAPNKTLA

AQLYGEMKEFFPENAVEYFVSYYDYYQPEAYVPSSDTFIEKDASVNEHIEQMRLSATKALLERRDVVVVA

SVSAIYGLGDPDLYLKMMLHLTVGMLIDQRAILRRLAELQYTRNDQAFQRGTFRVRGEVIDVFPAESDDI

ALRIELFDEEVERLSLFDPLTGHVEGTVPRYTIYPKTHYVTPRERIVQAMEEIKLELAERRKVLLANNKL

LEEQRLTQRTQFDLEMMNELGYCSGIENYSRFLSGRGPGEPPPTLFDYLPADGLLVIDESHVTVPQIGGM

YRGDRARKETLVEYGFRLPSALDNRPMKFEEFEALAPQTIYVSATPGAYELDKSGGEVVDQVVRPTGLLD

PIIEVRPVATQVDDLLSEIRLRTAINERVLVTTLTKRMAEDLTEYLEEHGERVRYLHSDIDTVERMEIIR

DLRLGEFDVLVGINLLREGLDMPEVSLVAILDADKEGFLRSERSLIQTIGRAARNVNGKAILYGDKITPS

MAKAIGETERRREKQQRYNEEHGIVPQGLNKKVVDILQLGQGLAKTKAKGRGKAKAVEPAGLSAVDMTPK

ALQQKIHELEGQMMQHAQNLEFEEAAQIRDQLHQLRELFIAAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004147680.1\_1868 [gene=pmrB] [locus\_tag=BN49\_RS10815] [protein=two-component system sensor histidine kinase PmrB] [protein\_id=WP\_004147680.1] [location=complement(1926415..1927512)] [gbkey=CDS]

MALFATETWTMRHRLLLTIGAILVVCQLISVFWLWHESKEQIQLLVASAIEGHNNQKHVEHEVREAVASL

LVPSLLIVGLALYISMLAVRKITRPLSRLQSELENRTPDNLTPIVLSESVPEVTAVTTALNQLVSRLNLT

LDRERLFTADVAHELRTPLAGLRLHLELLAKVHGMGVDPLIQRLDQMTTSISQLLQLARVGQSFSAGSYQ

QVLLLDDVVKPLQDELEAMLAQRQQRLLLTDIENEAVVSGDATLIRVILRNLVENAHRYSPEGSTIRVSV

KAGLMPVMAVEDEGPGIDEAKSGELSKAFVRMDSRYGGIGLGLSIVTRIAQLHDAQFFLHNRQPGPGVRA

WVLFPQRGGQNVSTH

>lcl|NZ\_FO834906.1\_prot\_WP\_002895659.1\_1869 [gene=pmrA] [locus\_tag=BN49\_RS10820] [protein=two-component system response regulator PmrA] [protein\_id=WP\_002895659.1] [location=complement(1927516..1928187)] [gbkey=CDS]

MKILVIEDDALLLQGLILAMQSEGYVCDGVSTAHEAALSLASNHYSLIVLDLGLPDEDGLHFLSRMRREK

MTQPVLILTARDTLEDRISGLDTGADDYLVKPFALEELNARIRALLRRHNNQGDNEISVGNLRLNVTRRL

VWLGETALDLTPKEYALLSRLMMKAGSPVHREILYNDIYSWDNEPATNTLEVHIHNLREKIGKSRIRTVR

GFGYMLANNIDTE

>lcl|NZ\_FO834906.1\_prot\_1870 [gene=eptA] [locus\_tag=BN49\_RS10825] [protein=phosphoethanolamine transferase EptA] [pseudo=true] [location=complement(1928187..1929822)] [gbkey=CDS]

MSLLPLRRPVVSRTTYLILFACYIGICLNLAFYRQVFPLLPVNSLHNWLVFLSMPIVAISVMNILTTLAS

FLKLDRLVISLFILLSASAQYFIWNFGVVIDRSMITNILDTTPAESFALLSGEMIAVLGLSGVLAVFVAW

WVKIRKPATRWRGDAPAQYRRFGAADYSGGRAVLQRLRLGVP\*QQRAGEIPEPFQQHCGRELLVCSSSDG

QPAAGEDWRRCHAESGDA\*RSP\*EPDDRRARRDFASG\*LLTGRLFARHQPADAAGRRDLFSAYHFLRHGN

RSFRAVHVLQYAARAL\*RRAGAPSGRRPGYSTARRDPGTVER\*RRRLQRRLRPGTTPERHRLEAHRAVHR

WRVLR\*RPVP\*SRQLYR\*PATGWHYCAAYHRQPRSDVLQSLSSGVSQIHAELRHQ\*DPGLYPGAVDQYL\*

QHHPLCRLCR\*\*SDKTTAI\*TG\*IYH\*PGLFVRPRRIAGRRWRLFAWSAVFHRAGYAETCADGAVALRRL

PAALRYFRALSAAAGAKRELLAG\*SVLHPARPARRQHPRVPGGR\*YLNAM\*RGWL

>lcl|NZ\_FO834906.1\_prot\_WP\_004142092.1\_1871 [gene=yvcK] [locus\_tag=BN49\_RS10830] [protein=uridine diphosphate-N-acetylglucosamine-binding protein YvcK] [protein\_id=WP\_004142092.1] [location=complement(1929927..1930832)] [gbkey=CDS]

MRNRTFADLDRVVALGGGHGLGRVMSSLSSLGSRLTGIVTTTDNGGSTGRIRRSEGGIAWGDMRNCINQL

IAEPSVASAMFEYRFGGNGELSGHNLGNLMLKALDHLSVRPLEAINLIRNLLKVDAFLIPMSEQPVDLMA

LDHEGHEVYGEVNIDQLDNVPQELMLTPPVPATREAVEAIAEADLILIGPGSFYTSLLPILLLDEMAQAL

RRTPAPMVFIDNLGKEHSPAARLSLAERIAIMERYVGKRVVDAVIAGPKADISGIDDRLVIQTPLEASDV

PYRHDRALLRGALEKAIQLPG

>lcl|NZ\_FO834906.1\_prot\_WP\_002895665.1\_1872 [gene=moaA] [locus\_tag=BN49\_RS10835] [protein=GTP 3',8-cyclase MoaA] [protein\_id=WP\_002895665.1] [location=1931167..1932156] [gbkey=CDS]

MASQLTDAFARKFYYLRLSITDVCNFRCTYCLPNGYKPGAVNNNGFLSVDEVRRVTRAFSALGTEKVRLT

GGEPSLRRDFTEIIAAVRENPAIRQIAVTTNGYRLARDVERWRDAGLTAINVSVDSLDARQFHAITGQDK

FHQVMDGIDAAFAAGFDKVKVNTVLMRDVNHHQLDTFLAWIQPRRIQLRFIELMETGEGSDLFRRHHLSG

MVLRDELLRRGWIHQIRQRSDGPAQVFCHPDYAGEIGLIMPYEKDFCATCNRLRVSSVGKLHLCLFGEGG

VDLRDLMAEDQQQAALEARIAEALTHKKQTHFLHQGNTGITQNLSYIGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002895668.1\_1873 [gene=moaB] [locus\_tag=BN49\_RS10840] [protein=molybdenum cofactor biosynthesis protein B] [protein\_id=WP\_002895668.1] [location=1932180..1932692] [gbkey=CDS]

MSQASAEFIPTRIAILTVSSRRGEEDDTSGHWLREAAQEAGHQVVEKAIVKENRYAIRAQVSAWIASDNV

QVVLITGGTGFTDGDQAPEALLPLFDREVEGFGEVFRMLSFEEIGTSTLQSRAVAGVANRTLIFAMPGST

KACRTAWDNIIAPQLDARTRPCNFIPHLKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002895670.1\_1874 [gene=moaC] [locus\_tag=BN49\_RS10845] [protein=cyclic pyranopterin monophosphate synthase MoaC] [protein\_id=WP\_002895670.1] [location=1932696..1933184] [gbkey=CDS]

MSQLTHINAAGEAHMVDVSGKAETVREARAEAYVEMQATTLAMIIDGSHHKGDVFATARIAGIQAAKRTW

ELIPLCHPLMLSKVEVNLQAQPEHNRVRIESLCRLTGKTGVEMEALTAASVAALTIYDMCKAVQKDMVIG

PVRLLAKSGGKSGDFKVGECHD

>lcl|NZ\_FO834906.1\_prot\_WP\_002895672.1\_1875 [gene=moaD] [locus\_tag=BN49\_RS10850] [protein=molybdopterin synthase sulfur carrier subunit] [protein\_id=WP\_002895672.1] [location=1933177..1933425] [gbkey=CDS]

MIKVLFFAQVRELVGTDSLTLDASELATVEAVRQQLAARGDRWALALEEGKLLAAVNQTLTSFEHPVASG

DEVAFFPPVTGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002895674.1\_1876 [gene=moaE] [locus\_tag=BN49\_RS10855] [protein=molybdopterin synthase catalytic subunit MoaE] [protein\_id=WP\_002895674.1] [location=1933427..1933879] [gbkey=CDS]

MTQTRIVVSPARFSVSEEYPWLAERDEDGAVVTFTGKVRNHNLGDSVKALTLEHYPGMTEKSLAEIVELA

RERWPLGRVTVIHRIGEMWPGEEIVFVGVTSAHRGSAFAAGEFIMDYLKTRAPFWKREATPDGERWVDAR

DSDRQAAERW

>lcl|NZ\_FO834906.1\_prot\_WP\_004142079.1\_1877 [locus\_tag=BN49\_RS10860] [protein=Bax inhibitor-1/YccA family protein] [protein\_id=WP\_004142079.1] [location=1933925..1934629] [gbkey=CDS]

MDRYPRSDSIVQGRTGLQTYMAQVYGWMTVGLLLTAFIAWFAANTPAVMMFVFSSKITFFGLIIAQLALV

FVLSGMVQRLSAGMATTLFMLYSALTGLTLSSIFIAYTYSSIASTFVVTGGMFGAMSLYGYTTKRDLSGF

GSMLFMGLIGIVLASLVNLWLKSEALMWAVTYIGVVLFVGLTAYDTQKLKNIGEQIDTRDSATLRKYSIL

GALTLYLDFINLFLMLLRIMGNRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002895728.1\_1878 [locus\_tag=BN49\_RS10865] [protein=lysylphosphatidylglycerol synthase domain-containing protein] [protein\_id=WP\_002895728.1] [location=complement(1935047..1936012)] [gbkey=CDS]

MSKSHPRWRMAKRVLTVLFFIAVIVLLVIYAQKVDWQDVWKVIRGYDRLALFSAIALVIVSYLIYGCYDL

LGRAYCGHKLAKRQVMLVSFICYAFNLTLSTWVGGIGMRYRLYSRLGLNGSTITRIFSLSITTNWLGYIL

LGGVIFTADLVKLPPHWYISQTTLRIIGGVMLILTLCYLFGCAFAKRRHLTIKGQRLVLPSWRFALLQMG

LSAANWMAMGAIIWLLLGSEINYFLVLGVLLVSSIAGVIIHIPAGIGVLEAVFIAMLSGEDISKGAIIAA

LLAWRALYYFLPLLLATVAYLLLESRAKKLRQKNQRKLARE

>lcl|NZ\_FO834906.1\_prot\_1879 [gene=clsB] [locus\_tag=BN49\_RS10870] [protein=cardiolipin synthase ClsB] [pseudo=true] [location=complement(1936009..1937253)] [gbkey=CDS]

MKCRWQEGNRITLLENGDQYYPALFAAIGRASRRVILESFIWFEDEVGRRLHAVLLEAARRGI\*VEVLLD

GYGSPDLSDEFVGELTAAGVIFRYYDPRPKLMGMRTNLFRRMHRKIVVIDDTTAFVGGINYSAEHMSDYG

PEAKQDYAVQVEGPVVLDILQFELENLPNSETARRWWRRRRHQPEINQPPGEAQALFVWRDNQDHRDDIE

RHYLKMLTSARREVIIANAYFFPGYRLLHAMRNAARRGVRVKLIVQGEPDIPIVKFGAHLLYHYLVKGGV

QIYEYRRRPLHGKVALADDHWATVGSSNLDPLSLSLNLEANLIIHDRVFNQTLRDNLNGLIARDCQRIDK

TMLPKRNWWRLGVSVMAFHFLRHFPAWVGWLPAHTPRLARVSPPVQPEIETQDRVESPARDNPL

>lcl|NZ\_FO834906.1\_prot\_WP\_004179098.1\_1880 [locus\_tag=BN49\_RS10875] [protein=endonuclease/exonuclease/phosphatase family protein] [protein\_id=WP\_004179098.1] [location=complement(1937250..1938011)] [gbkey=CDS]

MAEPTAGFSLNVLTINTHKGFTAFNRRFILPELRDAVRSVSADIVCLQEVMGAHEVHPLHIENWPDTTHY

EFLADTMWSDYAYGRNAVYPEGHHGNAVLSRFPIEYYENRDISVGNGEKRGLLYCRIVPPRSGITIHVIC

VHLGLRADQRQAQLTMLAEWVNTLPAGEPVVVAGDFNDWRQQANQPLKAQAGLEEIFTRARGRPARTFPV

SFPLLRLDRIYVKNAHASRPKALALKQWRHLSDHAPLSVEIHL

>lcl|NZ\_FO834906.1\_prot\_WP\_004176793.1\_1881 [locus\_tag=BN49\_RS10880] [protein=YbhQ family protein] [protein\_id=WP\_004176793.1] [location=1938143..1938580] [gbkey=CDS]

MKWQQRVRVATGLSCWQIMLHLLVVAVLVMGWMSGALVRVGLGLCVLYSVTLLAMLFLQRHHEARWRDVG

DFLEELTTTWYFGAAMIALWLLSRVLHNNLLLALAGLVILAGPAVVSLLAKDKSRYPKAFGLQQGGNAAN

PQKHR

>lcl|NZ\_FO834906.1\_prot\_WP\_004142068.1\_1882 [locus\_tag=BN49\_RS10885] [protein=ABC transporter permease] [protein\_id=WP\_004142068.1] [location=complement(1938641..1939747)] [gbkey=CDS]

MFHRLWTLIRKELQSLLREPQTRAILIMPVLIQVLLFPFAATLEVTNATIAIYNEDSGRHAVELTQRFAR

AKAFTHVLLLQSPQAIQPTIDEQKALLVVRFPADFSRNLDNYQTAPLQLLLDGRNSNSAQIAANYLQQIV

KNYQQELLEGKAKPNNSELVVRNWYNPNLDYKWFVVPSLIAMITTIGVMIVTSLSVAREREQGTLDQLLV

SPLATWQIFVGKAVPALIVATLQATIVLAIGIWAYQIPFAGSLLLFYFTMVIYGLSLVGFGLLISSLCAT

QQQAFIGVFVFMMPAILLSGYVSPVENMPQWLQDLTWINPIRHFTDITKQIYLKDASLEIVWGSLWPLLV

IAATTGSAAYAMFRRKIA

>lcl|NZ\_FO834906.1\_prot\_WP\_002895739.1\_1883 [locus\_tag=BN49\_RS10890] [protein=ABC transporter permease] [protein\_id=WP\_002895739.1] [location=complement(1939877..1941010)] [gbkey=CDS]

MGNSILSWRRVRALCVKETRQIVRDPSSWLIAVVIPLLLLFIFGYGINLDSSRLRVGVLLEQQSEEALDF

VHTMTGSPYIDATVSDSRRQLIEMMQAGRIRAMVVIPVDFDRQMARPGADAPLQLITDGSEPNTANFAQG

YVEGIWQIWQQQRAEDRGETFEPLIDVQMRYWFNPAAISQHFIIPGAITIIMTVVGAILTSLVVAREWER

GTMEALLSTEITRAELLLCKLIPYYFLGMLAMLLCMLVSVFILGVPYRGSLPILFVITSLFLLSTLGMGL

LISTITRNQFNAAQVALNAAFLPSIMLSGFIFQIDSMPAVIRAVTYVIPARYFVSTLQSLFLAGNIPVVL

LVNVLFLIASAVMFIGLTWLKTKRRLD

>lcl|NZ\_FO834906.1\_prot\_WP\_002895741.1\_1884 [locus\_tag=BN49\_RS10895] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_002895741.1] [location=complement(1941000..1942739)] [gbkey=CDS]

MSETVIALNGLSRRFPGMDRPAVAPLTCTIRAGYVTGLVGPDGAGKTTLMRMLAGLLKPDEGRASVIGFD

PLKDDSALHAVLGYMPQKFGLYEDLTVMENLTLYADLRSVTGEARKKIFDRLLEFTSLGPFTERLAGKLS

GGMKQKLGLACTLVGDPKVLLLDEPGVGVDPISRRELWQMVHELAGDGMLILWSTSYLDEAEQCRDVLLM

NEGKLLYQGEPTALTQTMAGRSFLVSSPQENNRRLLQRALKLPQVSDGVIQGKSVRLILKKDARIEEVQQ

HGDMPPLQVADTAPRFEDAFIDLLGGAGTAESPLGAIIHRVDGSKEETVIEAQSLTKKFGDFAATDHVDF

QVKRGEIFGLLGPNGAGKSTTFKMMCGLLVPTSGKALVLGMDLKVSSGKARQHLGYMAQKFSLYGNLSVE

QNLRFFSGVYGLRGRAQNEKIARMSDAFGLKSIARHAADELPLGYKQRLALACSLMHEPDILFLDEPTSG

VDPLTRREFWLHINSMVDKGVTVMVTTHFMDEAEYCDRIGLVYHGKLIASGTPDALKAQAADDSQTDPTM

EQAFITLINRWDKENSHGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529602.1\_1885 [gene=hlyD] [locus\_tag=BN49\_RS10900] [protein=secretion protein HlyD] [protein\_id=WP\_016529602.1] [location=complement(1942732..1943727)] [gbkey=CDS]

MKKTVVVILLIVILLAALGGGWWWYQSSRQQPLTLYGNVDIRTVNMSFRVGGRLASLTVDEGDSIRAGQT

LGALDRAPYENALLQAQANVSTAQAQYDLMMAGYRAEEIAQAAAAVKQAQAAYDYAQNFYQRQLGLRASS

AISANDLENARSSRDQAQATLKSAQDKLRQYRAGNRPQEIAQAKASLEQAQAALAQAKLDLHDTVLTAPS

DGTLMTRAVEPGTMLNAGGTVLTLSLTHPVWVRAYVDEKNLGQAQPGQEVLLYTDSRPDKPYHGKIGFVS

PSAEFTPKTVETPDLRTDLVYRLRIVVTDADGALRQGMPVTISFSHGNGHE

>lcl|NZ\_FO834906.1\_prot\_WP\_002895746.1\_1886 [gene=cecR] [locus\_tag=BN49\_RS10905] [protein=transcriptional regulator CecR] [protein\_id=WP\_002895746.1] [location=complement(1943727..1944386)] [gbkey=CDS]

MTSKGEQAKNQLIAAAIAQFGEYGQHATTRDIAAQAGQNIAAITYYFGSKDDLYLACAQWIADFIGDNFR

PQAEAAEHLLAGEAPDRQAIRDLILSACHNMILLLTQDDTVNLSKFISREQLAPTAAYHLIHQQVIAPLH

HYLTRLIAAWTGCEASDTQMILHTHALLGEVLAFRLGRETILLRTGWTQFDAQKTEQIFEVITCHIDFIL

HGLSQRSLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004179102.1\_1887 [locus\_tag=BN49\_RS10910] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_004179102.1] [location=complement(1944460..1945383)] [gbkey=CDS]

MSQPLPNKNLPMPSLRNIQAFIEVAATGSLNLAAENLNITASAVSHQIASLEHFLGKKLFSRSSKGVTLT

AVGEKYLKEVSGALNMIGQATSQVINDIHQDYLRIHSAPSFGLLWLMPRLDKFRQAWPALKISLTCSYES

IQFSRDNIDIDIRHGLSQWPTLLVRTIKNERVLPYSAASYLASHPVQAVEDLLACDLIHSDSTLINWSNW

LSWHKVRGWHKNFIFNFDRSYMSIEAARMGMGVILESNLLAGGHVRQGQLTPVFADERSMPVGAHHFVLP

HANEQKEKVQRFFAWVAGELKEEGFHI

>lcl|NZ\_FO834906.1\_prot\_WP\_004142057.1\_1888 [locus\_tag=BN49\_RS30965] [protein=hypothetical protein] [protein\_id=WP\_004142057.1] [location=1945375..1945512] [gbkey=CDS]

MAHGGILRGARIKENSEQRGAAGMYSIGKSEKTTLICDGLNNLSC

>lcl|NZ\_FO834906.1\_prot\_WP\_002895749.1\_1889 [locus\_tag=BN49\_RS10920] [protein=MFS transporter] [protein\_id=WP\_002895749.1] [location=1945800..1947131] [gbkey=CDS]

MSRIDTLVCTDARKTKYRFVVLTMIFLVYAINYADRTNIGAVLPFIIDEFHINNFEAGAIASMFFLGYAV

SQIPAGFFIAKRGTRGLVSLSIFGFSAFTWLMGTVSSVFGLKLVRLGLGLSEGPCPVGLASTINNWFPPK

EKATATGVYIAATMFAPIIVPPLAVWIAVTWGWRWVFFSFAIPGIVAAIAWYLLVKSKPAESGFVSQSEL

AEINAGRESHNNSVRENILIAERFTWLDKIIRVKKMAPIDTAKGLFTSKNILGDCLAYFMMVSVLYGLLT

WIPLYLVKERGFDVMSMGFVASMPCIGGFIGAIGGGWVSDKLLGRRRKPTMMFTAVSTVVMMLIMLNIPA

STLAVCIGLFFVGFCLNIGWPAFTAYGMAVSDSKTYPIASSIINSGGNLGGFVAPMAAGFLLDKTGSFNS

VFTYFGICAAIGLVVILFLDEPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004223790.1\_1890 [locus\_tag=BN49\_RS10925] [protein=glucose 1-dehydrogenase] [protein\_id=WP\_004223790.1] [location=1947182..1947931] [gbkey=CDS]

MLLKDKVAIITGAASARGLGFATAKLFAENGAKVVIIDLNGEASKTAAAALGEGHLGLAANVADEVQVQA

AIEQILAKYGRVDVLVNNAGITQPLKLMDIKRTNYDAVLDVSLRGTLLMSQAVIPTMRAQKSGSIVCISS

VSAQRGGGIFGGPHYSAAKAGVLGLARAMARELGPDNVRVNCITPGLIQTDITAGKLTDDMTANILAGIP

MNRLGDAIDIARAALFLGSDLSSYSTGITLDVNGGMLIH

>lcl|NZ\_FO834906.1\_prot\_WP\_004223794.1\_1891 [locus\_tag=BN49\_RS10930] [protein=transketolase] [protein\_id=WP\_004223794.1] [location=1947945..1948790] [gbkey=CDS]

MKMTESQKVAAAAWRIRRYALQMGEVQGQGYIGQALGYADVLATAFSYAMTYRPEDPDWEGRDRFLLSHG

HYAIAYYAALLEAGIIPEAELETYGSDDSRLPMSGMATYTPGMEMSGGSLGQGLSIAVGMALGLRQKQSK

AWVYNSMSDGELDEGSTWEAAMSAAHYGLSNLINLVDVNKQQADGDSRKILGFEPLQDKWAAFGWYVQRV

DGNDLPAVMAAFDNAKSYSGNQPRVILCDTLMGKGVPFLETRDKNHFIRVDADEWQKAIAVLDANKPEGV

L

>lcl|NZ\_FO834906.1\_prot\_WP\_016529604.1\_1892 [locus\_tag=BN49\_RS10935] [protein=transketolase family protein] [protein\_id=WP\_016529604.1] [location=1948790..1949782] [gbkey=CDS]

MSQSQPRLKTSAMIASIADEGQATVPAPFGVALSKLAAQRPDIVGMTADLSKYTDLHIFAQAFPDRFFQM

GMAEQLLMAAAGGMAKEGFIPFATTYAAFATRRAYDFIHQVIAEEHLNVKICAALPGLTTGYGPSHQATE

DLAIMRGIPRMVIVDPCDALEIEQAVPAIADHQGPVYMRLLRGKVPLVLDKYDYQFELGKAKLLEDGNDV

LIISSGLMTMRALEAAEKLRADNIGVAVLHVPTIKPLDEKAIIEQASKPGRLVVTAENHTVVGGLGEAVA

ALLMRKGVRCELDSVGLPDAFLLAGALPTLHDRYGISTAKIVEKIKYRLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151702.1\_1893 [gene=rhlE] [locus\_tag=BN49\_RS10940] [protein=ATP-dependent RNA helicase RhlE] [protein\_id=WP\_004151702.1] [location=1949997..1951352] [gbkey=CDS]

MSFDSLGLNPDILRAVAEQGYVEPTPIQQQAIPAVLQGRDLMASAQTGTGKTAGFTLPLLQRLIQNEPHA

KGRRPVRALILTPTRELAAQVGENVRDYSKYLNIRSLVVFGGVSINPQMMKLRGGVDILVATPGRLLDLE

HQNAVSLDKVEILVLDEADRMLDMGFIHDIRRVLAKLPARRQNLLFSATFSDEIKGLAEKLLHNPLEVEV

ARRNTASEQITQHVHFVDKNRKRELLSQLIGEGNWQQVLVFTRTKHGANHLAEQLNKDGIRSAAIHGNKS

QGARTRALADFKSGGIRVLVATDIAARGLDIEELPHVVNYELPNVPEDYVHRIGRTGRAAATGEALSLVC

VDEHKLLRDIERLLKKEIPRIAIAGYEPDPSIKAEPIQNGRQQRGGGRGQGQGRGGQGQGRSGQPRSQNN

APRRQDGEAPKARTQDGKPPRRRRPRKPAGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004147693.1\_1894 [gene=dinG] [locus\_tag=BN49\_RS10945] [protein=ATP-dependent DNA helicase DinG] [protein\_id=WP\_004147693.1] [location=1951540..1953696] [gbkey=CDS]

MALTAALKAQIAAWYKALQEQIPDFIPRPPQRQMIADVAKTLAGEEGRHLAIEAPTGVGKTLSYLIPGIA

IAREEQKTLVVSTANVALQDQIYSKDLPLLRKIIPDLRFTAAFGRGRYVCPRNLTALASTEPSQQDLLAF

LDDDLTPNNQAEQKLCATLKQDLDSYRWDGLRDHTDKAIDDGLWSRLSTDKASCLNRNCHYYRECPFFVA

RREIQEAEVVVANHALVMAAMESEAVLPEPKNLLLVLDEGHHLPDVARDALEMSAEITAPWFRLQLDLFC

KLVATCMEQFRPKTTPPLANPERLTAHCEELFELIASLNNILNLYMPAGQEAEHRFPMGELPQEVMEICQ

RLAKLTELLRGLAELFLNDLSEKTGSHDVVRLHRVLLQMNRALGMFESQSKLWRLASLAQSSGAPVTKWA

TRVVRDGQIHVWFHCVGIRVSDQLERLLWRSVPHIVVTSATLRSLNSFSRLQEMSGLKEKAGDRFVALDS

PFNHVEQGKIIIPQMRYEPLMDNEEQHIAEMAAYFRQQVESKKHLGMLVLFASGRAMNRFLEHVTDLRLM

LLVQGDQPRYRLVELHRKRVESGERSVLVGLQSFAEGLDLKGDLLSQVHIHKIAFPPIDSPVVITEGEWL

KSLNRYPFEVQSLPSASFNLIQQVGRLIRSHNCWGEVVIYDKRLLTKNYGARLLNALPVFPIEQPGVPEV

IVKRKAKQTAKQTGRKRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179105.1\_1895 [gene=ybiB] [locus\_tag=BN49\_RS10950] [protein=DNA-binding protein YbiB] [protein\_id=WP\_004179105.1] [location=1953726..1954694] [gbkey=CDS]

MEYSKIIKEVGRGKNHARDLDEETARALYARMLNGEVPELELGGILIALRIKGEGEAEMKGFYAAMQQHT

LRLTPPAGKPMPIVIPSYNGARKQANLTPLLAMLLHKLGFPVVVHGVSHDPTRVLTETIFTLLDIPATLH

AGQAQAQLEGHEPVYIPVGAFCPPLEKQLAMRWRMGVRNSAHTLAKLATPFGEGEALRLSSVSHPEYVPR

VANFFRETGGRALLMHGTEGEVYANPQRCPQISLIDEQGVRVLYERQTEMAAEAVVLPTSKDPEVTARWI

ERCVAGVEPVPNSLKIQLACCLLACGEVTSLEQGLSRVNDCW

>lcl|NZ\_FO834906.1\_prot\_WP\_004176772.1\_1896 [gene=ybiJ] [locus\_tag=BN49\_RS10955] [protein=DUF1471 family protein YbiJ] [protein\_id=WP\_004176772.1] [location=complement(1954804..1955064)] [gbkey=CDS]

MKNIKYAAAAIALTALSFGAFAAEPVTPAQAESMNKIGVVSAQGATTLDGLEAKLAAKAEAAGATGYSIT

SANTNNKLSGTAVIYK

>lcl|NZ\_FO834906.1\_prot\_WP\_004179107.1\_1897 [locus\_tag=BN49\_RS10960] [protein=DksA/TraR family C4-type zinc finger protein] [protein\_id=WP\_004179107.1] [location=complement(1955350..1955616)] [gbkey=CDS]

MASGWAGDGAVQDQIDSTIDDAVARARRKLPRGESNKFCDECGEPIPEARRQAIPGVRYCVKCQQEKDLH

NNTFSGYNRRGSKDSQLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004183485.1\_1898 [locus\_tag=BN49\_RS10965] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_004183485.1] [location=complement(1955637..1955897)] [gbkey=CDS]

MKFVSLLFAAALTAHATAASPLPPPPVLPYNGPLRPVGTVSAFGASTLDDLAAALADKAHRHGAIAWRIN

AASSGNRLYGSAIIYQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529094.1\_1899 [locus\_tag=BN49\_RS10970] [protein=flavin reductase family protein] [protein\_id=WP\_016529094.1] [location=complement(1956037..1956651)] [gbkey=CDS]

MYFYQPSQGHGLPHDPLNAIIGPRPIGWIASQDAEGQRNLAPYSFFNCFNYRPPIIGFASSGWKDSVRNI

VETKEFVWNLATRPLAMAMNETSASIPHHEDEFVRAGLTAVASRLVSAPRVAESPVNFECRLSQCIQLTT

ADGNPVDTWLVLGEVVAVHIDESLLDNGIYQTARAQPILRAGGPSAYYGIDDSLRFDMIRPDAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002895831.1\_1900 [gene=rlmF] [locus\_tag=BN49\_RS10975] [protein=23S rRNA (adenine(1618)-N(6))-methyltransferase RlmF] [protein\_id=WP\_002895831.1] [location=1956748..1957662] [gbkey=CDS]

MKAQKPGLHPRNRHHQRYDLPALCQAHPDLQGYITLNPLGEQTIDFANPQAVKALNKALLAHFYAVKHWD

IPDGFLCPPVPGRADYIHHLADLLAGDSGEVPKDATILDIGTGANLIYPLIGAHEYGWRFTGSEINPQAF

ASAQAIINGNPGLTRQIRLRRQKESQAIFHGVIHKNETYDATLCNPPFHDSAESARAGGERKRRNLGLGA

ESGLNFGGQQQELWCEGGEVAFISQMIRESQAFARQVKWFTSLVSRGDNLPPLYRLLTEVGAVKVVKKEM

AQGQKQSRFIAWSFMDDAKRRRPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004142041.1\_1901 [gene=ybiO] [locus\_tag=BN49\_RS10980] [protein=mechanosensitive channel protein] [protein\_id=WP\_004142041.1] [location=complement(1957665..1959860)] [gbkey=CDS]

MPWILLLLAALFTAPLSAATLPGVPTANTDKNSASEPDVEQKRAAYAALADVLANDSARQELIDQLRKAA

ATPPPDSTPTLTPPAVKEETTVLENVTQISREYGEQLSSRFSQLWRNITGSPHKPFNPQTFTSAAWHFLL

LAGLVFAFWWLVRLAALPLYRKMGEWGRHKNRDRGNWLQLPLTIAGAFIIDLLLLALTLFVGQLLSDRLN

GNNPTIAFQQSLFLNAFALIEFFKAILRLIFCPRIPALRPFNLSDEAASYWSLRLSALSSLIGYGLIVAV

PIISNQVNVQVGALANVVIMLCITLWALYLIFHNKAVITQGLIHLADHSLAFFSLFIRAFALVWHWLACA

YFVVLFFFSLFDPGNSLKFMMGATLQSLAIIGGAALVSGILSRWIAKTITLSPATQRNYPELQKRLNGWI

SASLKAARILTVCVAIMLLLSAWGLFDFREWLHNDAGQKTVDVLIRIALILFFSAIGWTVLASLIENRLA

SDIHGRPLPSARARTLLTLFRNALAVVISTITVMILLSEIGVNIAPLLAGAGALGLAISFGAQTLVKDII

TGIFIQFENGMNTGDLVTIGPLTGTVERMSIRSVGVRQDTGAYHIIPWSSITTFANFVRGIGSVVANYDV

DRHEDLDKASQALKAAVDDLLAQEEIRGLIIGEPSFAGLVGLSNTAFTLRVSFTTLPLKQWTVRFALDTQ

VKKHFDRAGVRAPVQTWQQLPMPGADSPAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004142040.1\_1902 [gene=glnQ] [locus\_tag=BN49\_RS10985] [protein=glutamine ABC transporter ATP-binding protein GlnQ] [protein\_id=WP\_004142040.1] [location=complement(1959972..1960694)] [gbkey=CDS]

MIEFKNVSKHFGPTQVLHDISLKINQGEVVVIIGPSGSGKSTMLRCINKLEEITSGDLIVDGLKVNDPKV

DERLIRQEAGMVFQQFYLFPHLTALENVMFGPLRVRGASKQAAEKQAKELLAKVGLAERAHHYPSELSGG

QQQRVAIARALAVKPKMMLFDEPTSALDPELRHEVLKVMQDLAEEGMTMVIVTHEIGFAEKVASRLIFID

KGRIAEDGNPQELVKNPPSPRLREFLQHVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002895837.1\_1903 [gene=glnP] [locus\_tag=BN49\_RS10990] [protein=glutamine ABC transporter permease GlnP] [protein\_id=WP\_002895837.1] [location=complement(1960691..1961350)] [gbkey=CDS]

MQFDWSAIWPAIPILLEGAKMTLWISVLGLAGGLIIGLVAGFARCFGGWIANHIALVFIEIIRGTPIVVQ

VMFIYFALPMAFSDLRIDPFSAAVVTIMINSGAYIAEITRGAVLSIHKGFREAGLALGLSRRETIRHVIL

PLALRRMLPPLGNQWIISIKDTSLFIVIGVAELTRQGQEIIAGNFRALEIWSAVAVIYLIITLVLSFILR

RLERRMKIL

>lcl|NZ\_FO834906.1\_prot\_WP\_002895839.1\_1904 [gene=glnH] [locus\_tag=BN49\_RS10995] [protein=glutamine ABC transporter substrate-binding protein GlnH] [protein\_id=WP\_002895839.1] [location=complement(1961476..1962222)] [gbkey=CDS]

MKSVFKVSLAALTLAFAVSSHAANKTLVVATDTAFVPFEFKQGDKYVGFDVDLWAAIAKELKLDYTLKPM

DFSGIIPALQTKNIDLALAGITITDERKKAIDFSDGYYKSGLLVMVNANNNDIKDVKDLNGKVVAVKSGT

GSVDYAKANIKTKDLRQFPNIDNAYMELGTGRADAVLHDTPNILYFIKTAGNGKFKAVGESLEAQNYGIA

FPKGSDELREKVNGALKTLRDNGTYNEIYKKWFGTEPK

>lcl|NZ\_FO834906.1\_prot\_WP\_002895841.1\_1905 [gene=dps] [locus\_tag=BN49\_RS11000] [protein=DNA starvation/stationary phase protection protein Dps] [protein\_id=WP\_002895841.1] [location=complement(1962631..1963134)] [gbkey=CDS]

MSTAKLVKSKASNLVYTRNDVADSEKKATIELLNRQVIQFIDLSLITKQAHWNMRGANFIAVHEMLDGFR

TALTEHLDTMAERAVQLGGVALGTTQVINSKTPLQSYPLDIHHVQDHLKALADRYAVVANDVRKAIDEAK

DEDTADIFTAASRDLDKFLWFIEANIE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529095.1\_1906 [gene=rhtA] [locus\_tag=BN49\_RS11005] [protein=threonine/homoserine exporter RhtA] [protein\_id=WP\_016529095.1] [location=complement(1963372..1964259)] [gbkey=CDS]

MPGPSRKAAAWLPILVILVAMTSIQSGASLAKSLFPVVGAPGVTALRLTLGTLILVVVFKPWRLRFSPAQ

RVPLLLYGLALGAMNYLFYLSLQRIPLGVAVALEFTGPLAVALFGSRRPLDFVWVALAILGLWYLLPLGQ

NVAQVDLTGALFALGAGACWAVYILTGQRAGEEHGPATVAMGSLIASLVFVPLGMAQATDTLWQWSLLPL

GLGIAILSTALPYSLEMMALTRLPTRTFGTLMSLEPALAALSGMIFLGETLKLSQTLALGAIIIASMGAT

LTMQRQSKVEQVDIN

>lcl|NZ\_FO834906.1\_prot\_WP\_002895845.1\_1907 [gene=ompX] [locus\_tag=BN49\_RS11015] [protein=outer membrane protein OmpX] [protein\_id=WP\_002895845.1] [location=1964611..1965123] [gbkey=CDS]

MNKIARLSALAVVLAASVGTTAFAATSTVTGGYAQSDMQGKANKAGGFNLKYRYEQDNNPLGVIGSFTYT

EKDNNSNGTYNKGQYYGITAGPAYRLNDWASIYGVVGVGYGKFQNNNYPHKSDMSDYGFSYGAGLQFNPI

ENVALDFSYEQSRIRNVDVGTWIAGVGYRF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529096.1\_1908 [locus\_tag=BN49\_RS11020] [protein=phosphoethanolamine transferase] [protein\_id=WP\_016529096.1] [location=complement(1965214..1966794)] [gbkey=CDS]

MNVTTLKDTLVARRLALNPWTGFYFLQSLLINLALGYEFSLLYTVAFTCVLHLLWRAFPRVQKAVVGAYS

LLAALYYPFGQAYGAPNFNTLLALHATNVEESTEILTIFPWYNYLLAVFIFALGVIAVRRRIVEPSRWGK

MDTLGLLFSIGIFFLQPVQNLAWGGVFKVIDTGYPAFRFVKDVVVNNNEVLDEQARMAQLAGMKDSWHVL

AVKPKYHLYVVVIGESARRDALGAFGGHWDNTPFASSVNGYLFNNYIAASGSTQKSLGLTLNRVVDGKPQ

YQDNFVTLANRAGFQTWWFSNQGQIGEYDTAIASIAKRADEVQFLKNGDFEANKNTQDEQLLKLTEQVLS

TQRTQPQLIVLHLMGSHPQACDRTTGKYTVFVQSKETSCYLYSMTQTDSLLAKLYHQLQNSGDTFSLTYF

SDHGLAFKERGKEVQYLAHDDKFQQNFQVPFMVLSSDDKAHKVIKAQRSANDFLSFFSQWTGIQAAEITP

RYRFISEQKAGPVYITNFQLQKVDYAHLGTDEFTVN

>lcl|NZ\_FO834906.1\_prot\_WP\_002895851.1\_1909 [gene=mntS] [locus\_tag=BN49\_RS11025] [protein=manganase accumulation protein MntS] [protein\_id=WP\_002895851.1] [location=complement(1967062..1967187)] [gbkey=CDS]

MNEFKRCINVFSHSPFKVRLMLIGMLCEMINGKPQQGKPNS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176765.1\_1910 [gene=mntR] [locus\_tag=BN49\_RS11030] [protein=manganese-binding transcriptional regulator MntR] [protein\_id=WP\_004176765.1] [location=1967373..1967846] [gbkey=CDS]

MNRRAGKPITKKVTQLVNVEEHVEGFRQVREAHRRELIDDYVELISDLINEVGEARQVDMAARLGVSQPT

VAKMLKRLASVGLIEQIPWRGIFLTPEGEKLAQESRERHQIVENFLLAIGVSPEIARRDAEGMEHHVSEE

TLAMFLKFTQTQGSQEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002895863.1\_1911 [locus\_tag=BN49\_RS11035] [protein=anion transporter] [protein\_id=WP\_002895863.1] [location=1967843..1968955] [gbkey=CDS]

MTLPFVQSLLRDRFLHLLLIIACVLSAIVPFVPASWPAAIDWHTIVTLSGLMLLTKGIELSGYFDVLGRK

MARRFVTERQLAIFMVLAAALLSTFLTNDVALFIVVPLTLTLKKWCAIPVNRLIIFEALAVNAGSLLTPI

GNPQNILLWGRSGLSFFGFIGQMLPLAAAMMLTLLALCWFCFPAKRLSYQSSDRAPSWQPKLVWSCLGLY

VVFLTALEMNQALWGLALVLLGFLVLARAVIVHVDWSLLLVFMVMFIDVHLLTQLPALHQVLSGVGTLSG

GGLWLTAIGLSQVISNVPSTILLLNYVPPSILLAWAVNVGGFGLLPGSLANIIALRMASDRRIWWRFHLY

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>lcl|NZ\_FO834906.1\_prot\_WP\_004223813.1\_1912 [locus\_tag=BN49\_RS11040] [protein=glycoside hydrolase family 1 protein] [protein\_id=WP\_004223813.1] [location=1969125..1970501] [gbkey=CDS]

MKNRLPADFLWGNSVSSMQTEGAWNEGGKGMSVYDIRQPAEFASDWKVATDSYHRYREDFDLMQDLGMNC

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RYGQKMIACYGDKVKYWLTFNEQNLYHSPEAFLISGYLQGEKTLRELYLIQHHVMMAHVHLTHYLHQTKP

QCLMGGMLAHALVYPATCKPRDILCAQQLDEFLNQNLLRAYAGEGYSPEVMHFVAAEGFDDIYRPEDLAL

MATVKVDYLAFSYYASRTLNSDAIPPGTAVNNYMLFGNQDNPFLKATEWNWQIDPLGFRTIITRYYNDWR

LPVFPIENGIGVIESWDGEHPIADDYRIAYHRDHINAMKAAIFEDGAQVIGYLGWGLIDILSSQGDMRKR

YGVVYVNRENHDLKDLRRVPKKSYAWLKQVFRSNGEAM

>lcl|NZ\_FO834906.1\_prot\_WP\_004151705.1\_1913 [locus\_tag=BN49\_RS11045] [protein=GntR family transcriptional regulator] [protein\_id=WP\_004151705.1] [location=1970570..1971286] [gbkey=CDS]

MTAKYLQIAREIKKRIISQQYPASAPLPDQFALAAEFSTSRMTIQQAMRQLIVEGLIYTRKGQGTFVRKN

FLQLSQWELPGSDYFGATKTWEHLGEVQSEVVRFAVRFPSDKEQSSLLIDADAPVYDFVRLRLLNGEPVS

LDLTVMPVGLVPGLTKSHLEGSVFRYVQETLGLKLMGSYRVVRAMKPGELDKQHLHCEPTDPVLEVEQVI

YLEDGTPLEYAHCHYRYDHGGIILVNNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002895871.1\_1914 [gene=ldtB] [locus\_tag=BN49\_RS11050] [protein=L,D-transpeptidase] [protein\_id=WP\_002895871.1] [location=complement(1971431..1972345)] [gbkey=CDS]

MKLSTLLAAAFAIVGFCNTASAVTYPLPTDGSRLVGQNQVITIPDDNKQPLEYFAAKYQMGLSNMLEANP

GVDTYLPKGGSVLNIPQQLILPDTVHEGIIINSAEMRLYYYPKGTNTVIVLPIGIGQLGKDTPINWTTKV

ERKKAGPTWTPTAKMHAEYAAAGNPLPAVVPAGPDNPMGLYALYIGRLYAIHGTNANFGIGLRVSHGCVR

LRNDDIKFLFENVPVGTRVQFIDEPVKATTEPDGSRYIEVHNPLSTTEAQFQGGEIVPITLTQPVQAVTS

QSDVDQNVVEQAIQNRSGMPVRLN

>lcl|NZ\_FO834906.1\_prot\_1915 [locus\_tag=BN49\_RS11055] [protein=tyrosine-protein phosphatase] [pseudo=true] [location=complement(1972546..1973461)] [gbkey=CDS]

MPANDTLFTACGKFHRGACAKVFVR\*AGNPRSNGYSVRIYKESHDQQPIATPGFFIPAGRHQFSRPGRPA

CRRRTPRPQRQAIAIRRAKPVNGGGSQPPRYFAAQPGARLSRPRRGSPYSGQA\*PAYPLSQRAGQSAGER

G\*CEGHRAECRPP\*RAERRAVYAATLPPAAV\*QPGLSPARRLADHAF\*RRFTATLRGWQRSYRHRLRVNA

VRRRLRQRNGDGGVSPYPRHADAGGGLDVGAARQRPHCPGAPKPGGYFDGKRVLSRRRAVGYSPALWHRR

RLAGGRVPAYRAGSRRAAGPAAGRV

>lcl|NZ\_FO834906.1\_prot\_WP\_002895876.1\_1916 [locus\_tag=BN49\_RS11060] [protein=ABC-F family ATPase] [protein\_id=WP\_002895876.1] [location=1973511..1975103] [gbkey=CDS]

MLVSSNVTMQFGSKPLFENISVKFGGGNRYGLIGANGSGKSTFMKILGGDLEPTLGNVSLDPNERIGKLR

QDQFAFEAFTVLDTVIMGHGELWEVKQERDRIYALAEMSEEDGYKVADLEVKYGEMDGYSAEARAGELLL

GVGIPVEQHYGPMSEVAPGWKLRVLLAQALFSNPDILLLDEPTNNLDIDTIRWLEQTLNDRDSTMIIISH

DRHFLNMVCTHMADLDYGELRVYPGNYDEYMTAATQARERLLADNAKKKAQIADLQSFVSRFSANASKSR

QATSRARQIDKIKLEEVKASSRQNPFIRFEQDKKLFRNALEVEALTKGFDEGPLFKNVNLLLEVGEKIAI

LGANGVGKSTMLKTLVGELQPDNGSVKWSENAQIGYYAQDHEYEFENDLTVFEWMSQWKQEGDDEQAVRS

ILGRLLFSQDDIKKPAKVLSGGEKGRMLFGKLMMQKPNILVMDEPTNHLDMESIESLNMALEMYQGTLIF

VSHDREFVSSLATRVLEITPDRVIDFSGNYEDYLRSKGIE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529855.1\_1917 [locus\_tag=BN49\_RS11065] [protein=glycoside hydrolase family 31 protein] [protein\_id=WP\_016529855.1] [location=complement(1975237..1977600)] [gbkey=CDS]

MKTLKHWSLHQQLEHHVELTVDGQHTLCLYVLEENLFRVLLKRQGQLALDRTWSIAPQQDVPWEGRARDD

LSGFSLPAWQLAQEGDTLTIATRQLRVTVHQPLWLEWSYRDEAGEWQPLANDRPTSAYLANAHGDGVAHY

LSRRKDERFYGLGEKAGDLQRTGKRYEMRNLDAMGYNAVSTDPLYKHIPFTITQRSDISYGLFYDNLSSC

WLDLGNEIDNYHTAYRRWQAEAGDIDYYLFTGKQVLDVTKAFVRLTGKTLFGPKWSLGYSGSTMHYTDAP

DAQNQLMNFIRLCEQHAIPCDSFQLSSGYTSINGKRYVFNWNYDKVPQPKVMSQSFHDAGLKLAANIKPC

LLQDHPRYGEVAERGLFIRDSQTDAPERSSFWDDEGSHLDFTNPQTVAWWQEGVTTQLLEMGIDSTWNDN

NEYEVWDGEARCYGFGREIAIKHIRPVMPLLMMRASLEAQQRFAPQKRPYLISRSGCAGMQRYVQTWSGD

NRTNWDTLRYNIRMGLGMSLSGLFNVGHDVGGFSGDKPEPELFVRWVQNGVMHPRFTIHSWNDDQTVNEA

WMYPAITPAIRSAIELRYRLLPYLYTLLWQAHADDEPMLRPTFLDHQHDAQTFAECDDFLLGRDLLVASV

VEPGARQREVWLPDNQAGWYDFYSHQWFAGGQWVTLDAPLEKLPLLVRAGAGLPLSERISHVDAQKDDSR

ELQLFPLKGTGSTRGLLFEDDGESWGYKQGDALWLEWEMTCSASSINLDINARGNYRPAWKALKLSLPVG

EKRKLLVNGVEGTEWRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002895884.1\_1918 [locus\_tag=BN49\_RS11070] [protein=MFS transporter] [protein\_id=WP\_002895884.1] [location=complement(1977616..1978917)] [gbkey=CDS]

MSQGLNNDIAVSKTRRVVKNLRWWVLVLFLLGVTVNYITRNSLGIIAPELKATLGITTEQYSWIVGAFQL

AYTIFQPLCGWLIDVIGLKLGFMICATLWALACIAHAGAGSWLHLAMLRFFMGGAEAAATPANAKTIGEW

FPKSERPIAAGWAGVGFSIGAMLAPPIIYFAHASFGWQGAFMFTGALALLWVVLWWAFYQTPEKHPNLSK

SELEYIKQDNEAPPVKQPFFTALKTVSKNKRFYGIAIPAFMAEPAWAVLSFWVPLYLAKEHGMDLKQIAM

FAWLPFLAADLGSVVSGYLTRLYVRWFGCTRVNSVIASSVTGAFLMLSLALVAITRDPYITIILISIGGF

GHQIISCMLSALVVESFDKGQMATVNGMRGSAAWIASFLFSLLIGVTADKIGFNPLFIAMGFFDLIGAVF

LVAFIAERRAKRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004219745.1\_1919 [locus\_tag=BN49\_RS11075] [protein=LacI family transcriptional regulator] [protein\_id=WP\_004219745.1] [location=1979159..1980289] [gbkey=CDS]

MCFGDYENSFIFQSELDHKMDKKLRVAEIAARTGLSPSTVSRVLAGKANTSDKARRAVLDCARELGVMQG

LAAGRLLLNHLLVFAPQRAFDERSDIFYYRVIQSINNALAAHEVRLRYCALDENDSDANLFLARMNEPET

QAAVLLGIDDPHIHGLAADLGKPCVLINCRDEGMRLPSIAPDHRLIGQCAARYLFDMGHRAVMNVMCLRR

YTMELRLGGIQEAWRARNLRFTASRDLISVANFSARETEEQVGAWLDGLQGRPLPTAFLVGGDFMAAGTV

SALQKRGLRVPQDVSVMSIDGFNLAAIQEVPLTAVHVPRDELGSEAVHLLQQRLLRPEAPHGSLLLHGTL

VVRDSVRRIRPGKGHTAVEPQGLYDD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529964.1\_1920 [locus\_tag=BN49\_RS11080] [protein=DUF1479 domain-containing protein] [protein\_id=WP\_016529964.1] [location=complement(1980286..1981551)] [gbkey=CDS]

MAALPTHETLPADHKAAIRQMKQALRAQIGDVQAVFDKLSARISERLQEIETLKAAGQEVWPTVPFRDIA

EGTVSDEQRAAIKRRGCAVIKGHFPREQALAWDTAMLEYLDRNHFDDVYKGPGDSFFGSLEASRPEIYPI

YWSPSQMQARQSDEMAAVQSFLNRLWRFEQNGKRWFDPDVSVIYPDRIRRRPPGTTSKGLGAHTDSGALE

RWLLPAYQQVFANVFNGNIDAYDPWDAAHRTEVEEYTVDNTTKCSVFRTFQGWTALSDMIPGQGLLHVVP

IPEAMAYVLLRPLLDDVPEDELCGVAPGRVLPISEQWHPLLIKALSSIPALNAGDSVWWHCDIIHSVAPV

ENQQGWGNVMYIPAAPMCEKNLAYAQKVKIALEKGASPGDFPREDYEASWQGRFTLEDLNIHGKRALGML

V

>lcl|NZ\_FO834906.1\_prot\_WP\_016529963.1\_1921 [locus\_tag=BN49\_RS11085] [protein=Cof-type HAD-IIB family hydrolase] [protein\_id=WP\_016529963.1] [location=complement(1981691..1982506)] [gbkey=CDS]

MTVKVIVTDMDGTFLNDAKTYDRSRFLAQFAQLQQRGIEFVVASGNQYYQLISFFPEIREQISFVAENGA

LVYEHGTQLFHGELTRHESQVVIGELLKDPQLNFVACGLQSAYVSDKAPDAFVELMSKHYHRLHRVSDYH

AIDDTLFKFSLNLPDSEIPQLIDKLHVSLDGIMKPVTSGFGFVDLIIPGLHKANGISRLLKRWDLSPQQC

VAIGDSGNDAEMLKLVKYAFAMGNAADSIKAIAGYATDDNNHDGALNVIQAVLDNTPPFNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004179127.1\_1922 [locus\_tag=BN49\_RS11090] [protein=formate C-acetyltransferase/glycerol dehydratase family glycyl radical enzyme] [protein\_id=WP\_004179127.1] [location=complement(1982683..1985115)] [gbkey=CDS]

MTTLKLNTLSARIQAHKMALVHIVKPPVCTERARHYTEMYQRHLDKPIPVRRALALAHHLAERTIWIKHD

ELIVGNQASEVRAAPIFPEYTVSWIEKEIDDLADRPGAGFSVSEENKRVLHEVCPWWRGQTVQDRCYGMF

TDEQKALLATGIIKAEGNMTSGDAHLAVNYPLLLEKGLDGMRAKVAERRSRINLTVLEDLHGEQFLKAID

IVLEAVSDHSKRFAALAREMATAESRESRRHELLTIAENCDVIAHEPPKTFWQALQLCYFIQLILQIESN

GHSVSFGRMDQYLYPYYRRDVELQQSLDREQAIELLHSCWLKLLEVNKIRSGSHSKASAGSPLYQNVTIG

GQNLVDGKPQDAVNPLSYAILESCGRLRSTQPNLSVRYHAGMSNDFLDACVQVIRCGFGMPAFNNDEIVI

PEFIKLGIEPQDAYDYAAIGCIETAVGGKWGYRCTGMSFINFARVMLATLEGGRDATSGQVFLPQEHALS

KGNFANFDQVLADWDRQIRYYTRKSIEIEYVVDTMLEENVHDILCSALVDDCIERAKSIKQGGAKYDWVS

GLQVGIANLGNSLAAVKKLVFDQGAIGQQELAKALAEDFDGLTHEQLRQRLINGAPKYGNDDDSVDQLLA

RAYQTYIDELKQYHNPRYGRGPIGGNYYAGTSSISANVPFGAQTMATPDGRKAHTPLAEGASPASGTDHL

GPTAVISSVGKLPTGAILGGVLLNQKLNPSTLENESDKQKLMVLLRTFFEVHKGWHIQYNIVSRDTLLEA

KKHPDQYRDLVVRVAGYSAFFTALSPDTQDDIIARTEHTL

>lcl|NZ\_FO834906.1\_prot\_WP\_004176738.1\_1923 [locus\_tag=BN49\_RS11095] [protein=glycyl-radical enzyme activating protein] [protein\_id=WP\_004176738.1] [location=complement(1985120..1986019)] [gbkey=CDS]

MIFNIQRYSTHDGPGIRTVVFLKGCSLGCRWCQNPESRARSEDLLYDSRLCLPGCELCQQAAPAVITRTL

DGLIIHRQNVNDSHIAALRDCCPTTALTVCGEEKSVEEIMATVLRDKPFYDRSGGGITLSGGEPFMNPTL

AQALFEASHQAGIHTAVETCLHVPWKYIEPSLPFVDLFLADLKHVDEAVFQQWTDGSARRVLDNLQRLAQ

AGKKMIIRVPLIQGFNASEADIAAITDFAADRLQVSEIHYLPYHTLGMNKYQLLSQPYTAPDKPLDAPEL

LAFAQDYAQSKGLTAILRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004176736.1\_1924 [gene=moeB] [locus\_tag=BN49\_RS11100] [protein=molybdopterin-synthase adenylyltransferase MoeB] [protein\_id=WP\_004176736.1] [location=complement(1986174..1986929)] [gbkey=CDS]

MTVELSDEEMLRYNRQIVLRGFDFDGQERLKAARVLVVGLGGLGCAAAQYLAAAGVGQLTLLDFDTVSLS

NLQRQTLHSDATLGQPKVDSAREALARINPHVRLVPLNALLDEAALAAQIADHDLVLDCTDNVAIRNQLN

VGCFQHKTPLVSGAAIRMEGQISVFTYQDGEPCYRCLSRLFGENALTCVEAGVMAPLVGTIGSLQAMEAI

KLLSGYGTPASGKIVIYDAMTCQFREMRLMRHPQCEVCGSH

>lcl|NZ\_FO834906.1\_prot\_WP\_032104926.1\_1925 [gene=moeA] [locus\_tag=BN49\_RS11105] [protein=molybdopterin molybdotransferase MoeA] [protein\_id=WP\_032104926.1] [location=complement(1986929..1988164)] [gbkey=CDS]

MDFTAGLMPLDTALAQMLDRITPLNATETVPLLQAFSRVTAHDIVSPLDVPGFDNAAMDGYAVRLNDLRN

GAALPVAGKAFAGQPFNDAWPSGTCIRIMTGAPVPEGCDAVVMQEETEQTEAGVRFIAPVKAGQHIRRRG

EDIAHGAVVFPAGTPLTVAELPVLASLGIAEVEVVRKVRVAVFSTGDELQLPGQPLGDGQIYDTNRLAVH

LMLQQLGYEVINLGIIPDDPAKLRDAFIAADQQADVVISSGGVSVGEADYTKTILEELGEIGFWKLAIKP

GKPFAFGKLSSSWFCGLPGNPVSATVTFCQLVQPLLAKLSGKHGPLQAPRLRVRAATRLKKSPGRLDFQR

GILQRNPDGELVVNTTGHQGSHIFSSFSLGNCFIVLERERGHVEAGEWVEVEPFSHLFGGL

>lcl|NZ\_FO834906.1\_prot\_WP\_004147725.1\_1926 [gene=iaaA] [locus\_tag=BN49\_RS11110] [protein=beta-aspartyl-peptidase] [protein\_id=WP\_004147725.1] [location=1988400..1989341] [gbkey=CDS]

MGKAVIAIHGGAGAISRAQMTPEREREYVAALSTIVESGQKMLAAGASALDAVTEAVRLLEECPLFNAGM

GAVFTRDQTHELDACVMDGYSLQAGAVAGVKHLRNPVLAARLVLEKSPHVLLIGEGAENFAISHGMARVD

NDLFSTPERLLQLQEAKAGGEIILDHHAAPLDERQKMGTVGAVALDLAGNLAAATSTGGMTNKLPGRVGD

SPLPGAGCYANNASVAVSCTGTGEVFMRTLAAYDIAALMEYGQLSLYSACERVVMEKLPALGGSGGLIAV

DREGNVVLPFNSEGMYRAWCYAGDTPTIGIYRE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042951.1\_1927 [gene=gsiA] [locus\_tag=BN49\_RS11115] [protein=glutathione ABC transporter ATP-binding protein GsiA] [protein\_id=WP\_046042951.1] [location=1989359..1991218] [gbkey=CDS]

MSQTHETDTCEVLVVRNLNVAFRQQDAPEVQAVRQLSFSLRRGETLAIVGESGSGKSVTALALMRLLDAA

SSEVNSEGLWLRRRNRQVIALNEQTDAEMRRVRGADLAMIFQEPMTSLNPVFTIGEQIAESLRLHQGLGR

EEALRAAKKMLDQVRIPQAEEMLSRYPHQLSGGMRQRVMIAMALSCRPAVLIADEPTTALDVTIQAQILQ

LIAVLQKEMAMGVIFITHDMGVVADIADRVLVMYRGEAVETGSVEEIFRSPQHPYTQSLLAAVPRLGEMR

GQDLPRRFPLPGQPLAESETPDTVVAGEPILQVRDLVARFPVRGGLLNRVTREVHAVEKVSFDLWPGETL

SLVGESGCGKSTTGRALLRLVETQGGTITFDGQRIDTLAGGKLQALRRNIQFIFQDPYASLEPRQTVGDS

IMEPLRVHGLLRGEAARERVAWLLKRVGLQPEHAWRYPHAFSGGQRQRICIARALALNPKVVIADESVSA

LDVSIRAQIINLMLDLQREMGIAFLFISHDMAVVERISHRVAVMYRGRIVEIGPRRAVFENPQHPYTRKL

MAAVPVADPGHRHPQRVLLSDDVPGNIYKRGEEIASVPLQQVGPGHFVARESADVLGRT

>lcl|NZ\_FO834906.1\_prot\_WP\_016529999.1\_1928 [gene=gsiB] [locus\_tag=BN49\_RS11120] [protein=glutathione ABC transporter substrate-binding protein GsiB] [protein\_id=WP\_016529999.1] [location=1991251..1992792] [gbkey=CDS]

MTQPVSRKWWLALSIAAALASAPAFAAKDVVVAVGSNFTTLDPYDANDTLSQAVAKSFYQGLFGLDKEMK

LQNVLAESYTVSPDGLVYTVKLHSGVKFQDGTDFNAEAVKANLDRASNPDNHLKRYNLYKNIASTEAVDP

TTVKITLKQPFSAFINILAHPATAMISPAALKKYGKDIGFHPVGTGPYKLDTWNQTDFVKVSKFDGYWQP

GLPKLDSITWRPVVDNNTRAAMLQTGEAQFAFPIPYEQAPLLAKNSKLELVASPSIMQRYISMNVTQKPF

DNPKVREAINYAINRQALVKVAFAGYATPATGVVPPSIAYAQTYPAWPYDPAKARQLLKEAGYPNGFSTT

LWPSHNHSTAQKVLQFTQQQLAQVGIKAQVTAMDAGQRAAEVEGKGQKESGVRMFYTGWSASTGEADWAL

SPLFASQNWPPTLFNTAFYSNPQVDNALSEALKTTDPQQKTKLYKEAQDIIWKESPWVPLVVEKLVSAHS

KNLTGFYIQPDTGFSFEQADLTP

>lcl|NZ\_FO834906.1\_prot\_WP\_002892997.1\_1929 [gene=gsiC] [locus\_tag=BN49\_RS11125] [protein=glutathione ABC transporter permease GsiC] [protein\_id=WP\_002892997.1] [location=1992839..1993759] [gbkey=CDS]

MLNYVIKRLLGLIPTLLIVAVLVFLFVHMLPGDPARLIAGPEADAQVVAMVRQQLGLDQPLHVQFWHYIT

NVLRGDFGISMASRRPVASEIASRFMPTLWLTLASMSWAVLFGMAAGIAAAVWRNRWPDRLGMALAVSGI

SFPAFALGMLLMQVFSVELGWLPTVGADSWRHYILPSLTLGAAVAAVMARFTRASFVDVLHEDYMRTARA

KGVSETRVVLKHGLRNAMIPVVTMMGLQFGFLLGGSIVVEKVFNWPGLGRLLVDSVEMRDYPVIQAEVLL

FSLEFILINLVVDVLYAAINPAIRYK

>lcl|NZ\_FO834906.1\_prot\_WP\_004147729.1\_1930 [gene=gsiD] [locus\_tag=BN49\_RS11130] [protein=glutathione ABC transporter permease GsiD] [protein\_id=WP\_004147729.1] [location=1993761..1994672] [gbkey=CDS]

MRLLNWRRQAALNAMPGIRPGEIHTPWHEFWRRFRRQPVAMGAGIFVLLLIAVAIVAPWIAPYDAENYFD

YDRLNEGPSLVHWFGVDSLGRDIFSRVLVGAQISLAAGVLAVLIGAAIGTVLGLLAGYYEGWWDRLIMRL

CDVLFAFPGILLAIAVVAVMGSGMANVIIAVAIFSIPAFARLVRGNTLVLKQQTFIESARSIGASDATIL

FNHILPGTVSSIVVYFTMRIGVSIISAASLSFLGLGAQPPTPEWGAMLNEARADMVMSPHVALFPAVAIF

VTVLAFNLLGDGLRDALDPKLKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004141985.1\_1931 [gene=rimO] [locus\_tag=BN49\_RS11135] [protein=30S ribosomal protein S12 methylthiotransferase RimO] [protein\_id=WP\_004141985.1] [location=complement(1995373..1996698)] [gbkey=CDS]

MSNVTHQPKIGFVSLGCPKNLVDSERILTELRTEGYDVVPTYDNADMVIVNTCGFIDSAVQESLEAIGEA

LKENGKVIVTGCLGAKEDQIREVHPKVLEITGPHSYEQVLEHVHHYTPKPKHNPFLSLVPEQGVKLTPRH

YAYLKISEGCNHRCTFCIIPSMRGDLVSRPIGEVLAEAKRLADAGVKELLVISQDTSAYGVDVKHRTGFH

NGMPVKTSMVSLCEELAKLGIWVRLHYVYPYPHVDDVIPLMAEGKILPYLDIPLQHASPRILKLMKRPGS

ADRQLARIKQWREICPDLTLRSTFIVGFPGETEEDFQMLLDFLKEARLDRVGCFKYSPVEGATANELADQ

VPEEVKEERWNRFMQLQQQISAERLQEKVGREILVLVDEVDEEGAIGRSMADAPEIDGAVYLNGETRVKP

GDVVRVKVEHADEYDLWGTRV

>lcl|NZ\_FO834906.1\_prot\_WP\_004147732.1\_1932 [locus\_tag=BN49\_RS11140] [protein=oligosaccharide MFS transporter] [protein\_id=WP\_004147732.1] [location=complement(1996930..1998171)] [gbkey=CDS]

MTSGKRNYLLLSLFDFLYLFAWSSTMAFFVIWTTQHLGISATKTGLLYSVNAFIALLMQPFFGFISDKFG

LKKRLIWLLVALLLPVGPFFIYVYAPLLVHNFWFGALLGGIYLGIIFNSGCGVIDSYIDKISRRYQFEYG

RVRMWGSLGWAAAAWIVGKYIDSNPNLAFWLASLAIVIAAICFMLTKIELTDADVARSESLKVSHALELA

KNGQFWMLLLFTLFVTQIYDTYDQQFAQYFSLQFPTPEEGNRWYGILASIQVCGETLFLCLMPWFVNRTG

AKWALIIAGLIMSVRIVGSAVPLGPVWIGAVKMMHALEKPLILVSVFKFIAANFDHKLSSTVYLLVLFVA

SIATAIYSPLAGYLYDTIGFANTYLILGSVAGLFTLISIFTLQDKREPKKTGATPSAAINPAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004151712.1\_1933 [gene=bssR] [locus\_tag=BN49\_RS11145] [protein=biofilm formation regulator BssR] [protein\_id=WP\_004151712.1] [location=1998550..1998933] [gbkey=CDS]

MTVDRLYRHLLQKLINANIDIDAYLQLRKAKGYMSVSENDHLRDNLFELCREMRAQAPRLQNAISPEERD

VLRLAGESVAAAALCLMSGHHDCPLYIAVNVEKLERCLTGLTSNIHKLNKLAPITHA

>lcl|NZ\_FO834906.1\_prot\_WP\_004141981.1\_1934 [locus\_tag=BN49\_RS11150] [protein=PQQ-dependent sugar dehydrogenase] [protein\_id=WP\_004141981.1] [location=1999049..2000158] [gbkey=CDS]

MRPIPLLLILSALALPALSQAAVRVEVLQNRLAQPWGMAFLPDDQGILITLRGGELKRWQPGKGLSAPIA

GVPQVWANGQGGLLDVALAPDFAQSRRVWLSYAESDASGKAGTAVGYGRLSEDATQLTNFTVVFRQQPKL

SVGNHFGGRLVFDGKGYLFIGLGENNQRATAQDLSKLQGKVVRLTETGGVPPDNPFVGRADARPEIWAYG

IRNPQGMAMNPWSEALWLNEHGPRGGDEINIPQAGKNYGWPLATHGINYSGLPIPEAKGKTVPGTEPPLY

VWPVSPGVSGMAFYSAPTFPQWQHKLFIGALKETSLIVLAVDGNQVREEGRLLEARGKRIRDVRVGPDGY

LYVLTDESNGELLRLSPEA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530133.1\_1935 [locus\_tag=BN49\_RS11155] [protein=glutathione S-transferase family protein] [protein\_id=WP\_016530133.1] [location=complement(2000161..2000787)] [gbkey=CDS]

MITLWGRNNSTNVKKVRWVLEELDLPYQQILAGLEFGLNHDPEYLAMNPNGLVPLLKDDATGVVLWESNT

IIRYLAAQYGVDRLWLAAPAQRAQGEKWMDWSNGTLSPAHRPVLMGLVRTPPEQRDPAAIAAGISACEAL

FAMLDDELAKMPWLSGEQFGLGDIAVAPFVYNLLSILDNWQPRPHLQRWYQQISQRPAWREVVQIPVT

>lcl|NZ\_FO834906.1\_prot\_WP\_009485542.1\_1936 [locus\_tag=BN49\_RS30970] [protein=hypothetical protein] [protein\_id=WP\_009485542.1] [location=2002320..2002448] [gbkey=CDS]

MISFIKDIAPPSAECCGNRSPAEHGDQADPMERKVRALLLIS

>lcl|NZ\_FO834906.1\_prot\_WP\_004191175.1\_1937 [gene=dacC] [locus\_tag=BN49\_RS11165] [protein=serine-type D-Ala-D-Ala carboxypeptidase] [protein\_id=WP\_004191175.1] [location=2003101..2004303] [gbkey=CDS]

MMHDAFSLRGLAAGCALLFLVAPAVQAAEQLPDAPSIDARAWILMDYASGKVLSEGNADEKLDPASLTKI

MTSYVVGQAIKAGKIKLTDMVTVGRDAWATGNPALRGSSVMFLKPGMQVSVEDLNKGVIIQSGNDASIAI

ADYVAGSQDAFVSLMNGYAKKMGLTNTTFMTVHGLDAPGQFSTARDMALLTKAMIHDVPEEYAVHKEKEF

TFNKIRQPNRNRLLWSSNLNADGVKTGTTAGAGYNLVSSATQGDMRLIAVVLGTKTDRIRFNESEKLLTW

GFRFFETVTPIKPDATFVTQRVWFGDSNEAKLGAGEAGSITLPKGQLKNLKASYTLNQPQLTAPLEKGQV

VGTIDFKLNDKTIEQRPLIVMESVKEGGFFSRMIDFVLMKLHGWFGSWFS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151717.1\_1938 [gene=deoR] [locus\_tag=BN49\_RS11170] [protein=DNA-binding transcriptional repressor DeoR] [protein\_id=WP\_004151717.1] [location=complement(2004342..2005100)] [gbkey=CDS]

METRRDERISQLIQALKRSDKLHLKEAASLLGVSEMTIRRDLNGHSGPVVLLGGYIVLEPRSATHYLLSD

QKTRLVEEKRRAARHAAALLEAHQMAFFDCGTTTPWIIDAIDDALPFTGVCYSLNTFLALQEKPQCRAVL

CGGEFHASNAIFMPLSLEDTLSHLSPDIAFYSAAGIDCEQGATCYNLEELPVKHWAMRHARYHVLVVDHS

KFGKVRPARMGALAKFDVIASDICPDDELVALAKAQQISLLY

>lcl|NZ\_FO834906.1\_prot\_WP\_004141974.1\_1939 [gene=ybjG] [locus\_tag=BN49\_RS11175] [protein=undecaprenyl-diphosphate phosphatase] [protein\_id=WP\_004141974.1] [location=complement(2005202..2005795)] [gbkey=CDS]

MLENINYALFALLNATPASPQWAIEMAIFIAKDLILIVPLLVVTLWLWGPAQRQMVFKLMLALTISLTVS

WAIGHLYPHDRPFVAGVGYNFLHHAADDSFPSDHGTVSFTFALAFLFWHRLWSGALLMAIAAAIAWSRVY

LGVHWPLDMVGGLLAGMCGCLGAALIWHTFGPALYHQLQRLYRLCFSLPIRKGWVRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151718.1\_1940 [gene=kdeA] [locus\_tag=BN49\_RS11180] [protein=multidrug efflux MFS transporter KdeA] [protein\_id=WP\_004151718.1] [location=2006123..2007355] [gbkey=CDS]

MQNYSLSGRRLGRQALLFPLCLVLYEFSTYIGNDMIQPGMLAVVQEFQVGNEWVPTSMTAYLAGGMFLQW

LLGPLSDRIGRRPVMLTGVVWFIVTCLATLLAQTIEQFTLLRFLQGISLCFIGAVGYAAIQESFEEAVCI

KITALMANVALIAPLLGPLVGAAWVHVLPWEMMFVLFAVLAAISFFGLQRAMPETATRLGEKLSVKELGR

DYRLVLKNLRFVAGALATGFVSLPLLAWIAQSPVIIISGEQATSYEYGMLQVPIFGALIAGNLVLARLTA

RRTVRSLIIMGGWPIMFGLILSAAATVVSSHAYLWMTAGLSFYAFGIGLANAGLVRLTLFASEMSKGTVS

AAMGMLQMLIFTVGIELSKHAYELGGNGLFSLFNLLGGVLWLGLMIYFLKDKSVGNSQQG

>lcl|NZ\_FO834906.1\_prot\_WP\_004141971.1\_1941 [locus\_tag=BN49\_RS11185] [protein=Cof-type HAD-IIB family hydrolase] [protein\_id=WP\_004141971.1] [location=complement(2007393..2008205)] [gbkey=CDS]

MSIKLIAVDMDGTFLSDAKTYNRPRFLAQYQRMREQNIRFVVASGNQYYQLISFFPEIAHQIAFVAENGG

WVVSGNEDVFNCQLPVHHFNAVVDHLQTLPNIEIIACGKRSAYTLNRYNDALKTVAAKYYHRLELVDDFN

HLDDTILKFGLNVPDSLIPEIQPKLHAALGDMVTAVATGYGSIDLIIPGVHKANGLRILQQRWGIEDHEV

VAFGDSGNDIEMLQHAGFGFAMANAREDVKAVARYQAPHNNEEGVLQIIDKVLDREAPFA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042954.1\_1942 [locus\_tag=BN49\_RS11190] [protein=MFS transporter] [protein\_id=WP\_046042954.1] [location=complement(2008205..2009407)] [gbkey=CDS]

MTTQSSRRALQLRLWALFMFFFIPGLLMASWATRTPAIRDLLALSTAEMGVVLFGLSVGSMSGILCSAWL

VKRFGTRKVIRTTMSFAVLGMLVLSLALWVTSAPLFAFGLAIFGASFGSAEVAINVEGAAIEREMNKTVL

PMMHGFYSFGTLFGAGVGMAVTGFGLPAAPHILAAALVAILPIAIAIRAIPDGTGKNAAEVAHGEAKGLP

VWRDAQLLLIGVIVLAMAFAEGSANDWLPLLMVDGHGFSPTSGSLIYAGFTLGMTLGRFTGGWFIDRYSR

VAVVRGSAVMGALGIGLIIFVDNPWVAGISVLLWGIGASLGFPLTISAASDTGPDAPKRVSVVAITGYLA

FLVGPPLLGFLGEHFGLRSAMMVVLGLVIVAALVARAVAKPQSEPVMENS

>lcl|NZ\_FO834906.1\_prot\_WP\_004223846.1\_1943 [locus\_tag=BN49\_RS11195] [protein=TetR family transcriptional regulator] [protein\_id=WP\_004223846.1] [location=2009490..2010053] [gbkey=CDS]

MARRPNDPQRRERILQATLDTIAAHGIHAVTHRKIATCANVPLGSLTYYFSGIEALIEEAFSLFTAEMSA

QYQQGFVGVTNREQACDAIADLIFSAQVTTARNMELMYQLYAFCSSQPALKAVMQNWMRRSQQTLEQWFA

PDTARGLDAFIEGMTLHFVTDRAPLSKAAIRMMVGQLAGERAQEERR

>lcl|NZ\_FO834906.1\_prot\_WP\_004223848.1\_1944 [locus\_tag=BN49\_RS11200] [protein=hypothetical protein] [protein\_id=WP\_004223848.1] [location=complement(2010223..2010492)] [gbkey=CDS]

MNELQKQGAELRTKAKELALAVLAKHPDGQKNGKGIKQSEVFRLCGFDWGAKPKATSSNQQYWVVALLRE

LEEDGLVEQIKESGPWRLR

>lcl|NZ\_FO834906.1\_prot\_WP\_223271217.1\_1945 [locus\_tag=BN49\_RS31415] [protein=hypothetical protein] [protein\_id=WP\_223271217.1] [location=complement(2010737..2011363)] [gbkey=CDS]

MFNFYPDKTFSRTDVMSRPTPVPAANGIYFWWFKEIPSGVPTEGCITQNGYTLLYVGISPDKKGKPNSRA

NLRQRIKTHYSGNAEGSTLRRTLGVLLATESNFPLRRVGSGKRMTFTHPGEQWLDRWMDKNARVYWIEDD

EPWVLEEMLIATISLPLNLQGNKHTFKPILSSMRSKAIAEAQTMEIADETGFSRSVVTEMIKQAAEVE

>lcl|NZ\_FO834906.1\_prot\_WP\_123806901.1\_1946 [locus\_tag=BN49\_RS30380] [protein=hypothetical protein] [protein\_id=WP\_123806901.1] [location=2011439..2011696] [gbkey=CDS]

MMSLRVTTQQVDTWKKRIQRDGLKGSTYFCQQSGGVWVSASADHQAICQKVLGKDSGTSSLASYLRWDDV

GAVALVDLLYAIETA

>lcl|NZ\_FO834906.1\_prot\_WP\_074422434.1\_1947 [locus\_tag=BN49\_RS11210] [protein=tyrosine-type recombinase/integrase] [protein\_id=WP\_074422434.1] [location=complement(2011880..2012860)] [gbkey=CDS]

MRKQFATKGEALAFERHTMEETEAKPWLGESVDRRTLKDVVELWFKLHGKSLTAGQHVYDKLLLMVDALG

NPIATDLTSKMFAHYRDKRLTGEIYFSEKWKKGASPVTINLEQSYLSSVFSELSRLGEWSYPNPLENMRK

FTIAEKEMAWLTHEQIVELLADCKRQDPILALVVKICLSTGARWREAVNLTRSQVTKYRITFVRTKGKKN

RSIPISKELYEEIMALDGFNFFTDCYFQFLSVMGKTSIVLPRGQLTHVLRHTFAAHFMMSGGNILALQKI

LGHHDIKMTMRYAHLAPDHLETALRFNPLATLPSGDKVAAAVGITP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529336.1\_1948 [locus\_tag=BN49\_RS11215] [protein=hypothetical protein] [protein\_id=WP\_016529336.1] [location=complement(2013019..2014008)] [gbkey=CDS]

MNSENKKNENNDYVEKVNCEWKDLYNILNENLHKFNENERAYLVDLLKKGELDKFREYYWKLAQQEKMNY

SDKAGDIFINENNKIDELIKEQKHLREIMRSYTKRLLEAEESKATLHLRNENLEKLNSEKETIIEQAVSR

IKQLEASNSELQSRVQQERIDEKIPGYVDSVKSELSSDDLYFIKMSQVWAFTGCIFGLLAVCASFYTLYA

TIDFNNVKGFELFYFFTRGLIGISILSWLAYICLGNSKKYTHESILRKDRRHALMFGQVFLQIYGSTSTK

EDAVLVFKDWNMSGNSAFSDKTELPPGIQSLWDSTKEKLKPSTAEKAQE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529335.1\_1949 [locus\_tag=BN49\_RS28910] [protein=phage repressor protein CI] [protein\_id=WP\_016529335.1] [location=complement(2014019..2014957)] [gbkey=CDS]

MSTQKNTFRHVSESLKTSIMQNRGGQKVIERILVAYGFTSRQAFCNHLGISQSTMANRYARDTFPADWVI

ICSIETGASIDWLASGISCESSSVLLNDERLAHTKSDDLDRTNSIAQKFPIETSINPNKGGKAAIDRLVA

AYGFSTRQALANHLQVSKSTVANRYLRDTFPSDWIIQCALETGTSLLWLTNGNGPKFIDNSSSVAQLKHQ

TIIDGKLHDEGYLAFDKTLIPSGLKKPIGVTAEGKTFIADTEYDDVSDGSWLIEIEGKVSLRKLTRIPVG

KVKITSDTTDFVCKLEDITTIAKCCCVFSKEI

>lcl|NZ\_FO834906.1\_prot\_WP\_000188448.1\_1950 [locus\_tag=BN49\_RS28915] [protein=hypothetical protein] [protein\_id=WP\_000188448.1] [location=2015046..2015267] [gbkey=CDS]

MTPNISITLNTPHVTIERYSELTGLSIDTINDMLADGRIPRHRLRKDKKREKVMINLAALTVDALTDCNV

VFN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529334.1\_1951 [locus\_tag=BN49\_RS11225] [protein=phage regulatory CII family protein] [protein\_id=WP\_016529334.1] [location=2015300..2015809] [gbkey=CDS]

MFDYQVSKHPHFDEACRAFALRHNLVQLAERAGMNVQILRNKLNPSQPHLLTAPEIWLLTDLTEDSTLVD

GFLAQIHCLPCVPINEVAKEKLPHYVMSATAEIGRVAAGAVSGDVKTSAGRRDAISSINSVTRLMALAAV

SLQARLQANPAMASAVDTMTGLGASFGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_000956190.1\_1952 [locus\_tag=BN49\_RS11230] [protein=DUF2724 domain-containing protein] [protein\_id=WP\_000956190.1] [location=2015817..2016017] [gbkey=CDS]

MLTKEPSFASLLVKQSPAMHYGHGWIMGKDGKRWHPCRSQDELLAELSTKKRGNKWLLKALRRLFH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529332.1\_1953 [locus\_tag=BN49\_RS11235] [protein=DUF5347 domain-containing protein] [protein\_id=WP\_016529332.1] [location=2015981..2016322] [gbkey=CDS]

MAIEGAAATVPLSPGERLNGLNHIAELRAKVFGLNIESELERFIKDMRDPRDINNEKNKRALAAIFFMAK

IPAERHSISINELTTDEKRELIKAMNHFRAVVSLFPRRLTMPN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529331.1\_1954 [locus\_tag=BN49\_RS11240] [protein=DUF2732 family protein] [protein\_id=WP\_016529331.1] [location=2016390..2016623] [gbkey=CDS]

MRNIETLTTKTGPDDAWLNILLTEARLEERRARAEAMAARLDSLACHISSRQLNHVEAAELLRVTAEAIQ

NEAQEIH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529330.1\_1955 [locus\_tag=BN49\_RS11245] [protein=TraR/DksA family transcriptional regulator] [protein\_id=WP\_016529330.1] [location=2016623..2016850] [gbkey=CDS]

MADAMDLVQQRVEEERQRHIRAARAKTPGMSRVLCIECEAPIPPARRRAIPGVQLCITCQEIAELKGKHY

NGGAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529329.1\_1956 [locus\_tag=BN49\_RS11250] [protein=DNA adenine methylase] [protein\_id=WP\_016529329.1] [location=2016847..2017704] [gbkey=CDS]

MSTILKWAGNKTAIMSELKKHLPAGPRLVEPFAGSCAVMMETDYPSYLVADINPDLINLYKKVAADCESF

IFRARFLFEIANREVAYYNIRQEFNYSTEITDFMKAVYFLYLNRHGYRGLCRYNKSGHFNIPYGNYKNPY

FPEKELRTFAEKAQRATFVCASFDETLAMLKAGDVVYCDPPYDGTFSGYHTDGFTEDDQYHLASVLEHRS

SEGHPVIVSNSDTSLIRSLYRNFTHHYIKAKRSIGVAAGESKSATEIIAVSGPRCWVGFDPSRGVDSSAV

YGVRA

>lcl|NZ\_FO834906.1\_prot\_WP\_046042959.1\_1957 [locus\_tag=BN49\_RS11255] [protein=replication endonuclease] [protein\_id=WP\_046042959.1] [location=2017701..2020115] [gbkey=CDS]

MSHADMNNCSGFNEAAAAFSWNSPKKAINPYLDPAEVAPVSALSNLITLYAADNEQEQLRREALSDQVWE

RYFFNASRDPVQREMEQDKLISRAKLAHEQQRFNPDMIILADVNAQPSHISKPLMQRIEYFSSLGRPKAY

SRYLRETIKPCLERLEHVRDSQLSTSFRFMASHEGLDGLLILPEMSQDQVKRLSTLVAAHMSMCLDAACG

DLYATDDVKPEEIRKTWEKVAAETLRLDVIPPAFEQLRRKRNRRKPVPYELIPGSLARMLCADWWYRKLW

KMRCEWREEQLRAVCLVSKKASPYVSYEAVMHKREQRRKSLEFFRSHELVNEDGDTLDMEDVVNASSTNP

AHRRNEMMACVKGLELIAEMRGDCAVFYTITCPSRFHSTLNNGRPNPTWTNATVRQSSNYLVGMFAAFRK

AMHKAGLRWYGVRVAEPHHDGTVHWHLLCFMRKKDRRAITALLRKFAIREDREELGNNTGPRFKSELINP

CKGTPTSYIAKYISKNIDGRGLAGEISKETGKSLRDNAEYVNAWASLHRVQQFRFFGIPGRQAYRELRLL

AGQVARQQGDKKAGAPVLDNPRLDAILAAADAGCFATYIMKQGGVLVPRKYHLIRTAYEINEEPTAYGDH

GIRIYGIWSPIAEGKICTHAVKWKMVRKAVDVQEAAADQGACAPWTRGNNCPLAENLNQQGKDKSADGDT

RTEITRMDDKELHDYLHSMSKKERRELAARLRLVKPKWRKDYKQRITEHQRQQLVYELKSRGFDGSEKEV

DLLLRGGSIPSGAGLRIFYRNQRLQEDDKWRNLY

>lcl|NZ\_FO834906.1\_prot\_WP\_001154434.1\_1958 [locus\_tag=BN49\_RS11260] [protein=hypothetical protein] [protein\_id=WP\_001154434.1] [location=2020269..2020457] [gbkey=CDS]

MQDYFLESLKLQRIDFFLKLVAASECSDEEKGLALQWVSELTDELMAKIRTHEYNRSMDVIS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529212.1\_1959 [locus\_tag=BN49\_RS11265] [protein=DinI family protein] [protein\_id=WP\_016529212.1] [location=2020468..2020701] [gbkey=CDS]

MRIEIMIDKEQKISQSTLDALESELYRNLRPLYPKTAIRIRKGSANGIELTGLKLDEDKQRVMEIMQQVW

EDDSWLH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529211.1\_1960 [locus\_tag=BN49\_RS11270] [protein=hypothetical protein] [protein\_id=WP\_016529211.1] [location=2020988..2021206] [gbkey=CDS]

MSSIAALKLGNPVERLARVLKENQDKLNLSKDGFVSVDLSNEEAMKAIRDQMDKLEGIKTSTVKAKYYYR

TR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529210.1\_1961 [locus\_tag=BN49\_RS11275] [protein=hypothetical protein] [protein\_id=WP\_016529210.1] [location=2021206..2022048] [gbkey=CDS]

MATLLLAVILVSGFIYVNLSLSTRYRYKRSNGWDAYFFVAAWGIVFFLAGGFLTFALNISGGFRWFSNAL

NLTPDSFNGMLSTTTDKPQRINEIKQIAWVVISIVLAALFGWLNKRRTSKGDRRWDALAKAVGNNAFESL

LMEASARQFPIIATLSSRKIYVGLVTCPALENGLSEHLEILPLLSGYRDKDDLTINITTNYHQHYLDSGV

INGMSRLNIQDFRVLLPKDEVETISFFDTETYNKFKENEARDRKDCRKLGGKKPSARRRKTAGDAEQGSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529209.1\_1962 [locus\_tag=BN49\_RS11285] [protein=TIR domain-containing protein] [protein\_id=WP\_016529209.1] [location=2022264..2023697] [gbkey=CDS]

MIQPKVFISYSWSSKTHQQHIKDMAERLAADGVETVIDIYDLKEGDDKNYYMERMVQDETVTHVLVICDK

KYSEKADLRKDGVGVESMIISQEIYSSVSQSKFIPLIFEYKDNGEPYTPIFLKSRIYIDFSTPEKENDNW

ERLIRLLYGKPEFTKPPLGKPPVYLEQDTSKPTYEIHAKFQTLKSAVLNQKQTLKDCRRQFLEVCRNYCI

SLQVVTNPTTEDFAAEVLQIHKELIAVRDAITDWVLLEGDTQGEDFSKALLQFMEVMLAIRNRPKNVNSY

NEIWFLPHQIFAYETFLYILAALIKIEAFQHVHTLLHTSYLLPDHITSPGMEFANYSELYLSSDYLQSKL

SPENYRLYSPVAELVKQSATRDDVSFDDLKQADLVALMISFINPGIFWYPQMLLYSGHYEKYPLFTRAIQ

HRGFKSIAVITGIDDSKLLAQKLTEGEAQRNTNNWYHFGFNRDFLNKMNVSRLDSIE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529208.1\_1963 [locus\_tag=BN49\_RS11290] [protein=phage portal protein] [protein\_id=WP\_016529208.1] [location=complement(2023732..2024772)] [gbkey=CDS]

MSKRKNKNNRAAVDHNANSGGAAAEAFSFGDPVPVLDRRELLDYVECVQMDRWYEPPVSFDGLARTYRAA

VHHSSPIAVKRDILSSTYIPHRLLSQQAFARFVQDYLVFGNAYLEKRTNRLGSVLSLEPALAKYTRRGVD

LDTYWFVQYGMTTQPYEFTQGNIFHLLEPDINQEIYGLPGYLSAIPSTLLNESATLFRRKYYINGSHAGF

IMYMTDAAQNQEDVNNIRQAMKSAKGPGNFRNLFMYSPNGKKDGIQIIPLSEVAAKDEFLNIKNVSRDDM

MAAHRVPPQMMGIIPNNTGGFGDVEKASRVFVRNELMPLQKRLQELNDWLGEEVIRFEPYTLDIEN

>lcl|NZ\_FO834906.1\_prot\_WP\_227504838.1\_1964 [locus\_tag=BN49\_RS11295] [protein=terminase family protein] [protein\_id=WP\_227504838.1] [location=complement(2024769..2025449)] [gbkey=CDS]

MDSSFFAYQYEWNTSPKSRNRVLTKMRQAGADFFFSYEALNDALHTGRNQIFLCCSTASALTVKTYMSAF

IDQAATWTHLGKIKSGKAHLELPNGAVIYFIGPKSLAAALHGNVYVSEYAWADSPKNMIALAKSLSMHAR

YHATYYTTPSPSPEAWREYKKLIARNSTTSMIFTADDAAASGATLATGAALFDDEWLNDMKKELSAEDWK

MLFMCEWPQTDKEQAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529206.1\_1965 [locus\_tag=BN49\_RS11300] [protein=terminase ATPase subunit family protein] [protein\_id=WP\_016529206.1] [location=complement(2025494..2027260)] [gbkey=CDS]

MNTTLTPADLDPRRQAMLLYFQGYRVARIAEMLGEKVATVHSWKKRDKWGDYGPLDQMQLTTAARYCQLI

MKEHKEGKDFKEIDLLARQSERHARIGKFNNGGNEADLNPNVANRNKGPRRQPEKNVFTDEQIEKLEEIF

HSSMFNYQRHWWEAGKTNRIRNLLKSRQIGATFYFAREALIDALLTGRNQIFLSASKAQAHVFKQYIIDF

AKEVEVELKGDPMVLPNGATLYFLGTNARTAQSYHGNLYLDEYFWIPKFQELRKVASGMAIHKKWRQTYF

STPSSLTHSAYPFWSGALFNRGRNKADKVDIDLSHSNLAPGLLCADGQYRQIVTVEDAVRGGCNLFDLDQ

LRMEYSPDEYQNLLMCEFVDDLASVFPLSELQACMVDSWEVWTDFHALALRPFGWREVWIGYDPAKGTQN

GDSAGCVVVAPPAVPGGKFRILERHQWRGMDFRAQADAIKKLTEQYNVTYIGIDSTGVGHGVYENVKAFF

PAVREFVYNPNVKNALVLKAYDIISHRRLEFDAGHTDIAQSFMAIRRATTASGNRLTYEASRSEEASHAD

LAWATMHALFNEPLQGESANTSNIVEIF

>lcl|NZ\_FO834906.1\_prot\_WP\_046042962.1\_1966 [locus\_tag=BN49\_RS11305] [protein=GPO family capsid scaffolding protein] [protein\_id=WP\_046042962.1] [location=2027403..2028236] [gbkey=CDS]

MTVKAKRFRIGVEGATTDGREIQREWLEQMAASYNPAVYTALINLEHIKSYLPDSTFNRYGKVTALFAEE

ITEGPLAGKMALYADVEPTESLVELVKKGQKLFTSMEVSPKFADTGKAYLVGLAATDDPASLGTEMLTFS

ASAAHNPLANRKQNPANLFTAAEETVIELEEIQDDKPSLFARVTALFTKKEQSDDARFSDVHKAVELVAT

EQQNLSVRTEKSLSEQEERLSELETALQAQQTAFNELVNKLSQEDSRQDYRQRATGGNAPADTLTNC

>lcl|NZ\_FO834906.1\_prot\_WP\_000742511.1\_1967 [locus\_tag=BN49\_RS11310] [protein=phage major capsid protein, P2 family] [protein\_id=WP\_000742511.1] [location=2028253..2029311] [gbkey=CDS]

MKKNTRFAFNAYLQQLARLNGVAVEELSSKFTVEPSVQQTLEDQIQQSAAFLTLINVTPVTEQSGQLLGL

GVGSTIAGTTDTTAKEREPVDPTLMVDVEYKCEQTNFDTVLTYAKLDLWAKFQDFQVRIRDAIVKRQALD

RIMIGFNGVKRAKTSNRSENPLLQDVNKGWLQKIREDAPDHVMGSTTTGGETTPGAVKVGKGGEYANLDA

VVMDAVNELIDVVYQDDDDLVVICGRELLSDKYFPLVNKEQENSEKLAADMIISQKRMGGLQAVRAPFFP

PNALLITRLDNLSIYWQEDTRRRSVIDNPKRDRIENFESVNEAYVVEDYRCAALVENIQIGDFSAAAAET

GA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531514.1\_1968 [locus\_tag=BN49\_RS11315] [protein=terminase endonuclease subunit] [protein\_id=WP\_016531514.1] [location=2029315..2029965] [gbkey=CDS]

MSLSPARQHRLRVQAEQAAREGGSVRHASGYDLMLLQLAEDRRRLKGVQSTVKKAEIKVELLPKYAAWAE

GVLTAGGVQQDDVLMYVMLWRIDAGDYAGALEIGRHALRHGWVMPLGNRNVQTVLAEEMADAAQSAMLAA

TGFDADLLLQTLELTDGLDMPDQSRARLHKAIGAVLSESNPASALNHLNHALQLDPRCGVKKDKQQLERR

LRNDSR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531513.1\_1969 [locus\_tag=BN49\_RS11320] [protein=head completion/stabilization protein] [protein\_id=WP\_016531513.1] [location=2030061..2030525] [gbkey=CDS]

MKFVAPEQAPEQAEIIRNTPFWPDVDLSEFRSVMRTDGTVTQPRLKQVALSAISEVNAELYEFRRRQQML

GYSSLAEVPAEQLDGKSERIHHYFNAVYCWARAMLNERYQDYDATASGVKRGEELAEASGDLWRDARWAI

SRVQDAPHCTVELI

>lcl|NZ\_FO834906.1\_prot\_WP\_000868192.1\_1970 [locus\_tag=BN49\_RS11325] [protein=tail protein X] [protein\_id=WP\_000868192.1] [location=2030525..2030728] [gbkey=CDS]

MKVRAYQYDTVDALCWRHYGRTQGVTEQVLKANPGLAEYGPFLPHGLQVELPDIPTTTTVQTVQLWD

>lcl|NZ\_FO834906.1\_prot\_WP\_000171568.1\_1971 [locus\_tag=BN49\_RS11330] [protein=phage holin] [protein\_id=WP\_000171568.1] [location=2030732..2030947] [gbkey=CDS]

MTLERISAFITYCIAVVLAWLGDLSIKDASTLGGLMIGVLMLAINWYYKHKAYQLLRDGQISREDYESIN

R

>lcl|NZ\_FO834906.1\_prot\_WP\_001513678.1\_1972 [locus\_tag=BN49\_RS11335] [protein=lysozyme] [protein\_id=WP\_001513678.1] [location=2030928..2031440] [gbkey=CDS]

MNPSIVKRCLVGTVLAIAATLPGFQQLHTSVEGLKLIADYEGCRLQPYQCSAGVWTDGIGNTSGVIPGKT

ITERQAAEGLISNVLRVERALERCVKQQPPQKVYDAAVSFAFNVGTGNACSSTLVKLLNQRRWADACRQL

PRWVYVKGVFNQGLDNRRAREMAWCLQGAN

>lcl|NZ\_FO834906.1\_prot\_WP\_016531512.1\_1973 [locus\_tag=BN49\_RS11340] [protein=DNZ54\_00345 family protein] [protein\_id=WP\_016531512.1] [location=2031442..2031819] [gbkey=CDS]

MKKKLISGLFLMLWMALLIAAMVYPQGIFPVLSASGVWVACLLTWAVIPVALAALIKNGPLWQELRASLL

KTITRKENVFISWVMRLLIVVSLAWTGWAITLVFYLLTVIAFWMTRNQMAQQVSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531511.1\_1974 [gene=lysB] [locus\_tag=BN49\_RS11345] [protein=Rz-like lysis system protein LysB] [protein\_id=WP\_016531511.1] [location=2031816..2032244] [gbkey=CDS]

MNRLLLVVLALLLAALGWQKWRLADASQTISTQADELQSKSQALAKSNSQLISLSILTETNNREQARLYA

EAEQTSALLRQRQHRIEELKRENEDLRRWADTPLPADIIRLRERPALTGGAAYRQWLSASDAVLAGSDSA

AH

>lcl|NZ\_FO834906.1\_prot\_WP\_227504845.1\_1975 [gene=lysC] [locus\_tag=BN49\_RS31420] [protein=Rz1-like lysis system protein LysC] [protein\_id=WP\_227504845.1] [location=2032129..2032377] [gbkey=CDS]

MLTLSGCGNVRHSPEVQLTVSGCPRVTPCWLDQTAPRTNGDLNALLDETEAAWAVCADKVDMIIACQERN

SEQTTIPAPRPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_001039939.1\_1976 [locus\_tag=BN49\_RS11355] [protein=phage tail protein] [protein\_id=WP\_001039939.1] [location=2032340..2032771] [gbkey=CDS]

MNKPQSLRHALNKAVPYVRNNPDKLHLFVDNGSLVATGASSMSWEYRYTLNVVIEDFSGDQNLLMAPVLL

WLRDNQPDAINNPALREKLFTFDVDILRNDVCDISLNLQLTERVLVSTDGSVSSVEAVAEPDEPEEMWTV

KRG

>lcl|NZ\_FO834906.1\_prot\_WP\_000829146.1\_1977 [locus\_tag=BN49\_RS11360] [protein=phage virion morphogenesis protein] [protein\_id=WP\_000829146.1] [location=2032764..2033210] [gbkey=CDS]

MAELQKVDDWLSALLANLEPATRSRMMRQLAQELRRTQQQNIRMQRNPDGSSYEPRRVTARSKKGRIKRQ

MFAKLRTTKYLKTAASADSASVQFEGKVQRIARVHHYGLRDRVSRKGPEVRYAERRLLGVNDDVEAMTRD

MILQWLAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016531508.1\_1978 [locus\_tag=BN49\_RS11365] [protein=phage baseplate assembly protein V] [protein\_id=WP\_016531508.1] [location=2033279..2033857] [gbkey=CDS]

MNAQLTEIMRLITNLIRTGVVTEVDRENWLCRVKTGDLETNWINWLTLRAGNARTWWKPSEGEQVVLLSL

GGNLETAFALPAVYSNQFAPPSKSADACVTEHPDGGWFEYEPATGRWYVRGIKSMVIEAVDNITMKTSEF

VLEADRTRINSEVVINGGVTQGGGAMSSNGIVVDAHQHTGVLKGGDTTGGPV

>lcl|NZ\_FO834906.1\_prot\_WP\_046042963.1\_1979 [locus\_tag=BN49\_RS11370] [protein=GPW/gp25 family protein] [protein\_id=WP\_046042963.1] [location=2033854..2034213] [gbkey=CDS]

MTLYSGMNNTSGKAITDIDHLRQSVRDILLTPQGSRIARREYGSLLSALIDQPQNPALRLQVMSAVYVAL

SRWEPRLTLDSITINSIFDGSMVVELTGRRNNGVPVSLSVSTGAENGSD

>lcl|NZ\_FO834906.1\_prot\_WP\_046042965.1\_1980 [locus\_tag=BN49\_RS11375] [protein=baseplate assembly protein] [protein\_id=WP\_046042965.1] [location=2034200..2035108] [gbkey=CDS]

MAVIDLSQLPAPQIVDVPDFETLLAERKAEFVALHPKDEQEAVMRTLELESEPVTKLLQENAYRELLLRQ

RINEAAQAVMVAYAIGSDLDQLAANYNVKRLTVTPADNDAVPPVAAVMESDEALRLRVPAAFEGLSVAGP

TAAYEFHARSADGRVADASATSPAPAEVVLTVLSREGDGTAEKDLLDVVEKALNSENVRPVADRLTVRSA

EIIPYRVEATIFLYPGPEAEPVMAAAKASLQKYIASQTRLGRDIRRSAIFAALHVEGVQRVELASPLADV

VLNKTQAASCTQWSVTNGGTDE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042967.1\_1981 [locus\_tag=BN49\_RS11380] [protein=phage tail protein I] [protein\_id=WP\_046042967.1] [location=2035101..2035706] [gbkey=CDS]

MNSLLPPGSTSLERRLAQTCSGISDLQVPLRDLWNPATCPVSFLPYLAWAFSVDRWDEGWTESVKRQVVK

DAFYIHQHKGTTSAVRRVVEPFGFLIRIIEWWQTGETPGTFRLDIGVQDQGITEDTYLELERLISDAKPC

SRHMIGMSINLQTSGPYWVGAASYLGEEITIYPYINETIISGGTAHEGGAVHVIDTMRVNP

>lcl|NZ\_FO834906.1\_prot\_WP\_046042969.1\_1982 [locus\_tag=BN49\_RS11385] [protein=phage tail protein] [protein\_id=WP\_046042969.1] [location=2035703..2037424] [gbkey=CDS]

MSTKFYTLLTDIGAAKLASVAALGVPLKITHMAVGDGGGTLPTPDAKQTALVNEKRRAALNMLYIDPQNS

SQIIAEQVIPENEGGWWIREVGLFDESGALIAVGNCPESYKPQLAEGSGRTQTVRMVLITSSTDNITLKI

DPAVVLATRKYVDDKVLELKVYADDQMAKHLAAPDPHSQYAQKESPTFTGTPKAPTPAAGNNTTQVATTA

FVQEALTALINGAPATLDTLKEIAVAINNDPKFSTTINNALALKAPLSSPALTGTPTAPTAAQSVNNTQI

ATTAFVKSAIAAMVGSAPAELDTLNELAAALGNDPNFATTMLNALAGKQPLDNTLTNLSGKDVTGLLTYL

GLGDASGYVGRLLKIQVFTASGTVTKTPGAKKWRIKCLGAGAGSSAAPATGSNEVSVSNGGGAGAYAEGI

YDVSSITTASVVIGSGGAGGTAGSIYGADGGASSVGSFISSPGGKAGLPAGPATPPFQPVANNNSDSPTG

WNIVGSSGAGAEPAVAVANSYAAGSRGSNSIFGVGGSIPAINSPANPGGGYGSGASGCSNGPSQSAKSGA

AGRPGIVIIEELA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529754.1\_1983 [locus\_tag=BN49\_RS11390] [protein=hypothetical protein] [protein\_id=WP\_016529754.1] [location=2037424..2037606] [gbkey=CDS]

MSNYALVKNGVVENVVVWDGTGGIFDDYITVNIDDISAGIDWTYDGEAFAPPPEITPQGV

>lcl|NZ\_FO834906.1\_prot\_1984 [locus\_tag=BN49\_RS28920] [protein=tail fiber assembly protein] [pseudo=true] [partial=5'] [location=complement(2037587..>2037742)] [gbkey=CDS]

EISWRQDAVDAGIATTEEAAALSEWKKYRVLLMRIDTSKAPDIEWPTPPAE

>lcl|NZ\_FO834906.1\_prot\_1985 [locus\_tag=BN49\_RS11395] [protein=IS1 family transposase] [pseudo=true] [partial=5'] [location=complement(2037760..>2038207)] [gbkey=CDS]

KPQSVNSRIQPGSDVIVCAEMDEQWGYVGAKSRQRWLFYAYDRIRRTVVVHVFGERTMATLERLLGLLSA

FEVVVWMRDGWPLYEPRLKGELHVISKRYTQRIERHNLNLRQEVTVVLKIGGAA\*QSHRALSEHKTLSES

WSHYQKSTL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529756.1\_1986 [locus\_tag=BN49\_RS11400] [protein=recombinase family protein] [protein\_id=WP\_016529756.1] [location=2038403..2038969] [gbkey=CDS]

MLIGYVRVSTNDQNTDLQRNALNCAGCERIFEDKISGTKSDRPGLKKLLRTLSAGDTLVVWKLDRLGRSM

RHLVTLIEELRQRGVNFRSLTDSIDTSTPMGRFFFHVMGVLAEMERELIVERTMAGLAAARAKGRVGGRR

PKLTTEQWAQIGRLLEAGESRQRIALIFDVGVSTIYRKFPANKSNESP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529757.1\_1987 [locus\_tag=BN49\_RS11405] [protein=phage tail sheath protein] [protein\_id=WP\_016529757.1] [location=2039112..2040284] [gbkey=CDS]

MAQDYHHGVRVVEVNEGTRSITTVSTAIVGMVCTGDDADAKMFPLNKPVLITDVLTASGKAGESGTLARS

LDAIADQAKPVTIVVRVPQGETEEETTTNIIGAVTAEGKKTGMKALLSAQSQLGVKPRILGVPGHDTKAV

ATELLSVAQSLRGFAYLSAYGCKTVQEAITYRENFSQREGMLIWPDFTGWDTVLNAEATAYATARALGLR

AKIDEQTGWHKSLSNVGVNGVTGISADVFWDLQDTATDAGLLNQNDVTTLIRKDGFRFWGSRCLSDDPLF

AFENYTRTAQVLMDTMAEAHMWAVDKPLNPSLARDIIEGIRAKMRSLVSQGYLIGGDCWLDESVNDKDTL

KAGKLTIDYDYTPVPPLENLMLRQRITDQYLVNFSSQVSA

>lcl|NZ\_FO834906.1\_prot\_WP\_001504081.1\_1988 [locus\_tag=BN49\_RS11410] [protein=phage major tail tube protein] [protein\_id=WP\_001504081.1] [location=2040294..2040809] [gbkey=CDS]

MALPRKLKHLNLFNDGNNWQGIVESLTLPKFTRKYEKYRGGGMPGAVDVDLGLDDSALDTEFSIGGTELL

LFKQMGKSTVDGIQLRFTGSIQRDDTGEVQAVELVVRGRHKEVDSGEWKTGESNTTKVTSTNSYAKLTIN

GEVLYEVDLINMVEIVDGVDLMEAHRNALGL

>lcl|NZ\_FO834906.1\_prot\_WP\_001281009.1\_1989 [locus\_tag=BN49\_RS11415] [protein=phage tail assembly protein] [protein\_id=WP\_001281009.1] [location=2040864..2041166] [gbkey=CDS]

MSDKQTEKTIQLDTPIKRGKTEITEIVLRKPQSGALRGTRLQAIMDMDVNAMMTVIPRISSPALTAQEIA

EMDPADLTAMSVEVVTFLLKKSVLAGLPTA

>lcl|NZ\_FO834906.1\_prot\_WP\_000763311.1\_1990 [locus\_tag=BN49\_RS11420] [protein=GpE family phage tail protein] [protein\_id=WP\_000763311.1] [location=2041181..2041300] [gbkey=CDS]

MADIATIFHWPPSVTDVMPLTEVLEWRYKAIQRSGANDE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042972.1\_1991 [locus\_tag=BN49\_RS11425] [protein=phage tail tape measure protein] [protein\_id=WP\_046042972.1] [location=2041293..2044370] [gbkey=CDS]

MSDNNLRLQVILNAVDKLTRPFRAAQASSKELAGAIRNSRDALKQLNQAGNSLEKFRKLQADNKRLGDRL

NYARQKANLLSSELEAMEQPSQRHLVALGRQTLAVQRLEEQQKYLQKQTALVRAELYRAGISANDDAGAT

ARLARETSRYNQELSKQEARLKRLGEAQRRMNAARASYARSLEVRDRIAGAGATTTAAGLAMGTPVMAAV

KSYTSMEDAMKGVAKQVNGLRDDNGNRTARFYEMQDAIKAASEQLPMENGAVDFAALVEGGARMNVANPD

DSWEDQKRDLLAFASTAAKAATAFELPADELSESLGKIAQLYKIPTRNIEQLGDALNYLDDNAMSKGADI

IDVMQRLGGVADRLDYRKAAALGSTFLTLGAAPEVAASAANAMVRELSIATMQSKSFFEGMNLLKLNPEV

IEKQMTKDAMGTIQRVLEKVNALPQDKRLSAMTMLFGKEFGDDAAKLANNLPELQRQLKLTAGNDALGSM

QKESDINKDSLSAQWLLVKTGAQNTFSSLGETLRQPLMDILYTVKSITGALRRWVEANPELTGTLMKVAA

VVAAVTVGLGTLAVALAAVLGPLAVIRLGFSVLGIKTLPSVTAAVTRTSSALSWLAGAPLALLRRGLASS

GNAAGLLTALLSSLHRTASLTGNVLKTVAGAPVALLRSGLSGLRAVAVMFMNPLAALRGGLAATGTVLRV

LASGPLAMLRVALYAVSGLLGALLSPIGLVVTALAGVALVVWKYWQPITAFLGGVVEGFKAAAGPISAAF

EPLKPVFQWIGDKVQALWGWFTDLLTPVKSTSAELQSAAAMGRRFGEALAEGLNMVMHPLDSLKSGVSWL

LEKLGIVSKEAAKAKLPESVTRQQPATVNADGKVMMPLGGFPSWGYGFAGMYDSGGYIPRGQFGIVGENG

PEIVNGPANVTSRRNTAALAAVVAGMMGVAAAPAELPPLHPLALPAKGGEAMLSRAATVPPVQRIEAPTQ

IIIQTQPGQSAQDIAREVARQLDERERRLKAKARSNYSDQGGYDA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529761.1\_1992 [locus\_tag=BN49\_RS11430] [protein=phage tail protein] [protein\_id=WP\_016529761.1] [location=2044367..2044852] [gbkey=CDS]

MMMVLGLYVFMLRTVPYQELQYQRSWRHAANSRVNRRPSTQFLGPDNDMLTLSGVLMPEITGGRLSLLAL

EQMAEQGKAWPLIEGSGTIYGMYVIEGLNQTKTEFFRDGMPRRIEFTLSLKRVDESLSDMFGDLSAQLNN

LQGTETSALSDISKTVGGLLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002896225.1\_1993 [locus\_tag=BN49\_RS11435] [protein=phage late control D family protein] [protein\_id=WP\_002896225.1] [location=2044849..2045949] [gbkey=CDS]

MNFSSELLNKGNKTPAFSISIEGRDITTVLDNRLMGLTLTDNRGFEADQLDLELDDADGKIVLPRRGAVI

TLALGWKGQPLFPKGAFTVDEIEHTGAPDRLTIRARSADFRETLNTRREKSWHNTTIGEVVKEIAARHKL

KMALGKELSDKPVEHIDQTNESDGSFLMRLARQYGAIASVKNGNLLFIRQGQGKSATGKPLPVITITRKD

GDSHRFTLADRGAYTGVIASWLHTREPAKKESTTVKRKRRTKKQKKEPEAKQGDYLVGTDENVLVLNRTY

ANRSNAERAAKMQWERLQRGVASFSLQLAEGRADLYTEMPVKVSGFKQPIDDAEWTITTLTHTVSPDNGF

TTSLELEVKIDDFEME

>lcl|NZ\_FO834906.1\_prot\_WP\_000972391.1\_1994 [locus\_tag=BN49\_RS28925] [protein=ogr/Delta-like zinc finger family protein] [protein\_id=WP\_000972391.1] [location=2046040..2046258] [gbkey=CDS]

MMICPLCGSAAHTRSSFQVSSLTKERYNQCQNINCSHTFVTHETFVRSIATPKESNPVQPHPMKSGQVAL

SL

>lcl|NZ\_FO834906.1\_prot\_WP\_004179131.1\_1995 [locus\_tag=BN49\_RS11450] [protein=aspartate:alanine antiporter] [protein\_id=WP\_004179131.1] [location=complement(2046479..2048164)] [gbkey=CDS]

MNINVADLLNGNYILLLFVVLALGLCLGKLRLGSVQLGNSIGVLVVSLLLGQQHFAINTDALNLGFMLFI

FCVGVEAGPNFFSIFFRDGKNYLMLALVMVGSAMLIAMVLGKVFGWDIGLTAGMLAGAMTSTPVLVGAGD

TLRHFGLPSDQLAQSLDHLSLGYALTYLVGLVSLIVGARYMPKLQHQDLQTSAQQIARERGLDTDSKRKV

YLPVIRAYRVGPELVAWADGKNLRELGIYRQTGCYIERIRRNGILANPDGDAVLQMGDDIALVGYPDAHA

RLDPSFRNGKEVFDRDLLDMRIVTEEIVVKNHNAVGRRLAQLKLTDHGCFLNRVIRSQIEMPIDDNVVLN

KGDVLQVSGDARRVKTVADRIGFISIHSQVTDLLAFCAFFIVGLMIGMITFQFSSFSFGIGNAAGLLFAG

IMLGFLRANHPTFGYIPQGALNMVKEFGLMVFMAGVGLSAGAGINNGLGAVGGQMLAAGLIVSLVPVVIC

FLFGAYVLRMNRAMLFGAMMGARTCAPAMEIISDTARSNIPALGYAGTYAIANVLLTLAGTLIVIIWPGL

Q

>lcl|NZ\_FO834906.1\_prot\_WP\_002896351.1\_1996 [locus\_tag=BN49\_RS11455] [protein=inner membrane protein YbjM] [protein\_id=WP\_002896351.1] [location=2048431..2048814] [gbkey=CDS]

MKSERSWAGIICGFVLFIVVCLSLLLHMKGAFRASGNPELGLLFFLLPGAAASCLSPGRRVLRPLLGAIL

AAPVCMVTMRLFFVTHRTFWQEMAWVLSAVFWCALGALCFLFICAWLDTWRSHSSSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002896352.1\_1997 [locus\_tag=BN49\_RS11460] [protein=GrxA family glutaredoxin] [protein\_id=WP\_002896352.1] [location=complement(2048821..2049084)] [gbkey=CDS]

MFTVIFGRPGCPYCVRAKELAEKLTNERDDFNYRYVDIHAEGISKADLEKTVGKPVETVPQIFVDQKHIG

GCTDFEAWAKENLGLFA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529762.1\_1998 [locus\_tag=BN49\_RS11465] [protein=YbjC family protein] [protein\_id=WP\_016529762.1] [location=2049287..2049574] [gbkey=CDS]

MRKFAPLPKSILLVEILGMGLLTLAWLSLNQYVQLPAPIASPTAALVMILSGIALMIPAALVVMWRVAQI

VAPQLTHSPKPESLSDREKRNDADH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529763.1\_1999 [gene=nfsA] [locus\_tag=BN49\_RS11470] [protein=nitroreductase NfsA] [protein\_id=WP\_016529763.1] [location=2049558..2050280] [gbkey=CDS]

MTPTIELLRSHRSIRHFTDAPVSDEQRAAIIASAQAASTSSFLQCTSIIRITDPALRERLVPLTGGQQHV

AQAAEFWVFCADFNRHLQICPQAQLGLAEQLLIGVVDTALLAQNALTAAESLGLGGVYIGGLRNSIEAVT

ELLELPQHVLPLFGLCLGWPADNPDIKPRMPAAMLVHENRYQPLDNALLAEYDEQLAHYYLSRGSNARRD

TWSDHIRRTIVKESRPFILDYLHKQGWATR

>lcl|NZ\_FO834906.1\_prot\_WP\_002896363.1\_2000 [gene=rimK] [locus\_tag=BN49\_RS11475] [protein=30S ribosomal protein S6--L-glutamate ligase] [protein\_id=WP\_002896363.1] [location=2050395..2051297] [gbkey=CDS]

MKIAILSRDGTLYSCRRLREAAQQRGHQIEILDPLSCYMNVSPVASSIHYKGRQLPHFDAVIPRIGSAIT

YYGTAALRQFELLGSYPLNESVAITRARDKLRSLQLLARQGIDLPLTGIAHSPDDTSDLIAMVGGAPLVV

KLVEGTQGIGVVLAETRQAAESVIDAFRGLNAHILVQEYIAEAKGCDIRCLVVGNEVVAAIERRAKEGDF

RSNLHRGGMATVAQISDEERAIAIKATQTLGLDAAGVDILRAARGPLVMEVNASPGLEGVETTTGVDVAG

KMIAWIERQATPEFCLKIGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002896365.1\_2001 [locus\_tag=BN49\_RS11480] [protein=YbjN domain-containing protein] [protein\_id=WP\_002896365.1] [location=2051386..2051865] [gbkey=CDS]

MDSLVVPGLDTLRRWLDEIGISFFECDSCQALHLPHMQNFDGIFDAKIDLVDNVVLFSALAEVKPSALLA

LSADLSAINASSLTVKAFIDIQDDNLPKLVVCQSLSIGPGVTMEQFAWFFRQSEEQISMVILEAGANQLL

YKGEEEEPAAENVQYHFLH

>lcl|NZ\_FO834906.1\_prot\_WP\_002896368.1\_2002 [gene=potF] [locus\_tag=BN49\_RS11485] [protein=spermidine/putrescine ABC transporter substrate-binding protein PotF] [protein\_id=WP\_002896368.1] [location=2052214..2053326] [gbkey=CDS]

MTAFGKKWLTGLVTGALMAVSAGSLAAEQKTLHVYNWSDYIAPDTVANFEKETGIKVVYDVFDSNEVLEG

KLMAGSTGFDLVVPSASFLERQLAAGVFQPLDKSKLPNWKNLDPEVLKLVAKHDPENKYAMPYLWATTGI

GYNVDKVKAVLGKDAPVDSWDLVLKPENLEKLKSCGVSFLDAPEEIFATVLNYLGKDPNSSKADDYTGPA

TDLLLKLRPNIRYFHSSQYINDLANGDICVAIGWAGDVWQAANRAKEAKNGVNVSYFIPKEGALAFFDVF

AMPADAKNKDEAYQFLNYLMRPDVIAKISDQVFYANGNKASTPLVSETIRNNPAIYPPADVFAKLFTLKV

QDPKIDRVRTRAWTKVKSGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002896370.1\_2003 [gene=potG] [locus\_tag=BN49\_RS11490] [protein=putrescine ABC transporter ATP-binding subunit PotG] [protein\_id=WP\_002896370.1] [location=2053490..2054623] [gbkey=CDS]

MNDVMPRPQAKAPKALTPLLEIRNLTKSFDGQHAVDDVSLTIYKGEIFALLGASGCGKSTLLRMLAGFEQ

PTAGQIMLDGVDLARVPPYQRPINMMFQSYALFPHMTVEQNIAFGLKQDRLPKAEITARVQEMLALVHMQ

EFAKRKPHQLSGGQRQRVALARSLAKRPKLLLLDEPMGALDKKLRDRMQLEVVDILERVGVTCVMVTHDQ

EEAMTMAGRIAIMNRGKFVQIGEPEEIYEHPTTRYSAEFIGSVNVFEGLVKERLEDGLVLSSPGLMHPLK

VDPDASVVDNVPVWVALRPEKIMLCDEPPADGYNFAVGEVIHIAYLGDLSIYHVRLQSGQMISAQLQNEH

RHRKGTPTWGDEVRLCWDADSCVVLTV

>lcl|NZ\_FO834906.1\_prot\_WP\_002896371.1\_2004 [gene=potH] [locus\_tag=BN49\_RS11495] [protein=putrescine ABC transporter permease PotH] [protein\_id=WP\_002896371.1] [location=2054634..2055587] [gbkey=CDS]

MNTVESPSGAKKPGGFALWAARLQMAHGRKLVIALPYLWLILLFMLPFLIVFKISLAEMARAIPPYTELM

EWADGQLTLTLNFANFLQLTDDPLYFEAYLQSLQVAGISTICCLLLGYPLAWAVAHSKPSTRNILLLLVI

LPSWTSFLIRVYAWMGLLKSNGVLNNFLLWLGVIDQPLEILHTNLAVYIGIVYAYLPFMVLPIYTALTRI

DYSLVEASLDLGARPLKTFFQVIVPLTKGGIIAGSMLVFIPAVGEFVIPELLGGPDSIMIGRVLWQEFFN

NRDWPVASAVAIVMLLLLIVPIMWFHKHQQKQMGEQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002896372.1\_2005 [gene=potI] [locus\_tag=BN49\_RS11500] [protein=putrescine ABC transporter permease PotI] [protein\_id=WP\_002896372.1] [location=2055584..2056429] [gbkey=CDS]

MNDLPVVRSPWRILILVLGFTFLYAPMLMLVIYSFNSSKLVTVWAGWSTRWYSELFHDDAMMSAVGLSLT

IAACAATAAAILGTIAAVVMVRFGRFRGSNGFAFMITAPLVMPDVITGLSLLLLFVALGHAIGWPSDRGM

LTIWLAHVTFCTAYVAVVISSRLRELDHSIEEAAMDLGAAPLKVFFVITLPMIMPAVISGWLLAFTLSLD

DLVIASFVSGPGATTLPMLVFSSVRMGVNPEINALATLILGVVGIVGFIAWYLMARAEKQRVRDIQRARQ

G

>lcl|NZ\_FO834906.1\_prot\_WP\_002896376.1\_2006 [locus\_tag=BN49\_RS11505] [protein=DUF2593 family protein] [protein\_id=WP\_002896376.1] [location=2056487..2056975] [gbkey=CDS]

MEDITLGLFTKTRSSHARLNVPALVQVAAFAIILIRGLDLLMILNLLGLQGLNEFIHRSVQTWNLTLVFL

GSLALVFIEIWCAFSLVKGRNWARWIYLLTQIIAAGYLWAASLGYGYPELFSIPGESKREIFHSLVMQKL

PDLLVLTLLFVPANCRRFFRLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002896378.1\_2007 [gene=rlmC] [locus\_tag=BN49\_RS11510] [protein=23S rRNA (uracil(747)-C(5))-methyltransferase RlmC] [protein\_id=WP\_002896378.1] [location=2057017..2058144] [gbkey=CDS]

MHCALYDAGRCRSCQWLERPVPQQLADKMADLRTLLAAIPVAAWGEPVSGPEAAFRNKAKMVVSGSVERP

LLGMLHRDGTPVDLTDCPLYPAEFAPVFAALKPFIARAGLTPYNVARKRGELKYLLLTASQQGEMMLRFV

LRSEAKVAQLRAALPWLQAQLPQLSVITANIQPVHMAIMEGEQEIFFTEQQALGEVFNGVPLWIRPQSFF

QTNPAVASRLYATARDWVRALPVQHMWDLFCGVGGFGLHCATPTMRLTGIEIAPEAIACARQSAAQLGLS

NLHFQALDSTQFATHEADAPQLVLVNPPRRGIGAELCDYLSRMAPPYIIYSSCNARTMATDIARLSGYRV

ERVQLFDMFPHTAHYEVLTLLVREV

>lcl|NZ\_FO834906.1\_prot\_WP\_002896380.1\_2008 [locus\_tag=BN49\_RS11515] [protein=response regulator transcription factor] [protein\_id=WP\_002896380.1] [location=2058223..2058939] [gbkey=CDS]

MAKTILLVEDDEDIATLLRLNLQDEGYQIVHEADGGQALARLETQVWDAVILDLMLPGVDGLEICRRIRQ

MTRYLPVIIISARTSEMHRVLGLEMGADDYLAKPFSLLELIARVKALFRRQEAMGQNLLMDAGRLSCHGL

SIDPLSREVKLRGETVDLTPREFDLLYYFARHPGEVFSRLALLEQVWGYQHEGYEHTVNTHINRLRSKIE

RDPAEPDIILTVWGKGYKFAPVTQEAAP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531909.1\_2009 [locus\_tag=BN49\_RS11520] [protein=ATP-binding protein] [protein\_id=WP\_016531909.1] [location=2058936..2060408] [gbkey=CDS]

MIRRLSLSQRLALVVVSLLMLCAVAVCAVQLHSSAQYGNAMVQRLSSGLAQQIVAREPLLDVHGEVNRQT

LKSLFDRLMTFNPSVELYLLSPDGDLLADAAPPGHIQRQRIDMAPVQAFLTGSASPVYGDDPRSPDGRKV

FSAAPLRVDGQLRGYLYIILQGETFNQLAADAWQKTLWSIVLWTLLLVALFGLLAGGLAWFWVTRPVRLL

TAQVAASGQDSISAIKTLAARRPEPRPGNEVAVLENRFIDLARQIADQWDRLADSDRQRREFVANISHDL

RTPLTSLLGYLETLTLKDEWLTAEERRQYLTIALRQGNKVRHLSQQLFELARLEHGGIKPQRERFAMGEL

ISDVAQKFELTARTREVNLHIDVPGPLPLINADVSMIERVVTNLLDNAMRHTPVGGEIRLAVWQENQQLQ

VEVADNGAGVDAALRDDLFQRPSALSTQASREDRGGLGLLIVKRMLELHGGDIRLVESVSGARFRFFVPL

>lcl|NZ\_FO834906.1\_prot\_WP\_002896384.1\_2010 [gene=artJ] [locus\_tag=BN49\_RS11525] [protein=ABC transporter substrate-binding protein ArtJ] [protein\_id=WP\_002896384.1] [location=complement(2060451..2061182)] [gbkey=CDS]

MKKLVLAALLTSFAFGAAAAEKISFGVSATYPPFESMDANNQIVGFDIDLAHALCKQMQAECTFTNHAFD

SLIPALKFKKYDAVISGMDITPERSKQVAFTDPYYANSALVIAKKDAFHSFDDLKGKRIGMENGTTHQKY

LQDKHPEVKTVAYDSYQNAIIDLKNGRIDGVFGDTAVVNEWLKTNPQLGAATPKVTDPQYFGTGLGIAVR

PDNKALLEKLNAALKAIKADGTYQKISNQWFPE

>lcl|NZ\_FO834906.1\_prot\_WP\_004141917.1\_2011 [gene=artM] [locus\_tag=BN49\_RS11530] [protein=arginine ABC transporter permease ArtM] [protein\_id=WP\_004141917.1] [location=complement(2061366..2062034)] [gbkey=CDS]

MLDYLPELLKGLHTSLTLTVASIIVALILSLIFTIILTLKTPGLVWIVRGYITLFTGTPLLVQIFLIYYG

PGQFPSLQEYPWLWHLISEPWLCALIALSLNSAAYTTQLFYGAIRAIPDGQWQSCSALGMSKKDTLAILL

PYAFKRALSSYSNEVVLVFKSTSLAYTITLMEVMGHGQLLYGRTYDVMVFGAAGIIYLIVNGLLTLLMRL

VERKALAFERRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002896386.1\_2012 [gene=artQ] [locus\_tag=BN49\_RS11535] [protein=arginine ABC transporter permease ArtQ] [protein\_id=WP\_002896386.1] [location=complement(2062034..2062750)] [gbkey=CDS]

MNEIFPLASAAGMTVGLAVCALVIGLVLAMLFAVLESVKWRPVAWLATGIVTILRGLPEILVVLFIYFGS

SQLLLTLSDGFTIPLGFTQIPVQMQIENFDVSPFLCGAIALSLLYAAYASQTLRGALKAVPQGQWESGQA

LGLSKAAIFFRLVMPQMWRHALPGLGNQWLVLLKDTALVSLISVNDLMLQTKSIATRTQEPFNWYIIAAA

IYLVITLLSQYILKRIDQRATRFERRPG

>lcl|NZ\_FO834906.1\_prot\_WP\_002896390.1\_2013 [gene=artJ] [locus\_tag=BN49\_RS11540] [protein=arginine ABC transporter substrate-binding protein] [protein\_id=WP\_002896390.1] [location=complement(2062757..2063488)] [gbkey=CDS]

MKKVLIAALLAGMSLSASAAQTIRFATEASYPPFELVDANNQIVGFDVDLANALCKEIDATCTFTNQAFD

SLIPGLKFRRFDAVMAGMDITPEREKQVLFSTPYYDNSALFVGQQGKFTSIDQLKGKKVGVQNGTTHQKF

ITDKHPEITTVPYDSYQNAKLDLQNGRIDAVFGDTAVVTEWLKSNPKLAAVGDKVTDKAYFGTGLGIAVR

QGNTDLQQKFNAALEKVKKDGTYQTIYNKWFQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002896392.1\_2014 [gene=artP] [locus\_tag=BN49\_RS11545] [protein=arginine ABC transporter ATP-binding protein ArtP] [protein\_id=WP\_002896392.1] [location=complement(2063509..2064237)] [gbkey=CDS]

MSIKLNGINCFYGAHQALFDITLDCPQGETLVLLGPSGAGKSSLLRVLNLLEMPRSGSLSIAGNQFDFTR

APSDKAIRELRQNVGMVFQQYNLWPHLTVQQNLIEAPCRVLGLSKDQALARAEKLLERLRLKPYSDRYPL

HLSGGQQQRVAIARALMMEPQVLLFDEPTAALDPEITAQIVSIIRELAETGITQVIVTHEVEVARKTASR

VVYMENGHIVEQGDASCFTHPQTDAFKNYLSH

>lcl|NZ\_FO834906.1\_prot\_WP\_002896394.1\_2015 [locus\_tag=BN49\_RS11550] [protein=lipoprotein] [protein\_id=WP\_002896394.1] [location=complement(2064464..2064979)] [gbkey=CDS]

MRYKLFAVLLPCALALSACTTVTPAYKDNGTRSGPCVEGGPDDVAQKFYDTQIQNRTQDPAALRPYLSDG

LAQLLNDARQDPANSKLLQANPFSSSSTPADSAVVASASTIPNRDARNIPLRVDLKQGTQSWKDEVLMIQ

EGQCWAVDDVRYLGNNSHAPAGTLRQSLEKR

>lcl|NZ\_FO834906.1\_prot\_WP\_225377445.1\_2016 [locus\_tag=BN49\_RS30390] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_225377445.1] [location=complement(2065281..2065469)] [gbkey=CDS]

MVLSGQCRLRRDFNKTAFDKVHTQYTKIGAISSTGQTASNDAREELIKKANEKGGRHCPLAR

>lcl|NZ\_FO834906.1\_prot\_2017 [locus\_tag=BN49\_RS11555] [protein=GGDEF domain-containing protein] [pseudo=true] [location=2065858..2066996] [gbkey=CDS]

MLTNKRERARQQRAALWATRDNVQRHALSMSMPWLAFVNIAFALMIFFRNFIFTYFDKRLLTHRAVIPYI

EAALIAVIIISAILVIIALTPRLAQGRYTLNIITGLLLALSLCWSLSNYCFIFSGPCPLPGRCW\*Y\*\*LP

ASPRCITIGPA\*PLLCCRYG\*PPCWREYSSTITPRSAF\*SSGPFLPRFCCMADVFCSAGMTKPGIPTRRI

CSLFSGWKVSPTRMP\*PEPLTVGRSMLTWRRSGSKKRRWR\*\*\*SMSIILSAITIAMAIRLVMSAYLLSRR

CLKWRSGRRAIWWLATAAKSLSSCCPGCP\*RMPPLLPSAFSRRSARQAYRTPLRRWRRRSP\*VSGSSPPM

ARSR\*RR\*SPGRTVRCIRRKIKDVINGLI

>lcl|NZ\_FO834906.1\_prot\_WP\_004209681.1\_2018 [locus\_tag=BN49\_RS11560] [protein=N-acetylmuramoyl-L-alanine amidase] [protein\_id=WP\_004209681.1] [location=2067028..2067858] [gbkey=CDS]

MKRMMRIVLLALLLTGCAGEKGIIDRDGYQLDTRHPAQAAYPRIKVLVIHYTADNFDVSLATLTDKEVSS

HYLIPEQPPRYQHKPRIWQLVPEEDLAWHAGVSYWRGSTRINDTSIGIELENRGWQKTAGVKSFTPFHPE

QIAALIPLARDIIARYHIAPQNVVAHADIAPQRKDDPGPLFPWQQLAQQGIGAWPDEQRVAFYLNGRPAS

EPVDPEIVLDLLSRYGYQVTPEMTPAQKKRVIIAFQMHFRPQRWDGVADAQTEAIAEALLEKYGQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002896399.1\_2019 [locus\_tag=BN49\_RS11565] [protein=NAD(P)-dependent oxidoreductase] [protein\_id=WP\_002896399.1] [location=complement(2067855..2068868)] [gbkey=CDS]

MKVLVTGATSGLGRNAVEYLRNKGISVRATGRNEAMGKLLSKMGAEFIPADLTELVSSQAKVMLAGIDTL

WHCSSFTSPWGTQQAFDLANVRATRRLGEWSVAWGVRNFVHISSPSLYFDYHHHRDIQEDFRPHRFANEF

ARSKAASEEVINLLAQANPHTRFTILRPQSLFGPHDKVFIPRLAQMMQHYGSVLLPRGGSALVDMTYYEN

AVHAMWLASQPACDHLPSARAWNISNGEPRTLRSIVQKLIDELGIKCRIRSVPYPMLDIIARSMERFGDK

TAKEPAFTHYGVSKLNFDFTLDITRAQDELGYQPVVTLDDGIVRTAAWLRDHGKLHR

>lcl|NZ\_FO834906.1\_prot\_WP\_002896401.1\_2020 [locus\_tag=BN49\_RS11570] [protein=SDR family oxidoreductase] [protein\_id=WP\_002896401.1] [location=complement(2068956..2070398)] [gbkey=CDS]

MSQSVLVLGASGYIGQHLVRALSARGYPVLAAARHIDRLQKLALPGVTCRSVDLNQPQDLPALLTGIDTL

YYLVHGMGEGGDFIAHERRVATYVRDALRQSSVRQVIFLSSLQAPAQEQSDHLRARQITGDLLRESGVPV

TELRAGIIVGAGSAAFEVMRDMVYNLPVLTPPRWVRSRTTPVALENLLVDLVELLNHPSDAHRVFEAAGP

EVLSYQQQFIRFMAVSGKHRPLIPIPLPTRWISVWFLNVITSVPPTIAKALIQGLKHDLIADDRALRALI

PQTLIPFDQAVRRTLKEEEQLVNSSDWGYDAQAFARWRPEYGYYPKQAGCTVATQASRQALWQVVNQIGG

EEGYFFGNLLWKTRGAMDLLVGHRLAKGRPQRAYLQTGDTVDSWKVIIVEEEKQLTLLFGMKAPGLGRLS

FTINDKGDRRELDVRAWWHPHGMPGLIYWLLMIPAHLFIFRGMAQRIARLAEQISGRVEG

>lcl|NZ\_FO834906.1\_prot\_WP\_004176702.1\_2021 [gene=ltaE] [locus\_tag=BN49\_RS11575] [protein=low-specificity L-threonine aldolase] [protein\_id=WP\_004176702.1] [location=complement(2070409..2071410)] [gbkey=CDS]

MIDLRSDTVTRPGRAMLEAMMAAPVGDDVYGDDPTVNELQRYAADLAGKEAALFLPTGTQANLVGLLSHC

QRGEEYIVGQGAHNYLYEAGGAAVLGSIQPQPIDAAADGSLPLDKVAAKIKPDDIHFAPTRLLSLENTHN

GKVLPRDYLQEAWAFTRQRNLALHVDGARIFNAVVAYGCELRDIAQYCDSFTICLSKGLGAPVGSLLLGS

EAYIRRAVRWRKMVGGGMRQAGILAAAGLYALKNNVQRLQEDHDNAAWMAEQLRAIGADVTRHDTNMLFV

RVGEEQAPALGKFMQAQGVLINASPVVRLVTHLDVNRQQLSEVVAHWQAFLQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176700.1\_2022 [gene=poxB] [locus\_tag=BN49\_RS11580] [protein=ubiquinone-dependent pyruvate dehydrogenase] [protein\_id=WP\_004176700.1] [location=complement(2071449..2073167)] [gbkey=CDS]

MKQTVAAYIAKTLEQAGVKRIWGVTGDSLNGLSDSLNRMGTIDWMPTRHEEVAAFAAGAEAQLTGELAVC

AGSCGPGNLHLINGLFDCHRNHVPVLAIAAHIPSSEIGSGYFQETHPQELFRECSHYCELVSTPEQIPQV

LAVAMRKAVINRGVSVVVLPGDVALKAAPESASSHWYHAPLPTVTPAEEELRKLAQLIRYSSNIALMCGS

GCAGAHQELVEFAAKIKAPIVHALRGKEHVEYDNPYDVGMTGLIGFSSGFHTMMNADTLILLGTQFPYRA

FYPTDAKIIQIDINPGSIGAHSKVDMALVGDIKSTLKALLPLLEEKTDRHFLDKALEHYRDARKGLDDLA

KPSDKAIHPQYLAQQISHFADEDAIFTCDVGTPTVWAARYLKMNGKRRLLGSFNHGSMANAMPQAIGAKA

TAPERQVVAMCGDGGFSMLMGDFLSLAQMKLPVKIVIFNNSVLGFVAMEMKAGGYLTDGTELHDTNFARI

AEACGIKGIRVEKASEVDEALQTAFRTDGPVLVDVVVAKEELAIPPQIKLEQAKGFSLYMLRAIISGRGD

EVIELAKTNWLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002896408.1\_2023 [locus\_tag=BN49\_RS11585] [protein=DoxX family protein] [protein\_id=WP\_002896408.1] [location=2073319..2073753] [gbkey=CDS]

MVKGLLNTVNRRLSHDDAGKLLLRLAVGGLMLFHGIHKLIDGVDGISGMLAAQGLPGFIAYGVLVGEVVA

PCLLILGVLTRPAALVLAFTMVVAWLMVGLDKTFALDAVGAWAIENLVYFFVGALAIALLGAGRYSLAGQ

SAWR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529505.1\_2024 [gene=hcr] [locus\_tag=BN49\_RS11590] [protein=NADH oxidoreductase] [protein\_id=WP\_016529505.1] [location=complement(2073965..2074933)] [gbkey=CDS]

MTMPTSQCPWRMQVHHIHQETPDVWTLSLLCHDYYPYRAGQYALVSVRNSAETLRAYTLSSTPGVSEYIT

LTVRRIDEGTGSQWLTREVKRGDYLWLSDAMGEFTCDDKAEDKFLLLAAGCGVTPIMAMRRWLAKHRPQA

DVQVIYNVRSPEDVIFAEEWRNYPVTLVAEHNATHGFVAGRLTRELLQSVPDLASRTVMTCGPAPYMEKV

EQDVAALGVTRFFKEKFFTPVAEAATSGLKFTKLQPAREFYAPVGTTLLDALESNKVPVTVACRAGVCGC

CKTKVVSGKYRVTSTMTLTDAEIADGYVLACSCHPQSDLVLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176696.1\_2025 [gene=hcp] [locus\_tag=BN49\_RS11595] [protein=hydroxylamine reductase] [protein\_id=WP\_004176696.1] [location=complement(2074944..2076596)] [gbkey=CDS]

MFCVQCEQTIRTPAGNGCSYAQGMCGKTAETSDLQDLLIASLQGLSAWALKAREYGIIDHQVDSFAPRAF

FSTLTNVNFDSPRIVGYARQAIALREALKAQCLAIDASAAVDSPVADLQLVSDDLGDLQRQAADYTPNKD

KAAIGENILGLRLLCLYGLKGAAAYMEHAHVLGQYDNAIYAQYHKIMAWLGTWPADMNALLECSMEIGQM

NFKVMSILDAGETTKYGHPTPTQVNVKATEGKCILISGHDLKDLYNLLEQTEGTGVNVYTHGEMLPAHGY

PELRKFKHLIGNYGSGWQNQQVEFARFPGPIVMTSNCIIDPTVGAYDDRIWTRSIVGWPGVNHLEGEDFS

PVIAQAQQMAGFPYSEIPHLITVGFGRQTLLGAADTLIDLVSREKLRHIFLVGGCDGARGERNYFTDFAT

SVPDDCLILTLACGKYRFNKLDFGDIEGLPRLVDAGQCNDAYSAIILAVTLAEKLGCGVNDLPLSLVLSW

FEQKAIVILLTLLSLGVKNIVTGPTAPGFFTPDLLAVLNEKFGLRSVTTVEQDMQQLLSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004147773.1\_2026 [locus\_tag=BN49\_RS11600] [protein=lysine exporter LysO family protein] [protein\_id=WP\_004147773.1] [location=complement(2076740..2077639)] [gbkey=CDS]

MFSGLFIILLPLVVGYLLPLRHSSALKLINRMLSWIVYVILFFMGISLAFLDNLASNLLAILHYAAVSVV

IILLCNIAALLWLESKMPWRSQHRQEKLPSRLAMALESLQLCGVVVLGFLLGLTRLPFLQHATEASEYTL

IFLLFLVGIQLRNNGMSLRQIVLNRRGMIVAVVVTASSLLGGILNAFILGLPLKTGLAMASGFGWYSLSG

ILLTESFGPVIGSAAFFNDLCRELLAIMLIPGLIRRSRSTALGLCGATSMDFTLPVLQRSGGVEIVPAAI

VHGFLLSLLVPILIAFFTA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529507.1\_2027 [gene=aqpZ] [locus\_tag=BN49\_RS11605] [protein=aquaporin Z] [protein\_id=WP\_016529507.1] [location=complement(2077755..2078450)] [gbkey=CDS]

MFRKLAAECFGTFWLVFGGCGSAVFAAAFPELGIGFAGVALAFGLTVLTMAFAVGHISGGHFNPAVTLGL

WAGGRFPAKEVIGYIIAQVVGGIIAAAVLYVVASGKAGFDAAASGFASNGYGEHSPGGFSMLSAIVIEIV

LTCGFLLVIHGATDKHAPAGFAPIAIGLALTLIHLISIPVTNTSVNPARSTAVAIFQGGWALQQLWLFWV

MPIVGGILGGVLYRTLLEKRD

>lcl|NZ\_FO834906.1\_prot\_WP\_004176693.1\_2028 [locus\_tag=BN49\_RS11610] [protein=ATP-dependent endonuclease] [protein\_id=WP\_004176693.1] [location=2078870..2080528] [gbkey=CDS]

MLLERVEIVGFRGINRLSLMLEQNNVLIGENAWGKSSLLDALTLLLSPEFDLYHFVRDDFWFPPGDIQGR

EHHLHIILTFRETEPGRHRVRRFRPLQRCWVPCDDGYHRVFYRLEGELAEDDSVMTLRSFIDGEGEALVL

EEIDELARHLVRLMPVLRLRDARFMRRIHNGTVPHSPQIEITARQLDFLSRELVSHPQNLSDGQIRQGLS

AMVQLLEHYFAEQSSAQTRHRLMRRRSHDEQRSWRYLDIINRMIDKPGGRSHRVILLGLFATLLQAKGTV

RLDRDARPLLLIEDPETRLHPIMLSVAWHLLNLLPLQRVTTTNSGELLSLTPVEQVCRLVRESTRVSAWR

LGPGGMNAEESRRIAFHIRFNRASSLFARCWLLVEGETETWVINELARQCGHHFDAEGVKVIEFAQSGLK

PLIKFARRMGIQWHVLVDGDEAGKKYAATVRGLLNNDRELERDHLTSLPALDMEHFMYRQGFDDVYHRVA

QIPDNVPMNMRRVITKAIHRSSKPDLAIEVAMEAGRRGVDAVPTLLKKMFSRVLWLARGRAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002896440.1\_2029 [gene=macA] [locus\_tag=BN49\_RS11615] [protein=macrolide transporter subunit MacA] [protein\_id=WP\_002896440.1] [location=2080675..2081790] [gbkey=CDS]

MKVKGKRRTVWWLLAIVVLGLAIWGWRILNAPLPNYQTLVVRKGDLQQSVLATGKLDALRKVDVGAQVSG

QLKTLHVNIGDKVKKDQLLGVIDPEQAQNQIKEVEATLMELRAQLNQARAESKLAQVTLARQQQLAQRQL

VSRQDLDTAATDLAVKQAQIGTIEAQIKRNQATLDTAKTNLDYTRILAPMAGEVTQITTLQGQTVIAAQQ

APNILTLADLSTMLVKAQVSEADVIHLRPGQKAWFTVLGDPLTRYEGKLKDILPTPEKVNDAIFYYARFE

VPNPQGILRLDMTAQVHIQLAEVKNVITIPLSALGDAVGDNRYHVRLLRTGEVKEREVIIGARNDTDVAV

VQGLEEGDEVIVGESASGAAK

>lcl|NZ\_FO834906.1\_prot\_2030 [gene=macB] [locus\_tag=BN49\_RS11620] [protein=macrolide ABC transporter ATP-binding protein/permease MacB] [pseudo=true] [location=2081787..2083714] [gbkey=CDS]

MTALLELRNIRRSYPSGDGSVEVLKGITLSIHAGEMVAIVGASGSGKSTLMNILGCLDKPTSGTYRVAGT

DIAQLDGDALARLRREHFGFIFQRYHLLSHLTAAQNVEVPAVYAGSERRALMSCWCGWGWASAPTINRHS

CPAVSSSGSVSPAP\*\*MAGR\*SSLMNRPARWTAIPAKR\*WRSCTS\*KRRGTRSSL\*PTIRRSPLRRSGSS

RSAMARSSATRPPVARAADCAPVRRRSLRRGVSLPAAFAKRW\*WPGERWRRIKCVPC\*PCSALLSVLPRW

CRSWWWGMPPSRWCWRIFAPSAPIPLMCILVRILATTTRAISRR\*SMTICWRSRSSRGCAPPRRRFQKAC

ACAPTILTLPPARRGSVHSILMSTA\*PLAKAIPSMNCSSTVGHRW\*CSTAIPVGSCFPIKRKWWER\*FWW

AICRPR\*LALRMKNSRCSAAAKFSASGCPTPPWREE\*WASRG\*TPSLCAFMKATTVKPQRNSCCVCWSCG

MVKKMYSPGIWTAS\*KPPKGPHIPYSCS\*HWWR\*LPWWSAGLA\*\*ILCWCR\*PNEPGRSASAWRLAPGPA

MCCSSFSLKRCWFAWSVVRWA\*HCR\*\*SPLFYSCFSPAGRLVFLRWRC\*RRFSVRR\*PGCCLVGCLRATR

RGSIRWMPWREN

>lcl|NZ\_FO834906.1\_prot\_WP\_002896516.1\_2031 [gene=cspD] [locus\_tag=BN49\_RS11625] [protein=cold shock-like protein CspD] [protein\_id=WP\_002896516.1] [location=complement(2083791..2084012)] [gbkey=CDS]

MEMGTVKWFNNAKGFGFICPEGGGEDIFAHYSTIQMDGYRTLKAGQAVRFDVHQGPKGNHASVIVPVEAE

TAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002896520.1\_2032 [gene=clpS] [locus\_tag=BN49\_RS11630] [protein=ATP-dependent Clp protease adapter ClpS] [protein\_id=WP\_002896520.1] [location=2084338..2084655] [gbkey=CDS]

MSKRDWLDFEHLVDDEVRDAIKPPSMYKVILVNDDYTPMEFVIDVLQKFFSYDVERATQLMLTVHYEGKA

ICGVFTAEVAETKVAMVNQYARENEHPLLCTLEKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532438.1\_2033 [gene=clpA] [locus\_tag=BN49\_RS11635] [protein=ATP-dependent Clp protease ATP-binding subunit ClpA] [protein\_id=WP\_016532438.1] [location=2084686..2086965] [gbkey=CDS]

MLNQELELSLNMAFARAREHRHEFMTVEHLLLALLSNPSAREALEACSVDLVALRQELEAFIEQTTPVLP

ATEEERDTQPTLSFQRVLQRAVFHVQSSGRSEVTGANVLVAIFSEQESQAAYLLRKHEVSRLDVVNFISH

GTRKDEPSQSSDNSGSQPGNEEQAGGEERMENFTTNLNQLARVGGIDPLIGREKELGRAIQVLCRRRKNN

PLLVGESGVGKTAIAEGLAWRIVQGDVPEVMADCTIYSLDIGSLLAGTKYRGDFEKRFKALLKQLEQDTN

SILFIDEIHTIIGAGAASGGQVDAANLIKPLLSSGKIRVIGSTTYQEFSNIFEKDRALARRFQKIDITEP

SVEETVQIINGLKPKYEAHHDVRYTAKAVRAAVELAVKYINDRHLPDKAIDVIDEAGARARLMPVSKRKK

TVNVADIESVVARIARIPEKSVSRSDRDTLKNLGDRLKMLVFGQDKAIEALTEAIKMARAGLGHEHKPVG

SFLFAGPTGVGKTEVTVQLAKALGIELLRFDMSEYMERHTVSRLIGAPPGYVGFDQGGLLTDAVIKHPHA

VLLLDEIEKAHPDVFNLLLQVMDNGTLTDNNGRKADFRNVVLVMTTNAGVRETERKSIGLIQQDNSPDAM

DEIKKIFTPEFRNRLDNIIWFDHLSTTVIHQVVDKFIVELQVQLDQKGVSLEVSQEARDWLATKGYDRAM

GARPMGRVIQDNLKKPLANELLFGSLVDGGQVTVSLDSDKNTLTYDFQSAPKHKPEAAH

>lcl|NZ\_FO834906.1\_prot\_WP\_001040187.1\_2034 [gene=infA] [locus\_tag=BN49\_RS11640] [protein=translation initiation factor IF-1] [protein\_id=WP\_001040187.1] [location=complement(2087095..2087313)] [gbkey=CDS]

MAKEDNIEMQGTVLETLPNTMFRVELENGHVVTAHISGKMRKNYIRILTGDKVTVELTPYDLSKGRIVFR

SR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898014.1\_2035 [gene=aat] [locus\_tag=BN49\_RS11645] [protein=leucyl/phenylalanyl-tRNA--protein transferase] [protein\_id=WP\_002898014.1] [location=complement(2087667..2088368)] [gbkey=CDS]

MRLVQLSRHSIAFPSPEGALREPNGLLALGGDLSPARLLMAYQRGIFPWFSPGDPILWWSPDPRAVLWPE

QFHLSRSMKRFHQRSPYRVTLNHAFGEVIEGCASDRDEGTWITSSIVRAYHQLHELGHAHSIEVWQENTL

VGGMYGVAQGALFCGESMFSRAENASKTALLVFCQDFAHSGGKLIDCQVLNNHTASLGAVDIPRRDYLDY

LSVLRGYRLPERFWVPRVLFPGG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532437.1\_2036 [gene=cydC] [locus\_tag=BN49\_RS11650] [protein=cysteine/glutathione ABC transporter ATP-binding protein/permease CydC] [protein\_id=WP\_016532437.1] [location=complement(2088413..2090134)] [gbkey=CDS]

MRALLPYLALYKRHKWMLLLGVVLAIVTLLASIGLLTLSGWFLSASAVVGVAGIYSFNYMLPAAGVRGAA

IIRTAGRYFERLVSHDATFRVLQHLRVFTFSKLLPLSPAGLARFRQGELLNRVVADVDTLDHLYLRVISP

LVGALVVIVVVTCGLSLLDVTLALTLGGIMLATLLVMPPLFYRAGKPAGESMTQLRGQYRQQLTAWLQGQ

AELMVFNASDRYRAQMEKTELSWQDAQRRQAELTALSQAVMLLIGGIAVVAMLWLASDGVGGNSQPGALI

ALFVFCALAAFEALAPVTGAFQHLGQVIASARRISQITDQQPEVTFVEDEASPPAQVALTLREVTFRYPQ

QPSPALENISLQIAAGEHIAILGRTGCGKSTLLQLLTRAWDPSQGEILLNNQPLSGLSEATLRQAMSVVP

QRVHLFSATLRDNLLLAAPEADDAHLSATLEKVGLEKLLQDGGLNGWLGEGGRQLSGGELRRLAIARALL

HDAPLMLLDEPTEGLDAATESQILHLLADVMRDKTVLMVTHRLRGLAGFNQIIVMDNGQIIEQGSHAELL

AKQGRYFQFKQRL

>lcl|NZ\_FO834906.1\_prot\_WP\_046042977.1\_2037 [gene=cydD] [locus\_tag=BN49\_RS11655] [protein=cysteine/glutathione ABC transporter permease/ATP-binding protein CydD] [protein\_id=WP\_046042977.1] [location=complement(2090135..2091901)] [gbkey=CDS]

MNKTRQQELTRWLKQQSIISRRWLMISRLLGVASGLLIVAQAWFLARILHRMVMENIPATALLLPLTLLV

LIFVLRAWVVWLRERVGFQAGQHIRYEIRRQVLDRLQQAGPAWIQGKPAGSWATLILEQIDDMHDYYARY

LPQMTLAACVPLLIVITIFPINWAAALILLGTAPLIPLFMALVGMGAADANRRNFQALARLSGHFLDRLR

GMETLRIFHRGQAETDNIRDASQDFRQRTMEVLRLAFLSSGVLEFFTSLSIALVAVYFGFSYLGELNFGH

YGAGVTLMAGFLTLILAPEFFQPLRDLGTFYHAKAQAVGAADSLKTFMETPLTQVERGEKTLNDNDLISV

EARDLVIKSPEGKVLAGPLNFALPAGARVVLVGQSGSGKSSLLNTLLGFLPYEGSLMVNGVELRELDAER

WRRLLSWVGQNPQLPAATLRENVLLAWPEASEAQLRLALGKAWVSEFIALLPQGIHTAVGDQAGRLSVGQ

AQRIAVARALLVPCRLLLLDEPAASLDAHSEQRVMQALTHASSEQTTLLVTHQLEGLADWDDVWVMQDGQ

IIEQGDYATLARAGGVFSALLAHRQEEI

>lcl|NZ\_FO834906.1\_prot\_WP\_002898019.1\_2038 [gene=trxB] [locus\_tag=BN49\_RS11660] [protein=thioredoxin-disulfide reductase] [protein\_id=WP\_002898019.1] [location=complement(2092016..2092984)] [gbkey=CDS]

MGTAKHSKLLILGSGPAGYTAAVYAARANLQPVLITGMEKGGQLTTTTEVENWPGDPNDLTGPLLMERMH

EHAAKFETEIIFDHISRVDLQNRPFRLTGDSGEYTCDALIIATGASARYLGLPSEEAFKGRGVSACATCD

GFFYRNQKVAVIGGGNTAVEEALYLSNIASEVHLIHRRDSFRAEKILIKRLMDKVASGNIVLHTDRTLEE

VTGDQMGVSGLRLRDTKNSDNVESLEVAGLFVAIGHSPNTAIFEGQLELENGYIKVQSGIHGNATQTSIP

GVFAAGDVMDHIYRQAITSAGTGCMAALDAERYLDGLADACK

>lcl|NZ\_FO834906.1\_prot\_WP\_000228469.1\_2039 [gene=lrp] [locus\_tag=BN49\_RS11670] [protein=leucine-responsive transcriptional regulator Lrp] [protein\_id=WP\_000228469.1] [location=2093517..2094011] [gbkey=CDS]

MVDSKKRPGKDLDRIDRNILNELQKDGRISNVELSKRVGLSPTPCLERVRRLERQGFIQGYTALLNPHYL

DASLLVFVEITLNRGAPDVFEQFNAAVQKLEEIQECHLVSGDFDYLLKTRVPDMSAYRKLLGETLLRLPG

VNDTRTYVVMEEVKQSNRLVIKTR

>lcl|NZ\_FO834906.1\_prot\_WP\_046042979.1\_2040 [gene=ftsK] [locus\_tag=BN49\_RS11675] [protein=DNA translocase FtsK] [protein\_id=WP\_046042979.1] [location=2094147..2098349] [gbkey=CDS]

MSQEYTEDKEVKLTKLSSGRRLLEAMLILCSLFAIWLMAALLSFNPSDPSWSQTAWHEPIHNLGGAPGAW

LADTLFFIFGVMAYTIPVIIIGGCWFAWRHQENDEYIDYFAVSLRLIGALALILTSCGLAAINADDIWYF

ASGGVIGSLLSTTLQPLLHSSGGTIALLCIWAAGLTLFTGWSWVSIAEKLGGGILSVLTFASNRTRRDDT

WVDEGEYEDDEEEYDDEEAARPQESRRARILRSALARRKRLAEKFTNPMGRKTDAALFSGKRMDDGEEVV

QYSASGAPVAADDVLFSGASAARPAEDDVLFSGASAVRPGDFDPYDPLLNGHSIAEPVSAAAAATAAPQA

WAESPVGHHGAAPAYQPEASYPPQQAYQPEPAPFQQAAYQPPAGQTAPQAYQPEPAPYQQPVYDPRAGQP

APQAYQPEPAPYQQPAYDPYAGQPAPQAYQPEPAPYQQPAYDPHAGQPAPQSYQPEPAPYQQPTYDPHAG

QPAPQAYQPEPAPYQQPAYDPNAGQLAPQTYQQPAYDPHAGQPAPQPYQPEPAAYQPQSAPVPPPEPEPE

VVQEEVKRPPLYYFEEVEEKRARERELLASWYQPIPEPESPIATKPLTPPTTASKPPVETTVVSAVAAGV

HQATAASGGAAAATSSTAASAAATPLFSPASSGPRVQVKEGIGPKLPRPNRVRVPTRRELASYGIKLPSQ

REAEQRARQAERDPHYDDELLSDEEADAMEQDELARQFAATQQQRYGHRWEDDNATDDDEADAAAEAELA

RQFAATQQQRYATEQPPGANPFSPADYEFSPMKTLVNDGPSEPLFTPTPEVQPQQPAQRYQQPAAAPQQS

YQPAQHQPIHHQPVPPQPQSYPTASQPVQPQQPVAPQGHQPAAPAPQESLIHPLLMRNGDSRPLQKPTTP

LPSLDLLTPPPSEVEPVDTFALEQMARLVEARLADFRIKADVVNYSPGPVITRFELNLAPGVKAARISNL

SRDLARSLSTVAVRVVEVIPGKPYVGLELPNKKRQTVYLREVLDNAKFRDNPSPLTVVLGKDIAGDPVVA

DLAKMPHLLVAGTTGSGKSVGVNAMILSMLYKAQPEDVRFIMIDPKMLELSVYEGIPHLLTEVVTDMKDA

ANALRWSVNEMERRYKLMSALGVRNLAGYNEKIAEAARMGRPIPDPYWKPGDSMDAVHPVLEKLPYIVVL

VDEFADLMMTVGKKVEELIARLAQKARAAGIHLVLATQRPSVDVITGLIKANIPTRIAFTVSSKIDSRTI

LDQGGAESLLGMGDMLYSGPNSTTPVRVHGAFVRDQEVHAVVQDWKARGRPQYVDGITSDSESEGGGGGF

DGGEELDPLFDQAVNFVTEKRKASISGVQRQFRIGYNRAARIIEQMEAQGIVSEQGHNGNREVLAPPPFE

>lcl|NZ\_FO834906.1\_prot\_WP\_002898132.1\_2041 [gene=lolA] [locus\_tag=BN49\_RS11680] [protein=outer membrane lipoprotein chaperone LolA] [protein\_id=WP\_002898132.1] [location=2098472..2099083] [gbkey=CDS]

MKKLAITCALLSGMVVSQVWADAASDLKSRLDKVSSFHASFTQKVTDGSGNAVQDGQGDLWVKRPNLFNW

HMTQPDESVLVSDGKTLWFYNPFVEQATATWLKDATSNTPFMLIARNQSSDWQQYNIKQNGDDFVLTPKS

GSGNLKQFTINVGRDGTIHQFSAVEQDDQRSSYQLKSQQNGAVDAAKFTFTPPKGVTVDDQRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002898137.1\_2042 [gene=rarA] [locus\_tag=BN49\_RS11685] [protein=replication-associated recombination protein RarA] [protein\_id=WP\_002898137.1] [location=2099092..2100435] [gbkey=CDS]

MSNLSLDFSDNAFQPLAARMRPENLAQYIGQQHLLAPGKPLPRAIEAGHLHSMILWGPPGTGKTTLAEVI

ARYASADVERISAVTSGVKEIREAIERARQNRNAGRRTILFVDEVHRFNKSQQDAFLPHIEDGTITFIGA

TTENPSFELNSALLSRARVYLLKSLTTDDIERVLDQAMNDKTRGYGGQDIILPDETRRAIAELVNGDARR

ALNTLEMMADMAESDDSGKRVLKAELLTEIAGERSARFDNKGDRFYDLISALHKSVRGSAPDAALYWYAR

IITAGGDPLYVARRCLAIASEDVGNADPRAMQVAISAWDCFTRVGPAEGERAIAQAIVYLACAPKSNAVY

TAFKAALADARDRPDYDVPVHLRNAPTKLMKEMGYGQEYRYAHDEPNAYAAGEQYFPQEMAQTRYYHPTN

RGLEGKIGEKLAWLAEQDQNSPIKRYR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898139.1\_2043 [gene=serS] [locus\_tag=BN49\_RS11690] [protein=serine--tRNA ligase] [protein\_id=WP\_002898139.1] [location=2100526..2101818] [gbkey=CDS]

MLDPNLLRTEPDAVAEKLARRGFKLDVDKLRALEERRKVLQVQTENLQAERNSRSKSIGQAKARGEDIEP

LRLEVNKLGEQLDAAKSELETLLAEIRDIALAIPNIPHDDVPVGRDENDNVEVSRWGTPRQFDFEVRDHV

TLGEMHGGLDFAAAVKLTGSRFVVMKGQLARLHRALAQFMLDLHTEQHGYSENYVPYLVNQDTLYGTGQL

PKFAGDLFHTRPLEEEADSSNYALIPTAEVPLTNLVRDEIIDEDDLPIKMTAHTPCFRSEAGSYGRDTRG

LIRMHQFDKVEMVQIVRPEDSMAALEEMTGHAEKVLQLLGLPYRKVALCTGDMGFSACKTYDLEVWVPAQ

NTYREISSCSNVWDFQARRMQARCRSKSDKKTRLVHTLNGSGLAVGRTLVALMENYQQADGRIEIPEVLR

PYMRGLEYIG

>lcl|NZ\_FO834906.1\_prot\_WP\_004147794.1\_2044 [gene=dmsA] [locus\_tag=BN49\_RS11695] [protein=dimethylsulfoxide reductase subunit A] [protein\_id=WP\_004147794.1] [location=2102019..2104457] [gbkey=CDS]

MKIKAPDALLAAEVSRRGLMKTTAIGGLALASNALTLPFTRLSHAADTPAPASEKVVWSACTVNCGSRCP

LRMHVVDGAIKYVETDNTGDDNYDGLHQVRACLRGRSMRRRVYNPDRLKYPMKRVGKRGEGKFEQISWEE

ALDTIASNMQRLIKEYGNESIYLNYGTGTLGGTLTRSWPPGKTLIARLMNCCGGYLNHYGDYSSAQIAAG

LNYTYGGWADGNSPSDIENSQLVVLFGNNPGETRMSGGGVTYYLEQARQKSNARMIIIDPRYTDTGAGRE

DEWIPIRPGTDAALVSGLAWVMITENLVDQPFLDKYCVGYDEKTLPAGAPANGHYKAYILGQGTDGIAKT

PEWASTITGIPRERIVKLAREIATAKPAYISQGWGPQRHANGEIATRAISMLAILTGNVGINGGNSGARE

GSYSLPFERMPTLENPVETSISMFMWTDAIERGPEMTALRDGVRGKDKLDVPIKMIWNYAGNCLINQHSE

INRTHEILQDDKKCEMIVVIDCHMTSSAKYADILLPDCTASEQMDFALDASCGNMSYVIFADQAIKPRFE

CKTIYEMTSELAKRLGVEEQFTEGRTQEGWMRYLYEQSRKAIPDLPDFDTFRQQGIYKQRDPQGHHVAYK

AFREDPQANPLTTPSGKIEIYSQDLAKIAATWELPEGDVIDPLPIYTPGFENYNDPLTAKYPLQLTGFHY

KSRVHSTYGNVDVLKAACRQEMWINPIDARKRGIANGDRIRIFNDRGEVHIEAKVTPRMMPGVVALGEGA

WYNPDASRVDQAGSINVLTTQRPSPLAKGNPSHTNLVQVEKL

>lcl|NZ\_FO834906.1\_prot\_WP\_004150845.1\_2045 [gene=dmsB] [locus\_tag=BN49\_RS11700] [protein=dimethylsulfoxide reductase subunit B] [protein\_id=WP\_004150845.1] [location=2104468..2105085] [gbkey=CDS]

MTTQYGFFIDSARCTGCKTCELACKDYKNLTPEVSFRRIYEYAGGDWQEDNGVWQQNVFAYYLSIACNHC

EDPACTKVCPSGAMHKREDGFVVVNEEVCIGCRYCHMACPYGAPQYNADKGHMTKCDGCHERVAEGKKPI

CVESCPLRALDFGPIAELRAKHGQLAAVAPLPSAHFTRPSIVIKPNANARPCGDTTGYLANPKEV

>lcl|NZ\_FO834906.1\_prot\_WP\_004183542.1\_2046 [locus\_tag=BN49\_RS11705] [protein=dimethyl sulfoxide reductase anchor subunit] [protein\_id=WP\_004183542.1] [location=2105087..2105950] [gbkey=CDS]

MGNGWHEWPLMVFTVFGQCVVGGFIVLALALMTGKLSREQEQRVVGSMLGLWVLMGIGFIASTMHLGSPL

RAFNSLNRVGASSLSNEIASGAIFFAVGGIGWLLAVCKKLPAGLRSLWLVVTMVLGVIFVWMMVRVYNTI

DTVPTWYTVWTPLSFFLTLFIGGPLLGYLLLRVAGVDGWALRLLPVVSLLALLVSIMVVVMQGSELATIR

SSVQQASALVPDYGLLMAWRVVLLALALACWCVPQIRGRKPAVSLLGLAFVLILAGEMIGRGVFYGLHMT

VGMAVAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004150843.1\_2047 [locus\_tag=BN49\_RS11715] [protein=MFS transporter] [protein\_id=WP\_004150843.1] [location=2106225..2107373] [gbkey=CDS]

MTIYTRPVQMLLCGLLLLTLAIAVLNTLVPLWLAHENMPTWQVGMVGSSYFTGNLAGTLLAGWVIKRLGF

NRSYYLASLIFAVGCVGLGITVGFWTWLSWRFIAGVGCAMIWVVVESALVCSGTSRSRGRLLAAYMMVYY

VGTVLGQLMVSKLPTDLMSVLPWVTGLALAAILPLLFTRIMGQAEEPHETVRIWPMLKLRQARHGVNGCI

ISGIVLGSLYGLMPLWLNHQGVSDSGIGFWMAVMVSAGILGQWPVGRLADRYGRLLVLRVQVFVVILGCL

AMLSQAAMAPALFVLGASGFTLYPVAMAWACEKVEHHQLVAMNQALLMSYTIGSLLGPTLTAMLMQNFSD

NLLFIMIASVSFIYLLTLLRKAGHHPTPVAHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898145.1\_2048 [gene=pflA] [locus\_tag=BN49\_RS11720] [protein=pyruvate formate lyase 1-activating protein] [protein\_id=WP\_002898145.1] [location=complement(2107536..2108276)] [gbkey=CDS]

MSVIGRIHSFESCGTVDGPGIRFITFFQGCLMRCLYCHNRDTWDTHGGKEITVEELMKEVVTYRHFMNAS

GGGVTASGGEAILQAEFVRDWFRACKKEGIHTCLDTNGFVRRYDPVIDELLEVTDLVMLDLKQMNDEIHQ

NLVGVSNHRTLEFAQYLAKKNINVWIRYVVVPGWSDDDDSAHRLGEFTRDMGNVEKIELLPYHELGKHKW

VAMGEEYKLDGVHPPKKETMERVKGILEQYGHKVMY

>lcl|NZ\_FO834906.1\_prot\_WP\_002898148.1\_2049 [gene=pflB] [locus\_tag=BN49\_RS11725] [protein=formate C-acetyltransferase] [protein\_id=WP\_002898148.1] [location=complement(2108468..2110750)] [gbkey=CDS]

MSELNEKLATAWEGFAKGDWQNEVNVRDFIQKNYTPYEGDESFLAGATEATTKLWDTVMEGVKQENRTHA

PVDFDTALASTITSHDAGYIEKGLEKIVGLQTEAPLKRAIIPFGGIKMVEGSCKAYNRELDPMLKKIFTE

YRKTHNQGVFDVYTPDILRCRKSGVLTGLPDAYGRGRIIGDYRRVALYGIDFLMKDKFAQFNSLQAKLES

GEDLEATIRLREEIAEQHRALGQIKEMAAKYGYDISGPATTAQEAIQWTYFGYLAAVKSQNGAAMSFGRT

SSFLDIYIERDLQAGKITEQDAQEMVDHLVMKLRMVRFLRTPEYDELFSGDPIWATESIGGMGVDGRTLV

TKNSFRFLNTLYTMGPSPEPNITILWSEKLPLSFKKFAAKVSIDTSSLQYENDDLMRPDFNNDDYAIACC

VSPMVVGKQMQFFGARANLAKTMLYAINGGVDEKLKMQVGPKSEPIKGDVLNFDEVMDRMDHFMDWLAKQ

YVTALNIIHYMHDKYSYEASLMALHDRDVIRTMACGIAGLSVAADSLSAIKYAKVKPIRDEDGLAIDFEI

EGEYPQFGNNDPRVDDMAVDLVERFMKKIQKLHTYRNAIPTQSVLTITSNVVYGKKTGNTPDGRRAGAPF

GPGANPMHGRDQKGAVASLTSVAKLPFAYAKDGISYTFSIVPNALGKDDEVRKTNLAGLMDGYFHHEASI

EGGQHLNVNVMNREMLLDAMENPEKYPQLTIRVSGYAVRFNSLTKEQQQDVITRTFTQTM

>lcl|NZ\_FO834906.1\_prot\_WP\_002898150.1\_2050 [gene=focA] [locus\_tag=BN49\_RS11730] [protein=formate transporter FocA] [protein\_id=WP\_002898150.1] [location=complement(2110802..2111659)] [gbkey=CDS]

MKADNPFDLLLPAAMAKVAEEAGVYKATKHPMKTFYLAITAGVFISIAFVFYITATTGTAAMPYGIAKLI

GGICFSLGLILCVICGADLFTSTVLIVVAKASGRITWGQLAKNWLNVYFGNLVGALLFVLLMWLSGEYMT

ANGGWGLNVLQTADHKMHHTFVEAVSLGILANLMVCLAVWMSYSGRSLMDKAMIMVLPVAMFVASGFEHS

IANMFMIPMGIVIRNFASPEFWTAIGSTPESFSHLTVMNFITDNLIPVTIGNIIGGGLLVGLTYWVIYLR

GNDHH

>lcl|NZ\_FO834906.1\_prot\_WP\_004150842.1\_2051 [locus\_tag=BN49\_RS11735] [protein=30S ribosomal protein S12 methylthiotransferase accessory protein YcaO] [protein\_id=WP\_004150842.1] [location=complement(2112045..2113805)] [gbkey=CDS]

MTQTFIPGKDAALEDSIARFQQKLLDLGFDIEEASWLNPVPHVWSVHIRDKACALCFTNGKGATKKAALA

SALGEYFERLSTNYFFADFWLGDTIANGPFVHYPNEKWFPLTEDDEVPEGLLDARLRAFYDPDDQLTASM

LVDLQSGNDERGVCGLPFTRQSDGETVYIPMNIVGNLYVSNGMSAGNTRNEARVQGLSEVFERHIKNRII

AESISLPEIPAEVMARYPGVVESIAKLEAEGFPIFAYDGSLGGKYPVICVVLFNPANGTCFASFGAHPDF

GVALERTVTELLQGRSLKDLDVFTPPTFDDEEVAEHANLETHFIDSSGLISWDMFKQDADYPFVDWSFSG

TTEEEFATLMAIFKAEDKEVYIADYEHLGVYACRIIVPGMSDIYPAEDLWLANNSMGAHLRDTILSLPGS

EWDKEDYLALIEQMDDEGLDDFTRVRELLGLATGKDNGWYTLRVGELKAMLALAGGDLEQALIWTEWTME

FNASVFSAERANYYRCLQTLLLLSQEEERQPLQYLNAFIRMYGADAVEAASAALSGEAPFYGLQAVDSDL

QAFPAHQSLLKAYEKLQRAKAAFWAK

>lcl|NZ\_FO834906.1\_prot\_WP\_046042983.1\_2052 [locus\_tag=BN49\_RS11740] [protein=DUF421 domain-containing protein] [protein\_id=WP\_046042983.1] [location=2113921..2114613] [gbkey=CDS]

MKAFDWQRMALDKVPVEFLAEVALRSLYTFVLVFIFLKITGRRGVRQMSLFEVLIILTLGSAAGDVAFYD

DVPLLPVLVVFVTLALLYRGIMWLMGHSEKLEDLLEGKPIVVVEEGQLAWEKLHAENMTEFEFFMELRVN

SVEQLGQVRLAILETNGQISVFYYPDDEVRAGLSILPAHCTTRYTTIPQEGIYACVRCSIVMAMQAGEKR

ICPRCANAEWSKASRAKRLT

>lcl|NZ\_FO834906.1\_prot\_WP\_002898155.1\_2053 [gene=serC] [locus\_tag=BN49\_RS11745] [protein=3-phosphoserine/phosphohydroxythreonine transaminase] [protein\_id=WP\_002898155.1] [location=2114802..2115890] [gbkey=CDS]

MAQVYNFSSGPAMLPAEVLKLAQQELCDWHGLGTSVMEISHRGKEFIQVAEEAEQDFRALLNIPSNYKVL

FCHGGGRGQFAGIPLNILGDKKVADYVDAGYWAASAVKEAKKYCTPNVIDAKITVDGKRAVKPMSEWQLT

PGAAYLHYCPNETIDGIAIDETPNFGDDVIVTADFSSTILSREIDVNRFGVIYAGAQKNIGPAGLTLVIV

REDLLGKASVACPSILDYTVLSENDSMFNTPPTFAWYLAGLVFKWLKQQGGVAAMDKINQQKAELLYGVI

DNSGFYRNDVAQANRSRMNVPFQLADSALDKLFLEESFAAGLHALKGHRVVGGMRASIYNAMPLDGVKAL

TDFMLDFERRHG

>lcl|NZ\_FO834906.1\_prot\_WP\_002898157.1\_2054 [gene=aroA] [locus\_tag=BN49\_RS11750] [protein=3-phosphoshikimate 1-carboxyvinyltransferase] [protein\_id=WP\_002898157.1] [location=2115964..2117247] [gbkey=CDS]

MESLTLQPIARVEGTVNLPGSKSVSNRALLLAALARGTTVLTNLLDSDDVRHMLNALSALGVQYTLSADR

TRCEVTGNGGPLRSAAALELFLGNAGTAMRPLAAALCLGSNDIVLTGEPRMKERPIGHLVDALRQGGAQI

DYLEQENYPPLRLRGGFQGGNVEVDGSVSSQFLTALLMTAPLAPQDTVIVIKGDLVSKPYIDITLHLMKT

FGVEVDNQSYQRFVVRGKQQYQSPGDYLVEGDASSASYFLAAGAIKGGTVKVTGIGRNSVQGDIRFADVL

EKMGATVTWGDDFIACTHGELKAVDMDMNHIPDAAMTIATAALFAQGTTTLRNIYNWRVKETDRLFAMAT

ELRKVGAEVEEGEDYIRITPPAKLKYAEIGTYNDHRMAMCFSLVALSDTPVTILDPKCTAKTFPDYFEQL

ARISTLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898160.1\_2055 [gene=cmk] [locus\_tag=BN49\_RS11755] [protein=(d)CMP kinase] [protein\_id=WP\_002898160.1] [location=2117422..2118105] [gbkey=CDS]

MTANIPVITIDGPGGAGKGTLCKAMAEALGWHLLDSGAIYRVLALAALHHHVDVESEEALVPLAAHLDVR

FISTDGNLEVVLEGEDVSSEIRTQEVANAASKVAAFPRVREALLRRQRAFRELPGLIADGRDMGTVVFPD

APVKIFLDASADERAHRRMRQLQEKGFDVNFERLLSEIKERDDRDRNRAVAPLVPAADALVLDSTELNIE

QVIEKALQYAREKLAVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898162.1\_2056 [gene=rpsA] [locus\_tag=BN49\_RS11760] [protein=30S ribosomal protein S1] [protein\_id=WP\_002898162.1] [location=2118239..2119912] [gbkey=CDS]

MTESFAQLFEESLKEIETRPGSIVRGVVVAIDKDVVLVDAGLKSESAIPAEQFKNAQGELEIQVGDEVDV

ALDAVEDGFGETLLSREKAKRHEAWITLEKAYEDAETVTGVINGKVKGGFTVELNGIRAFLPGSLVDVRP

VRDTLHLEGKELEFKVIKLDQKRNNVVVSRRAVIESENSAERDQLLENLQEGMEVKGIVKNLTDYGAFVD

LGGVDGLLHITDMAWKRVKHPSEIVNVGDEITVKVLKFDRERTRVSLGLKQLGEDPWVAIAKRYPEGTKL

TGRVTNLTDYGCFVEIEEGVEGLVHVSEMDWTNKNIHPSKVVNVGDVVEVMVLDIDEERRRISLGLKQCK

SNPWQQFAETHNKGDRVEGKIKSITDFGIFIGLDGGIDGLVHLSDISWNVAGEEAVREYKKGDEIAAVVL

QVDAERERISLGVKQLAEDPFNNYVALNKKGAIVVGKVTAVDAKGATVELADGVEGYLRASEASRDRVED

ATLVLSVGDEVEAKFTGVDRKNRVVSLSVRAKDEAEEKDAIATVNKQEDANFSNNAMAEAFKAAKGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002898165.1\_2057 [gene=ihfB] [locus\_tag=BN49\_RS11765] [protein=integration host factor subunit beta] [protein\_id=WP\_002898165.1] [location=2120064..2120351] [gbkey=CDS]

MTKSELIERLASQQSHIPAKAVEDAVKEMLEHMASTLAQGERIEIRGFGSFSLHYRAPRTGRNPKTGDKV

ELEGKYVPHFKPGKELRDRANIYEG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530945.1\_2058 [locus\_tag=BN49\_RS11770] [protein=ComEC family protein] [protein\_id=WP\_016530945.1] [location=2120557..2122821] [gbkey=CDS]

MRLPWLAGCAIIAMLPLLWLPVLPGPYSLAGASALALALIRLHGRAVAGVAMTLLLVVWGVLSAHQALWP

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QLNDGGFDSQRYALAQHRPLSGGIVAASALDARCSLRARYLTSLTRRLQTYPWRAVMLGLGMGERLSLPT

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ALRTCLGLAVCCALRLSGQRWTAWQVWLCCLGAILVADPLAVLSQSLWLSAFAVAGLIFWFQWLPLPAGR

WRWPWKTIIALVHLQAGVTLLLLPLQLLLFHGVSLTSMAANLLAVPLVTLLAVPLILTAMLVHLSGPDIV

ESLLWLAADRVLALLFWGLRRLPDGWLTLDARWLWISILPWLLVMGWRFQSWRHSPALCLSVLFLLTRPF

SRQPPADEWRVTMLDVGQGLAMVIERHGKALLYDTGPAWPQGDSGQQVIIPWLRWHHLQLQGIMLSHEHL

DHRGGLDSVLQAWPQAWVRSPLGWAHHLPCHRGERWQWQGLNFQALWPLPGSTAKGNNHSCVVRIDDGRS

SILLTGDIERQAEQAMISRYWRHLTSTLIQVPHHGSNTSSSALLVRRVDGAAALASASRYNAWRMPSYKV

VQRYRQRGYRWFATPQQGQITVVFSAEGWQIHSLRDQVLPRWYHQWFGAPADNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002898170.1\_2059 [gene=msbA] [locus\_tag=BN49\_RS11775] [protein=lipid A ABC transporter ATP-binding protein/permease MsbA] [protein\_id=WP\_002898170.1] [location=2122858..2124606] [gbkey=CDS]

MQNDKDLSTWQTFRRLWPIIAPFKAGLIVAAVALVLNAGSDTFMLSLLKPLLDDGFGKTDRSVLLWMPLV

VIGLMVLRGITSYISSYCISWVSGKVVMTMRRRLFGHMMGMPVAFFDKQSTGTLLSRITYDSEQVASSSS

SALITVVREGASIIGLFVMMFYYSWQLSLILIVLAPIVSVAIRVVSKRFRNISKNMQNTMGQVTTSAEQM

LKGHKEVLMFGGQEVETKRFDKVSNKMRLQGMKMVSASSISDPIIQLIASLALAFVLYAASFPSVMDTLT

AGTITVVFSSMIALMRPLKSLTNVNAQFQRGMAACQTLFAILDSEQEKDEGTRVIERAKGNLKFENVTFT

YPGREVAALRNINLDIPEGKTVALVGRSGSGKSTIASLITRFYDVDEGQILLDGHDLREYKLSSLRDQVA

LVSQNVHLFNDTVANNIAYARTEEYSREQIEEAARMAYAMDFINKMDNGLDTIIGENGVMLSGGQRQRIA

IARALLRNSPILILDEATSALDTESERAIQAALDELQKNRTSLVIAHRLSTIEQADEIVVVEDGRIVERG

THHDLLEHKGVYAQLHKMQFGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002898174.1\_2060 [gene=lpxK] [locus\_tag=BN49\_RS11780] [protein=tetraacyldisaccharide 4'-kinase] [protein\_id=WP\_002898174.1] [location=2124603..2125583] [gbkey=CDS]

MIARIWSGESPLWRLLLPLSWLYGLVSGVIRLSYQLGWQKAWRAPVPVVVVGNLTAGGNGKTPVVIWLVE

QLQQRGIRVGVVSRGYGGKADRYPLVLDDRTSTAQAGDEPVLIHQRTGAPVAVAPLRSDAVKALLSAHDL

QMIVTDDGLQHYKLARDREIVVIDGVRRFGNGWWLPAGPMRERASRLQSVDAVIVNGGVARPGEIPMRLR

PGMAVNLLTGERRDVSTFTNVVAMAGIGHPPRFFATLESCGVQPVKTVALADHQALSQADVAALVTADQT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530946.1\_2061 [locus\_tag=BN49\_RS11785] [protein=winged helix-turn-helix domain-containing protein] [protein\_id=WP\_016530946.1] [location=2125638..2126867] [gbkey=CDS]

MSVLQLSLNEARHLHLAAQGLLKKPRRRARPKDILSTIQQMSLLQIDTINVVARSPYLVLFSRLGSYPQH

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SADFTHPRKGASGWWEWKPHKRHLEGLFTAGEVMVVERRNFHRVYDLTRRVMPDWDDERDALSREDAEAI

MLRNSARSLGIFRAQWLADYYRLRQPALPGLLAAWQDEGLVVPVNVEALGEMWLHHEALAQLETAPGGKL

TASHSAVLSPFDPVVWDRKRAEQLFNFSYRLECYTPAPKRQYGYFVLPLLHQGKLVGRMDSKIHRKSREL

EIFALWLEEGVKITRGLEQGLRRAINDFTRWQSAERILCRRLPEGLFVGQEQGWEIDAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002898177.1\_2062 [gene=ycaR] [locus\_tag=BN49\_RS11790] [protein=protein YcaR] [protein\_id=WP\_002898177.1] [location=2126931..2127113] [gbkey=CDS]

MDHRLLEIIACPVCNGKLYYSQDKQELICKLDSLAFPLRDGIPVLLETEARPLALEESHS

>lcl|NZ\_FO834906.1\_prot\_WP\_002898180.1\_2063 [gene=kdsB] [locus\_tag=BN49\_RS11795] [protein=3-deoxy-manno-octulosonate cytidylyltransferase] [protein\_id=WP\_002898180.1] [location=2127110..2127856] [gbkey=CDS]

MSFVVIIPARFASTRLPGKPLQDINGKPMIVHVLERARESGADRIIVATDHEDVARAVEAAGGEVCMTRA

DHQSGTERLAEVVEKCAFSDDTIIVNIQGDEPMIPPAIVRQVAENLAASSSGMATLAVPIHDAEEAFNPN

AVKVVMDAKGYALYFSRATIPWDRDRFAQSRETIGDSLLRHIGIYGYRAGFIRRYVSWAPSPLEQIEMLE

QLRVLWYGEKIHVAVAAEVPGTGVDTPEDLERVRAELR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898182.1\_2064 [locus\_tag=BN49\_RS11800] [protein=YcbJ family phosphotransferase] [protein\_id=WP\_002898182.1] [location=2127994..2128887] [gbkey=CDS]

MEQLRTELSHLLGEKLSRVECVSEQAATALWFLYDAQGNPMPLLARSFTTPGVARQLAWKISTLARNGTV

RMPVVYGVMTHEEHPGPDVLLLERLRGVPVEAPTRTPARWEQLQEQIVEALLAWHRQDSGGCVGMVDNTQ

ENLWPNWYRQRVEILWSTLNLYQDTGLTMQDKRLLFRSRECLPELFRDFNDNAVLVHGNFTLRSMLKDPR

SDQLLAMVGPGMMLWAPREYELFRLAEGGQAEQLLWRYLQQAPVSEAFVWRRWLYLLWDEVDSLVNTGRF

DRARFDLAAKSLLPWLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004141786.1\_2065 [gene=elyC] [locus\_tag=BN49\_RS11805] [protein=envelope biogenesis factor ElyC] [protein\_id=WP\_004141786.1] [location=complement(2128864..2129643)] [gbkey=CDS]

MLFTLKKIVGGLLLPLPALLLLIGIGIALLWFSRFQRTGKLCVSLGWLLLTLLSLQPVADSLLKPIEDTY

PTWRGEQPVNYVVVLGGGYTWNPEWAPSSNLINNSLPRLTEGIRLWQANPGSKMIFTGAAAKTNPVSTAE

AGARVAESLGVPRSDIIVLDRPKDTEEEALAVKRAIGDAPFLLVTSASHLPRAMIFFRHAGLDPLPAPAN

QLAVTSPLNPWERAIPSPVWLMHSDRVGYETLGRVWQWLKGSSGEPGQE

>lcl|NZ\_FO834906.1\_prot\_WP\_002898187.1\_2066 [gene=cmoM] [locus\_tag=BN49\_RS11810] [protein=tRNA uridine 5-oxyacetic acid(34) methyltransferase CmoM] [protein\_id=WP\_002898187.1] [location=2129765..2130565] [gbkey=CDS]

MQDRNFDDIAEKFSRNIYGTTKGQLRQAILWQDLEPLLAQLGPGPLRVLDAGGGEGQTAIKVAQLGHHVT

LCDLSAEMVARARQAAADKGVIDNMHFVQCAAQDIAQHLESPVDLVLFHAVLEWVAEPQEILHTLWSTLR

AGGGLSLMFYNANGLLMHNMVAGNFDYVQLGMPKKKKRTLSPDYPREPQQVYHWLEEIGWQIVSKTGVRV

FHDYLREKRQQHDSYAALLALETRYCRQEPYLSLGRYIHVTALKSQAHSRRCKDKV

>lcl|NZ\_FO834906.1\_prot\_WP\_002898189.1\_2067 [gene=mukF] [locus\_tag=BN49\_RS11815] [protein=chromosome partition protein MukF] [protein\_id=WP\_002898189.1] [location=2130562..2131884] [gbkey=CDS]

MSEFSQTVPELVAWARKNDFSISLPVDRLSFLLAIATLNGERLEGEMSEGELVDAFRHVSDAFEQTSETI

SQRANNAINDLVRQRLLNRFTSEITEGNAIYRLTPLGIGITDYYIRQREFSTLRLSMQLSIVAGELKRAA

DAAEEGGDEFHWHRNVFAPLKYSVAEIFDSIDLTQRIMDEQQQLVKDDIAQLLNKDWRAAISSCELLLSE

TSGTLRELQDTLDAAGDKLQANLLRIQDSTMARDDLHFVDRLVFDLQSKLDRIVSWGQQAIDLWIGYDRH

VHKFIRTAIDMDKNRVFAQRLRQSVQTYFDEPWALTYANADRLLDMRDEEMALRDEEVTGELPADLEFEE

FNEIREQLAALIEAQLAVYKEKGIPLDLGLVAREFLAQYPRGRHFDVARIVVDQAVQLGVAQADFTGLPA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150840.1\_2068 [gene=mukE] [locus\_tag=BN49\_RS11820] [protein=chromosome partition protein MukE] [protein\_id=WP\_004150840.1] [location=2131865..2132569] [gbkey=CDS]

MSLTNIEQVMPVKLAQALANPLFPALDSALRAGRHIGLDELDNHAFLMDFQDYLEEFYARYNVELIRAPE

GFFYLRPRSTTLISRSVLSELDMMVGKILCYLYLSPERLANEGIFTQQELYDELLTLADESRLLKLVNNR

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MALENHLQLNDENEENQPDSGEEE

>lcl|NZ\_FO834906.1\_prot\_WP\_046042989.1\_2069 [gene=mukB] [locus\_tag=BN49\_RS11825] [protein=chromosome partition protein MukB] [protein\_id=WP\_046042989.1] [location=2132569..2137017] [gbkey=CDS]

MIERGKFRSLTLVNWNGFFARTFDLDELVTTLSGGNGAGKSTTMAAFVTALIPDLTLLHFRNTTEAGATS

GSRDKGLHGKLRAGVCYSVLDVINSRHQRVVVGVRLQQVAGRDRKVDIKPFAIQGLPTSILPTQLLTETL

NDRQACVVSLNELKDKLEAMEGVQFKQFNSITEYHSLMFDLGVVARRLRSASDRSKYYRLIEASLYGGIS

STITRSLRDYLLPENSGVRKAFQDMEAALRENRMTLEAIRVTQSDRDLFKHLISEATNYVAADYMRHANE

RRIHLDKALEYRRDLFTSRSQLAAEQYKHVDMARELQEHNGAEGDLEADYQAASDHLNLVQTALRQQEKI

ERYEADLDELQIRLEEQNEVVAEAVDRQEENEARAEAAELEVDELKSQLADYQQALDVQQTRAIQYNQAL

QALERAKALCHLPDLTPESADEWLEIFQAKEQEATEKMLSLEQKMSVAQTAHSQFEQAYQLVAAINGPLA

RNEAWDVARELLRDGVNQRHQAEQAQGLRSRLNELEQRLREQQDAERQLAEFCKRQGKRYDIDDLETLHQ

ELEARIASLADSVSNAQEQRMALRQELEQLQSRTQTLMRRAPVWLAAQNSLNQLCEQSGEQFASGQEVTE

YLQQLLEREREAIVERDEVGARKRAIDEEIERLSQPGGSEDPRLNALAERFGGVLLSEIYDDVSLDDAPY

FSALYGPSRHAIVVPDLSRVAEQLEGLEDCPEDLYLIEGDPQSFDDSVFSVDELEKAVVVKIADRQWRYS

RFPSLPLFGRAARENRIETLHAERESLSERFATLSFDVQKTQRLHQAFSRFIGSHLAVAFEDDPEEEIRK

LNSRRGELERALSAHESDNQQNRVQYEQAKEGVSALNRLLPRLNLLADDTLADRVDEIQERLDEAQEAAR

FIQQHGNQLAKLEPIVSVLQSDPEQFEQLKEDYAYAQQTQRDARQQAFALAEVVQRRAHFSYSDSAEMLS

GNSDLNEKLRQRLEQAESERSRARDAMRAHAAQLSQYNQVLASLKSSYDTKKELLNDLYKELQDIGVRAD

AGAEERARARRDELHMQLSNNRSRRNQLEKALTFCEAEMDNLTRKLRKLERDYCEMREQVVTAKAGWCAV

MRLVKDNGVERRLHRRELAYLSADELRSMSDKALGALRLAVADNEHLRDVLRISEDPKRPERKIQFFVAV

YQHLRERIRQDIIRTDDPVEAIEQMEIELSRLTEELTNREQKLAISSRSVANIIRKTIQREQNRIRMLNQ

GLQSVSFGQVNSVRLNVNVRETHSMLLDVLSEQHEQHQDLFNSNRLTFSEALAKLYQRLNPQIDMGQRTP

QTIGEELLDYRNYLEMEVEVNRGSDGWLRAESGALSTGEAIGTGMSILVMVVQSWEDESRRLRGKDISPC

RLLFLDEAARLDARSIATLFELCERLEMQLIIAAPENISPEKGTTYKLVRKVFNNHEHVHVVGLRGFAAP

LPEALPGTADAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002898195.1\_2070 [gene=ldtD] [locus\_tag=BN49\_RS11830] [protein=L,D-transpeptidase] [protein\_id=WP\_002898195.1] [location=2137218..2139008] [gbkey=CDS]

MLLKKRYGRPLSALSLSLAMAFAPLFNVQAAEPEVVPGDSSATPGELSVALSQSDGQSPAVAKLAGEQPL

SMEAAANSRAQIEALLPAGYKPVFMNPLVSLYAARDMKPMWENREAVQAFQQQLAEIAIAGFQPQFTTWV

SLLTDPAVTGMARDVVLSDAMMGYLHFISGIPTQGTRWLYSSTPYKMATPPLSVINQWQLALDNGSLPAF

IAGLAPRHPQYEAMHQSLLALVADSRPWPQMTGSGSLRPGEWSNDIGALREILQRTGMLENSANIVLPGD

VVSPSAKKKSKPAARGVYDRQLVEGVKRFQAMQGLGADGVIGQSTRDWLNVSSAQRAGVLALNIQRLRLL

PGKLSTGIMVNIPAFSLVYYQDGSQVLASRVIVGRPDRKTPMMSSALNNVVVNPPWNVPPTLARKDILPK

VRNNPGYLEQHGYTVMRGWNSKETIDPYRVDWSTITENNLPFRFQQAPGARNSLGRYKFNMPSSDAIYLH

DTPNHNLFQKDVRALSSGCVRVNKASELANMLLQDAGWNDTRISDALKQGDTRYVNIRQNIPVNLYYLTA

FVDADGRTQYRTDIYNYDITARSSAQILTKAEQLIR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898198.1\_2071 [locus\_tag=BN49\_RS11835] [protein=YcbK family protein] [protein\_id=WP\_002898198.1] [location=2139311..2139862] [gbkey=CDS]

MDKFDANRRRLLALGGAALGAAAILPAPAFATLSTPRPRILTLNNLHTGESLRAEFFDGRGYIQDELARL

NHFFRDYRANKIKSIDPNLFDHLYRLQGLLGTNKPVQLISGYRSLDTNDELRARSRGVAKHSYHTKGQAM

DFHIEGISLSNIRKAALSMRAGGVGYYPRSNFVHIDTGPVRHW

>lcl|NZ\_FO834906.1\_prot\_WP\_002898200.1\_2072 [locus\_tag=BN49\_RS11840] [protein=MBL fold metallo-hydrolase] [protein\_id=WP\_002898200.1] [location=2139876..2140523] [gbkey=CDS]

MNYRIIPVTAFAQNCSLIWCGQTRLAALVDPGGDAERIKAVVAEAGVTLMQILLTHGHLDHVGAAAELAQ

HYGVPVIGPEKEDEFWLEGLPAQSRMFGLEDCQPLRPDRWLNEGDVVNVGNVALQVLHCPGHTPGHVVFF

DDASRLLISGDVIFKGGVGRSDFPRGDHGQLIAAIKEKLLPLGDDVTFIPGHGPLSTLGEERRNNPFLQD

EMPVW

>lcl|NZ\_FO834906.1\_prot\_WP\_002898202.1\_2073 [locus\_tag=BN49\_RS11845] [protein=aspartate/tyrosine/aromatic aminotransferase] [protein\_id=WP\_002898202.1] [location=complement(2140592..2141782)] [gbkey=CDS]

MFENITAAPADPILGLADLFRADDRPEKINLGIGVYKDETGKTPVLTSVKKAEQYLLENETTKNYLGIDG

IPEFGRCTQELLFGKGNAIIADKRARTAQTPGGTGALRVAADFLAKNTDVKRVWVSNPSWPNHKSVFTSA

GLEVREYAYYDAANHALDFDGLLASLNEAQAGDVVLFHGCCHNPTGIDPTLDQWQQLAQLSVEKGWLPLF

DFAYQGFARGLEEDAEGLRAFAALHKELLVASSYSKNFGLYNERVGACTLVAADQETVDRAFSQMKSVIR

ANYSNPPAHGASVVATILSNDALRAIWEQELTDMRQRIQRMRLLFVNTLQEKGASRDFSFISQQNGMFSF

SGLTKEQVLRLREEFAIYAVASGRINVAGMTPDNMAPLCEAIVAVL

>lcl|NZ\_FO834906.1\_prot\_WP\_072269332.1\_2074 [gene=ompK35] [locus\_tag=BN49\_RS11850] [protein=porin OmpK35] [protein\_id=WP\_072269332.1] [location=complement(2141970..2143046)] [gbkey=CDS]

MKRNILAVVIPALLVAGAANAAEIYNKNGNKLDFYGKMVGEHVWTTNGDTSSDDTTYARIGLKGETQIND

QLIGYGQWEYNMDASNVEGSQTTKTRLAFAGLKAGEYGSFDYGRNYGAIYDVEAATDMLVKWGGDGWNYT

DNYMTGRTNGVATYRNSDFFGLVDGLSFALQYQGKNDHDRAIRKQNGDGFSTAATYAFDNGIALSAGYSS

SNRSVDQKADGNGDKAEAWATSAKYDANNIYAAVMYSQTYNMTPEEDNHFAGKTQNFEAVVQYQFDFGLR

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AVGIVYQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002898206.1\_2075 [gene=asnS] [locus\_tag=BN49\_RS11855] [protein=asparagine--tRNA ligase] [protein\_id=WP\_002898206.1] [location=complement(2143641..2145041)] [gbkey=CDS]

MSVVPVADVLQGRVAVDSEVTVRGWVRTRRDSKAGFSFLAVYDGSCFDPVQAVINNSLPNYNQEVLRLTT

GCSVIVTGKVVASQGQGQSFEIQATSVEVTGWVEDPDTYPMAAKRHSIEYLREVAHLRPRTNLIGAVARV

RHTLAQALHRFFNEQGFFWVSTPLITASDTEGAGEMFRVSTLDLENLPRNDQGKVDFDKDFFGKESFLTV

SGQLNGETYACALSKIYTFGPTFRAENSNTSRHLAEFWMLEPEVAFANLNDVAGLAEAMLKYVFKAVLEE

RADDMQFFAERVDKDAIDRLQRFITADFAQVDYTDAVTILENCGKQFENPVYWGVDLSSEHERYLAEEHF

KAPVVVKNYPKDIKAFYMRLNEDGKTVAAMDVLAPGIGEIIGGSQREERLDVLDARMAEMGLNKEDYWWY

RDLRRYGTVPHSGFGLGFERLIAYVTGVQNVRDVIPFPRTPRNATF

>lcl|NZ\_FO834906.1\_prot\_WP\_002898209.1\_2076 [locus\_tag=BN49\_RS11860] [protein=Lrp/AsnC family transcriptional regulator] [protein\_id=WP\_002898209.1] [location=complement(2145217..2145678)] [gbkey=CDS]

MKLDAWDKKILTLLQRNNRLSQREIADRISLSPSAVNRRIAALEDAGVIKGSVSLVDASKVGRPITIMVQ

VTIENERLDLLEEDKQRFVTCPQVQQVYYVTGDFDFLLVINVRDMAEYEALTRELFFASGNIKSFRTIVS

MQNAKQEMTVIIE

>lcl|NZ\_FO834906.1\_prot\_WP\_004147824.1\_2077 [gene=dpaL] [locus\_tag=BN49\_RS11865] [protein=diaminopropionate ammonia-lyase] [protein\_id=WP\_004147824.1] [location=2145990..2147201] [gbkey=CDS]

MDTIKYQLNARRQPYGQGADLSLLNESVGNEVLAFHQKFPDYRVTPLRKLEFLSQRLGLGSIHIKDEAQR

FGLNAFKGLGGSYAMGKYLAALLERDINTLSFAELNSPVIKARIKDIVFVTATDGNHGRGVAWAAEQLGL

RAVVYMPKGSSPVRAQNIRRHGAECTITELNYDDTVRLAAKTAREQGWVLLQDTAWQGYEQIPTWIMQGY

MTLAVEIWQQLAESGAPMPTHLFLQAGVGSFAGSIMGYFIEKMQQQAPTIIIVEPHKANCLYRSATINDG

LPHSVGGDMSTLMAGLACGEPNITSWPMLRDHATCFISADDCLAANGMRLLAAPRPGTDEPFVSGESGAI

GTGVLYALMTQPAYRELAESLRLNADAQVLLISTEGDTSPDVYEDIVWFGRNG

>lcl|NZ\_FO834906.1\_prot\_WP\_046042992.1\_2078 [locus\_tag=BN49\_RS11870] [protein=septum formation initiator] [protein\_id=WP\_046042992.1] [location=2147324..2148613] [gbkey=CDS]

MNTENIIINKGCSDPAKWHSEDTVWVLGLFGTAIGAGVLFLPINAGIGGFWPLLIVFVLAFPITYLAHRG

LARFIYSSNTPESSITDVIGEHFGALAGKVFTVIYFFAVYTILIMYAVAITNTAQSFITHQLAMAEPPRS

LVAIVLILGLMFIVRFGQRLIMRVMSTLVYPFIISLIFMALFLIPHWNGAILQTVSFSATGDGQGIMLSL

WMTFPVLVMSFNHYPIISPMVVRQKQRYGLALAEGKCAQIQRYGILLMTVVVLFFVLSCVLSLSPQQLAE

AKAQNLSILSYLANQYDTPIIAWLSPIIAFVAITKSFLGHYIGAYESLRDLILEAAGARGKKPGIRLVDA

VILVFMVLTCWFAAYKNPSILGIIECISGPTGAAILLLLPMYAIHKLPVLAPWRGKASNVFVTLIGLITV

SAIFYGMFQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530565.1\_2079 [locus\_tag=BN49\_RS11875] [protein=Zn-dependent hydrolase] [protein\_id=WP\_016530565.1] [location=2148638..2149876] [gbkey=CDS]

MSHYLQINGQRLIDSLYALGEHGALPGGGVCRLAATAEDKAGRDFVVARMKALGLSVSIDAIGNVTGVYH

GEETLPMVMMGSHIDTVATGGLYDGNYGVMAGLEVIATLQDAGIRTRRPLAVTFFTNEEGVRFQPDMMGS

VVFAGEYPLAQALAAKDLDGITLDEALRNIGYKGERQPGDMAVDSYVELHIEQGPILDKEQIDIGVVTGV

QGISWQEFTLRGVSNHAGTTPMSMRRDAGLAAAKIAVFARELALSLGGNQVATVGHFSVKPDLINVIPNH

VVMSVDLRNTDNAILCLAEQQLAEFVAKTSQEEGVEITSRSLVRFNPVIFADEIVNAVEAEAERQALSYR

RLPSGAGHDAQFMASVCPAGMIFVPCVDGISHNVKEHSAAKDLIAGANVLLQVVLQRAQRMD

>lcl|NZ\_FO834906.1\_prot\_WP\_004147828.1\_2080 [locus\_tag=BN49\_RS11880] [protein=M20 family metallopeptidase] [protein\_id=WP\_004147828.1] [location=2149895..2151061] [gbkey=CDS]

MNQQQLKQQLIAWRHYLHAHPESAFEEQNTSRFIAEKLEAMGIEVHRDIGKTGVVGRLKCGDGKGVIAIR

ADIDAIQLTEQGDWSYRSMTAERMHGCGHDGHTCIALGAAQLLLQRQNFNGTVCFVFQPAEEPGYGARAM

MDDGVIERFGIEEIYGLHNMPGMKAGTIATRVGGIMASEDNFIIRIKGQGAHAARPHMAKDPLVIAAEII

LALQTIVSRNVDPNVPAVISCTELHTDGIRNAIPTHVEIKGDTRSFAPEVQMLLEERMRTISEAICAMHG

ATCQFSYTHEFAPTVNWQQCVDVAVTAAINVVGAEKVDGNVAQMMISEDFGAFLQKIPGCFIFLGNGDSS

DAQGNTPLHNACYDFNDEILLTGAEYFAEVVRARLPQE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530566.1\_2081 [gene=pncB] [locus\_tag=BN49\_RS11885] [protein=nicotinate phosphoribosyltransferase] [protein\_id=WP\_016530566.1] [location=complement(2151104..2152306)] [gbkey=CDS]

MTQFTSPVLHSLLDTDAYKLHMQQAVFHRYGDVHVAAEFRCRGDDLLGIYADAIREQVESMRDLRLRDDE

YRWLSTLPFFRQDYLNWLRDFRYDPSQVTVSNDNGKLNIRLTGPWQEAIMWEVPLLAVISELVHRYRSPE

MGVDQALNTLEHKLGDFATMTADLDMSAFRLMDFGTRRRFSREVQEGIVRRLQQEPWFVGTSNYDLARRL

NLTPMGTQAHEWFQAHQQISPSLASSQRAALAAWLEEYPDQLGIALTDCITMDAFLRDFGPEFATRYQGL

RHDSGDPVEWGEKAIAHYQKLGIDPLSKVLVFSDNLDLAKAVDLYRHFASRVKLSFGIGTRLTCDLPQVK

PLNIVIKLVECNGKPVAKLSDSPGKTICHDKAFVRALREAFDLPPIKKAS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530567.1\_2082 [gene=pepN] [locus\_tag=BN49\_RS11895] [protein=aminopeptidase N] [protein\_id=WP\_016530567.1] [location=2152632..2155247] [gbkey=CDS]

MTQQPQAKYRHDYRAPEYLISDIDLTFDLDAAKTVVTAESKVSRHAAASDVPLRLDGEDLTLIALQVNGQ

PWSDYKEENNQLVIGGLPEHFTLTIVNEISPAANTALEGLYQSGEALCTQCEAEGFRHITWYLDRPDVLA

RFTTKIIADKAKYPFLLSNGNRMAEGELENGRHWVQWQDPFPKPCYLFVLVAGDFDVLRDSFRTRSGREV

ALELYVDRGNLDRAPWAMTSLKNSMKWDEERFGLEYDLDIYMIVAVDFFNMGAMENKGLNVFNSKYVLAR

TDTATDKDYLDIERVIGHEYFHNWTGNRVTCRDWFQLSLKEGLTVFRDQEFSSDLGSRAVNRINNVRTMR

GLQFAEDASPMAHPIRPDMVIEMNNFYTLTVYEKGAEVIRMLHTLLGEENFQKGMQLYFERHDGSAATCD

DFVQAMEDASNVDLSHFRLWYSQSGTPIVTVHDDYNPETEQYTLTISQRTPPTAEQAEKQPLHIPFAIEL

YDNEGKVIPLQKGGHPVHPVLNVTQAEQTFVFDNVYFQPVPALLCEFSAPVKLEYKWSDQQLTFLMRHAR

NDFSRWDAAQSLLATYIKLNVNRHQQGQPLSLPVHVADAFRAILLDEKIDPALAAEILTLPSANEIAEMF

AIIDPIAIAAVREALTRTLANELADEFLAVYNANKLDSYRVEHADIGKRALRNTCLRYLAFAEPTLGDKL

VATQYHQADNMTDALAALSAAVAAELPCRDALMQEYDDKWHQDGLVMDKWFILQSTSPAANVVETVRGLL

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RQALMRAALEQLKGLENLSGDLFEKISKALA

>lcl|NZ\_FO834906.1\_prot\_WP\_004150838.1\_2083 [gene=ssuB] [locus\_tag=BN49\_RS11900] [protein=aliphatic sulfonates ABC transporter ATP-binding protein] [protein\_id=WP\_004150838.1] [location=complement(2155452..2156225)] [gbkey=CDS]

MNTARLNPGIPLLLNGVTKRYGDNTILNELDLHIPSGQFVAVVGRSGGGKSTLLRLLAGLEKPNAGELLA

GATPLAAIQDDTRMMFQDARLLPWKTVIDNVGLGLKGAWRDAALQALASVGLESRAQEWPAALSGGQKQR

VALARALIHRPRLLLLDEPLGALDALTRLEMQELIVSLWQEHGFTVLLVTHDVSEAVAMADRVLLIEEKK

IGLDLSVDIPRPRRTGSAKLAELEAEVLDRVMKRGDSERAPRLFSHG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530316.1\_2084 [gene=ssuC] [locus\_tag=BN49\_RS11905] [protein=aliphatic sulfonate ABC transporter permease SsuC] [protein\_id=WP\_016530316.1] [location=complement(2156222..2157013)] [gbkey=CDS]

MAKSTHPLLLRLAPWLLPVGTVIVWQLASSVGWLSTRVLPSPEGVLKAFWTLSASGELWQHLAISSWRAL

VGFAIGGSIGLILGLISGLSRWGERLLDTSIQMLRNVPHLALIPLVILWFGIDETAKIFLVSLGTLFPIY

INTWHGIRNIDRGLVEMARSYGLSGFALFRHVILPGALPSVMVGVRFALGLMWLTLIVAETISANAGIGY

LAMNAREFLQTDVVVVAIILYAILGKLADVCAQLLERLWLSWNPAYHLQEANA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898293.1\_2085 [gene=ssuD] [locus\_tag=BN49\_RS11910] [protein=FMNH2-dependent alkanesulfonate monooxygenase] [protein\_id=WP\_002898293.1] [location=complement(2157024..2158169)] [gbkey=CDS]

MSLNMFWFLPTHGDGRYLGTEEGARPVDYGYLQQIAQTADRLGFTGVLIPTGRSCEDAWLVAASMIPVTQ

RLKFLVALRPSVVSPTVAARQAATLDRLSNGRALFNLVTGSDPAELAGDGVFLDHTERYEASAEFTHIWR

KLMEGETVTFNGKHQRVRDAKLLFPPLQQPRPPLYFGGSSEVAQELAAEQVDLYLTWGEPPAQVAEKIAQ

VREKAARHGRQVRFGIRLHVIVRETNEEAWQAADSLISHLDDETIARAQAAFARTDSVGQQRMAALHNGR

RDKLEISPNLWAGVGLARGGAGTALVGDAATVAERINEYAALGIDSFIFSGYPHLEEAYRVGELLFPLLD

VAVPSIPQPQNLRLQGEAVANEFIPRKVAQS

>lcl|NZ\_FO834906.1\_prot\_2086 [locus\_tag=BN49\_RS11915] [protein=sulfonate ABC transporter substrate-binding protein] [pseudo=true] [location=complement(2158129..2159128)] [gbkey=CDS]

MLNPLRALTLGGLLLFSTLGHAAPAAPDALRIGYQKGSVSMVLAKSHQLLEQRYPQTHISWIEFPAGPQM

LEALNVGSIDIGSTGDIPPIFAQAAGADLVYIGAEPPKPKAEVILVAQGSPIHNVAELKGKKVAFQKGSS

SHNLLLRALQLAGLKFSDIQPVYLAPADARAAFQQGNVDAWAIWDPYYSAALLQGGARVLTDGTDLKQTG

SFYLASRPYAERNGAFIEGVLDTFTQADALTHSQRAQSITLLAKTMGLPEAVIASYLDHRPPTAVTPVSA

ETAARQQQTADLFYENKLVPKKVDIRARIWQPTATQGAKS\*V\*ICSGFYRPMV

>lcl|NZ\_FO834906.1\_prot\_WP\_002898296.1\_2087 [gene=ssuE] [locus\_tag=BN49\_RS11920] [protein=NADPH-dependent FMN reductase] [protein\_id=WP\_002898296.1] [location=complement(2159121..2159696)] [gbkey=CDS]

MRVITLAGSPRYPSRSSALLEYARETLTAADIEVCHWHLQNFAPEDLLYARFDNPALQTLNEQLAGADGL

IIATPVYKASFSGALKTLLDLLPERALEGKIVLPLATGGTIAHMLAVDYALKPVLNALKAQEILHGVFAD

DSQVTDYQHKPQFTANLQRRLDDALETFWQALHRPSSRAPSLTSLRGVEHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898303.1\_2088 [gene=pyrD] [locus\_tag=BN49\_RS11925] [protein=quinone-dependent dihydroorotate dehydrogenase] [protein\_id=WP\_002898303.1] [location=2159946..2160956] [gbkey=CDS]

MYYPFVRKALFQLDPERAHEVTFQQLRRVTGTPLEMLVRQKVPARPVTCMGLTFKNPLGLAAGLDKNGEC

IDALGAMGFGSIEIGTVTPRPQPGNDKPRIFRLVDAEGLINRMGFNNHGVDNLVENVKKAHFDGVLGINI

GKNKDTPVEHGKDDYLICMEKVYPYAGYIAINISSPNTPGLRTLQYGEALDDLLSGIKNKQLELQQKHQK

YVPVAVKIAPDLLPEELIQVADSLVRHNIDGVIATNTTLDRSLVQGMKHCDETGGLSGRPLQLKSTEIIR

MLSAELNGRLPIIGVGGIDSVIAAREKIAAGASLVQIYSGFIFKGPPLIKEIVTHI

>lcl|NZ\_FO834906.1\_prot\_WP\_002898308.1\_2089 [gene=zapC] [locus\_tag=BN49\_RS11930] [protein=cell division protein ZapC] [protein\_id=WP\_002898308.1] [location=2161126..2161668] [gbkey=CDS]

MRIKPDDNWRWYYDEEHDRMMLDLANGMLFRSRFARRMLTPDAFAPSGFCVDDAALYFSFEEKCRDLELS

KEQRAELVLNALTAIRFLKPQMPKSWHFIAHTHHWQPSGGDAACVWLSDTGEQVNLLVVEPGDNAALCLL

AQPGLTLAGRVMQLGDVIKIMNDRLQPAQSAVSYSLGQAV

>lcl|NZ\_FO834906.1\_prot\_WP\_046042994.1\_2090 [locus\_tag=BN49\_RS11935] [protein=YcbX family protein] [protein\_id=WP\_046042994.1] [location=complement(2161665..2162774)] [gbkey=CDS]

MVTLSRLFIHPVKSMRGMGLTHAFADISGLAFDRLFMVTETDGTFITARQFPQMVKFIPAPLHDGLHLTA

PDGSSAVVRFSDFATQAEPTEVWGNHFTALIAPAAVNQWLSGFFKRDVQLRWLGPQLTRRVKRHDAVPLS

FADGYPYLLANEASLRDLQQRCPASVSIEQFRPNLVVTGAAAWDEDSWKVIRIGEVVFDVAKPCSRCIFT

TVSPERGQKHPAGEPLETLKRFRTALNNGDVDFGQNLIARNSGVIRVGDEVEILTRGPAKAYGAGESDDT

PAPEAQQQATVAIEWQGQQFTGNNQQVLLEQLEQQGIRVPYSCRAGICGSCRIRLEEGEVSPLKKNAVAG

DGTILACSCVPKTELRLAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004191110.1\_2091 [gene=rlmKL] [locus\_tag=BN49\_RS11940] [protein=bifunctional 23S rRNA (guanine(2069)-N(7))-methyltransferase RlmK/23S rRNA (guanine(2445)-N(2))-methyltransferase RlmL] [protein\_id=WP\_004191110.1] [location=2162874..2164979] [gbkey=CDS]

MNSLFASTARGLEELLKTELEGLGATDCQVVQGGVHFQGDTRLLYQSLMWSRLASRIMLPLGECRVYSDL

DLYLGVQAIPWTEMFNPGATFAVHFSGLNDEIRNSQYGALKVKDAIVDSFTRKNLPRPNVDRESPDLRIN

VWLNKETAHISLDLSGEGLHLRGYRDGTGMAPIKENLAAAIVMRSGWVPGTPLLDPMCGSGTLLIEAAML

ATDRAPGLHRGHWGFGGWAQHDDGIWKEVKAEAQTRARQGLAAYESRFYGSDVDARVIERARRNARRAGI

GELIDFDVKDVAQLNNPLPKGPYGTVISNPPYGERLESEPALIALHSLLGRIMKSQFGGWNLSVFSASPE

LLSCLQLRADKQFKAKNGPLDCVQKNYHLAESEGGKPAMLAEDFANRLRKNLKKFEKWARQEGIECYRLY

DADLPEYNVAIDRYADWVVVQEYAPPKTVDAHKARQRLFDIIAATIAVLDMAPNKLVLKTRERQKGKNQY

QKMAEKGDFIEVQEYNARLWVNLTDYLDTGLFLDHRIARRMLGQMSKGKDFLNLFSYTGSASVHAGLGGA

RSTTTVDMSRTYLEWAERNLRLNGLTGRAHRLMQADVLGWLRESTEQFDLIFIDPPTFSNSKRMEDAFDV

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A

>lcl|NZ\_FO834906.1\_prot\_WP\_004147848.1\_2092 [locus\_tag=BN49\_RS11945] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004147848.1] [location=2164992..2166899] [gbkey=CDS]

MSLISMHGAWLSFSDAPLLDNAELHIEDNERVCLVGRNGAGKSTLMKILNREQGLDDGRIIYEQDLIVAR

LQQDPPRNVAGTVYDFVAEGIAEQAAYLKAYHDVSHQVMTDPSDKNLNELARLQEQLDNLGLWQLDSRIN

EVIEQLGLDANAQLASLSGGWLRKAALGRALVSGPRVLLLDEPTNHLDIETIDWLEGFLKTFKGTIIFIS

HDRSFIRNMATRIVDLDRGKLVTYPGNYDQYLLDKEEALRVEELQNAEFDRKLAQEEVWIRQGIKARRTR

NEGRVRALKAMRRERGERREVMGSAKMQVEEASRSGKIVFEMENVNYQVDGKVLVKDFSAQIQRGDKIAL

IGPNGCGKTTLLKLMLGQLQADSGRIHVGTKLEVAYFDQHRAELDPDKTVMDNLAEGKQEVMVNGKPRHV

LGYLQDFLFHPKRAMTPVRALSGGERNRLLLARLFLKPSNLLILDEPTNDLDVETLELLEELIDGYQGTV

MLVSHDRQFVDNTVTECWIFEGGGRIGQYVGGYHDARGQQAQSLAQKQTVVKKTTEVAQPKAETVKRGGN

KLSYNLQRELEQLPQKLEALEAELQTLQDQVADPDFFGQPHDRTQQVLAQLAEAEQALEAAFERWEYLEG

LKNGA

>lcl|NZ\_FO834906.1\_prot\_WP\_004147849.1\_2093 [gene=pqiA] [locus\_tag=BN49\_RS11950] [protein=membrane integrity-associated transporter subunit PqiA] [protein\_id=WP\_004147849.1] [location=2166914..2168182] [gbkey=CDS]

MCDHHHAARHILCPQCDLLVALPQLEHRQKAACPRCGTTLTTTWDAPRQRPTAYALVALFMLLLANLFPF

IYMKVGGISSEIELLEIPNVLFTEDYASLGTFFLLFVQLVPAFCLVTILLLVNRVRMPAGLKTFLARILF

QLKTWGMAEIFLAGVLVSFVKLMAYGDIGIGLSFVPWCMFCLLQLRTFQCVDRRWLWDDIAPMPAITQPL

KVGVTGIRQGLRSCACCTAVLPVDQTVCPRCNSKGTARRKNSLQWTLALLVTSFILYLPANIMPIMITDL

LGDKMPSTIMAGVILLWSEGSYPVALVIFIASIMVPTLKMIAIAWLCWNANGNGARDSERMHLIYEVVEF

VGRWSMIDVFVIAVLSALVRMGGLMNIYPAIGAVMFALVVVMTMFSAMTFDPRLLWDREPDSSHEEIQQH

GK

>lcl|NZ\_FO834906.1\_prot\_WP\_004179201.1\_2094 [gene=pqiB] [locus\_tag=BN49\_RS11955] [protein=intermembrane transport protein PqiB] [protein\_id=WP\_004179201.1] [location=2168172..2169812] [gbkey=CDS]

MENKSGEAKVQKVKNWSPVWIFPIVTALIGAWILFYHYSHQGPEVTLITTNAEGIEGGKTRIKSRSVDVG

VVESATLTDDLTHVEIKARLNSGMQKLLHNDSVFWVVKPQVGREGISGLGTLLSGAYIELQPGTKGSVPA

QYPLLDSPPLASPDAKGIRILLESSKAGQLSPGDPVLFRGYRVGSVETSTFDTQKRRITYQLFINAPNDR

LVTTNVRFWKDSGIAVDLTSAGMRVEMGSLSTLFGGGVSFDIPEGLDLGEPVANKTEYHLFDDQKSIQDS

VFTEHIDYVMFFKDSVRGLQPGAPVEFRGIRLGTVGKVPFFIPGLKQRLNDDYRIPVEVRVEPQRLINQL

GGDPNIRAHIDDLINRGLRGSLKTGNLVTGALYIDLDFYPKAPPRGKIQEFNGYPIIPTISGGLAQIQQR

LMDALDKINNLPINPLLEQATSTLAQSEKTMQHVQTTLDNLNKITSSQSMQQLPADMQTTLRELNRSMQG

FQPGSAAYNKMVADMQRLDQVLRELQPVLKTLNDKSNALVFEAKDKKDPQPKGAKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002898392.1\_2095 [gene=pqiC] [locus\_tag=BN49\_RS11960] [protein=membrane integrity-associated transporter subunit PqiC] [protein\_id=WP\_002898392.1] [location=2169809..2170372] [gbkey=CDS]

MKKWLLAAAVCVLTACSSGGESKTYYQLPVVQGGAQSAASQGARLLWVEQVSIPDYLAGNGVVYQTTDVQ

YVIANNNLWASPLDQQLRTTLVANLSQQLPGWVVSSQPLGSEQDTLNVAVNGFHGRYDGRVIVSGEWLLK

HQGQLIKRPFNIVLRQEQDGYDAMVKTLAQAWSQEAAAIASELNRLP

>lcl|NZ\_FO834906.1\_prot\_WP\_002898396.1\_2096 [gene=rmf] [locus\_tag=BN49\_RS11965] [protein=ribosome modulation factor] [protein\_id=WP\_002898396.1] [location=2170626..2170793] [gbkey=CDS]

MKRQKRDRLERAHQRGYQAGIAGRSKEMCPYQSLNQRSWWLGGWREAMEDRVLTA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898398.1\_2097 [gene=fabA] [locus\_tag=BN49\_RS11970] [protein=bifunctional 3-hydroxydecanoyl-ACP dehydratase/trans-2-decenoyl-ACP isomerase] [protein\_id=WP\_002898398.1] [location=complement(2170862..2171380)] [gbkey=CDS]

MVDKRESYTKEDLLASGRGELFGAKGPQLPAPNMLMMDRVIKMTETGGNYDKGYVEAELDINPDLWFFGC

HFIGDPVMPGCLGLDAMWQLVGFYLGWLGGEGKGRALGVGEVKFTGQVLPTAKKVTYRIHFKRIVNRRLI

MGLADGEVLVDDRLIYTANDLKVGLFQDTSAF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529118.1\_2098 [locus\_tag=BN49\_RS11975] [protein=Lon protease family protein] [protein\_id=WP\_016529118.1] [location=complement(2171450..2173207)] [gbkey=CDS]

MTITKLTRTDLAPDLEAYQALFAQAELSHPAPSLSGDLQPRLFYGLEQLLYTPAVSSFMLVKAPEEPEYL

QWLAAETRTLHEPAAPLYGVRYEVTDAQVTLAPAQGAEDNFASTAPVVMADWVEAEQLFGCVRQFNGAIT

LQPGLVHQANGGVLVLSLRTLLAQPLLWVRLKNMVTRQRFDWLSMDESRPLPVSIPSMPLSLKIILVGER

ESLADFQEMEPELAAQAIYSEYEDTLQFADADTLKAWCQWVWQNAQQLALPGPAADAWPLLIDEGTRYTG

DQETLPLSPLWITRQLREAAAFCEGEEITGEAMQTMLARRVWREGYLAERMQDEILQEQILIETEGECVG

QINALSVIEFPGHPRAFGEPSRISCVVHIGDGEFIDVERKAELGGNIHAKGMMIMQAFLMSELELEQQLP

FTASLTFEQSYSEVDGDSASMAELCALISALANVPINQSIAITGSVDQFGRVQPVGGLNEKIEGFFTICQ

QRGLTGKQGVIIPAANVRHLSLSHELRQAVADNQFAIWAIDDITEALPMLTQLMWDGEGQTLRQTIQERI

AQATQQETRHRFPWPLRWLGGTSSN

>lcl|NZ\_FO834906.1\_prot\_WP\_002898404.1\_2099 [gene=matP] [locus\_tag=BN49\_RS11980] [protein=macrodomain Ter protein MatP] [protein\_id=WP\_002898404.1] [location=2173393..2173845] [gbkey=CDS]

MKYQQLENLESGWKWKYLVKKHREGELITRYIEASAAQAAVDDLLTLENEPVLVHAWIEQHMNPALMNRM

KQTIRARRKRHFNAEHQHTRKKSIDLEFVVWQRLAGLAQRRGKTLSETIVQLIEDAEHKEKYASKMSSLK

HDLQVLLGKE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529119.1\_2100 [gene=ompA] [locus\_tag=BN49\_RS11985] [protein=porin OmpA] [protein\_id=WP\_016529119.1] [location=complement(2173975..2175045)] [gbkey=CDS]

MKKTAIAIAVALAGFATVAQAAPKDNTWYAGGKLGWSQYHDTGFYGNGFQNNNGPTRNDQLGAGAFGGYQ

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VSRSEHDTGVSPVFAGGVEWAVTRDIATRLEYQWVNNIGDAGTVGTRPDNGMLSLGVSYRFGQEDAAPVV

APAPAPAPEVATKHFTLKSDVLFNFNKATLKPEGQQALDQLYTQLSNMDPKDGSAVVLGYTDRIGSEAYN

QQLSEKRAQSVVDYLVAKGIPAGKISARGMGESTPVTGNTCDNVKARAALIDCLAPDRRVEIEVKGYKEV

VTQPAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898418.1\_2101 [gene=sulA] [locus\_tag=BN49\_RS11990] [protein=cell division inhibitor SulA] [protein\_id=WP\_002898418.1] [location=complement(2175398..2175907)] [gbkey=CDS]

MFTSAHANRSAQASAPAGHYAHRSGEQNTNGLISEIVYREDQPMMTQLLLLPLLQQLGQQSRWQLWLTPQ

QKLSREWVQSAGLPLSKVMQISQLSPSHTIDSMIRALRTGNYSVVICWLAEELTADEHERLVNAAQVGSA

MGFIMRPVRNQGTLGRQLSGLKIHSNLYH

>lcl|NZ\_FO834906.1\_prot\_WP\_004179217.1\_2102 [locus\_tag=BN49\_RS11995] [protein=TfoX/Sxy family DNA transformation protein] [protein\_id=WP\_004179217.1] [location=2176256..2176852] [gbkey=CDS]

MRKLVCPRLPQFQACVSPLGQLHTRPLFGGYSLAIDDTVFAMVAEGNIYLKACEQSAAYRVEHRNPLLTL

RRHGRIVPLKYYQIDDTLWRDEQQLFRLSLLSWQSAQREKNCRRASGRLKDLPNISFHMELQLIHAGIPD

VRTLREVGAQEAWLRLRVNNASLSLSVLLALEGAIAGVHAAALPTPRRQELLEWAATR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529594.1\_2103 [gene=yccS] [locus\_tag=BN49\_RS12000] [protein=YccS family putative transporter] [protein\_id=WP\_016529594.1] [location=complement(2176866..2179001)] [gbkey=CDS]

MISPLLRRYTWNSAWLYNVRIFIALCGTTLFPWWIGEVKLTIPLTLGVVAAALTDLDDRLAGRLRNLAIT

LVCFFIASASVELLFPWPPLFALGLTVSTIGFILLGGLGQRYATIAFGALLIAIYTMLGVTLYDHWYLQP

LFLLAGAVWYNLLTLSGHLIFPIRPLQDNLARSYEQLARYLELKSRLFDPDLEDESQAPLYDLALANGQL

VATLNQTKVSLLTRLRGDRGQRGTRRTLQYYFVAQDIHERASSSHIQYQTLRDQFRYSDVMFRFQRMLSM

QAQACQKLSRAILLREPYQHDAHFERAFMHLDAALERVRAGGASDEQLNALGYLLNNLRAIDAQLATIES

VQTTAPAGSNTETLLADDRLGGLSDIWLRLQRNMSPESALFRHAVRMSLVLCAGYAFIQFTGLQHGYWIL

LTSLFVCQPNYNATRHRLALRIIGTLVGVAIGLPVLLLVPSVEGQLLLIVLTGVLFFAFRNVQYAHATMF

ITLLVLLCFNLLGEGFEVALPRIIDTLIGCAIAWAAVSFIWPDWKFRNLPRVLDRAMNANCRYLDAILEQ

YHQGRDNRLAYRVARRDAYNRDAELASVVSNLSTEPRADATQRETAFRLLCLNHTFTSYISALGAHREKL

STPEILALLDDAVCDVDDALHHTPADEQRVQQALNSLQSRIHHLEPRADSKEPLVLQQIGLLLALLPEIC

RLQQRVHAQTE

>lcl|NZ\_FO834906.1\_prot\_WP\_004224032.1\_2104 [locus\_tag=BN49\_RS12005] [protein=YccF domain-containing protein] [protein\_id=WP\_004224032.1] [location=complement(2179019..2179465)] [gbkey=CDS]

MRTILNILNFILGGFATTLGWLLATLVSIMLIVTLPLTRSCWEITRLSLFPYGNEAIHVDELEPGRKNGL

LNAGGTVLNILWFIFFGWWLCLMHIFSGIAQCLTIIGIPVGIANFKIAAIALWPVGRRVVSVETARAARE

ANARRRFQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043000.1\_2105 [gene=helD] [locus\_tag=BN49\_RS12010] [protein=DNA helicase IV] [protein\_id=WP\_046043000.1] [location=2179590..2181644] [gbkey=CDS]

MELKATTLGKRMAQHPYDRVQLLNAGVKVSGDRHEYLIPFNQLLSVHCKRGLVWGELEFVLPDGKVVRLH

GTEWSETQRFYHHLHTLWQQWSTEMSDIAAGVLKQQLATIEHTRAEGKWLTRQQVADVQDNIRHALTGLP

MPTSRLDAFDNCRELWRECQRWLGDIEATRLAHNQAFTEAMLEQYREFFDSVESSPLNASQARAVVNGER

SLLVLAGAGSGKTSVLVARAGWLLARGEAAADQILLLAFGRQAAQEMDERIRERLASDDITARTFHSLAL

HIIQQGSKKVPTISKLESDTAARHALLLKSWQKQCQEKKAQAKGWRLWLEEEMGWQLPEGDFWQDKKVQR

RMASRLDRWVSLMRMHGGSQAEMIAGAPEAVRDLFSKRVKLMSPLMKDWKAALKAENAVDFSGLIHQAVN

ILDKGRFVSPWKHILVDEFQDISPQRASLLAALRRQNSQTTLFAVGDDWQAIYRFSGAQLSLTTAFNHYF

GEGDCCALDTTYRFNGRIGEIANGFIQQNPHQLSKPLNSLTAGDKKAVTLLADDKLDDLLDKLSGYVKPE

QRILLLARYHHMKPEALNKAATRWPHLQLDFMTIHASKGQQADFVIVLGLQDGEDAFPAPARESIMEQAL

LPQPEDFPDAEERRLLYVALTRARHRVWLLFNKAQPSPFVEILQALDVPVARKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002898432.1\_2106 [gene=mgsA] [locus\_tag=BN49\_RS12015] [protein=methylglyoxal synthase] [protein\_id=WP\_002898432.1] [location=complement(2181656..2182114)] [gbkey=CDS]

MELTTRTLPAQKHIALVAHDHCKDMLMKWVARHQALLAQHILYATGTTGNLVSRATGLEVNAMLSGPMGG

DQQVGALISEGKIDVLIFFWDPLNAVPHDPDVKALLRLATVWNIPVATNVSTADFIIQSPHFGQPLDILI

PDYPRYLAERLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004144085.1\_2107 [locus\_tag=BN49\_RS12020] [protein=CoA-binding protein] [protein\_id=WP\_004144085.1] [location=2182269..2182682] [gbkey=CDS]

MKENDIAGILTSTRTIALVGASDKPDRPSYRVMKYLLDQGYHVIPVSPKVAGKTLLGQQGYATLADVPEK

VDMVDVFRNSEAAWGVAQEAIAIGAKTLWLQLGVINEQAAVLAREAGLSVVMDRCPAIELPRLGLAK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529813.1\_2108 [gene=hspQ] [locus\_tag=BN49\_RS12025] [protein=heat shock protein HspQ] [protein\_id=WP\_016529813.1] [location=complement(2182713..2183030)] [gbkey=CDS]

MIASKFGIGQQVRHTLLGYLGVIVDVDPEYSLAEPEEDEIAANDELRAAPWYHVVMEDDDGQPIHTYLAE

AQLSSETRDEHPEQPSLDELAKTIHQQLQAPRLRN

>lcl|NZ\_FO834906.1\_prot\_WP\_004141630.1\_2109 [gene=rlmI] [locus\_tag=BN49\_RS12030] [protein=23S rRNA (cytosine(1962)-C(5))-methyltransferase RlmI] [protein\_id=WP\_004141630.1] [location=complement(2183090..2184292)] [gbkey=CDS]

MTDSLFPRLVLAKGREKSLLRRHPWIFSGGVARMEGKARSGETIDIVDHQGKWLARGAYSPSSQIRARVW

TFDRNEAIDSAFFERRLQQAQTWRAWLAERDGLDSYRLIAGESDGLPGVTIDRFGNFFVLQLLSAGAEYQ

RAAIISALQNLFPDCAIYDRSDVAVRKKEGLELAQGPVVGELPPALLPITEHGMKLLVDIQGGHKTGYYL

DQRDSRLATRRYVADKRVLNCFSYTGGFAVSALMGGCRQVTSVDTSQEALDVARQNVEINGLDLSKAEFV

RDDVFKLLRKYRDQGEKFDVIVMDPPKFVENKSQLMGACRGYKDINMLAIQLLNPGGVLLTFSCSGLMTT

DLFQKIIADAAIDAGRDVQFIEQFRQAADHPVIATYPEGLYLKGFACRVM

>lcl|NZ\_FO834906.1\_prot\_WP\_004210995.1\_2110 [locus\_tag=BN49\_RS12035] [protein=YbhB/YbcL family Raf kinase inhibitor-like protein] [protein\_id=WP\_004210995.1] [location=2184483..2185037] [gbkey=CDS]

MKTGIRMAVAMVAAVSSGAMAAPFSVSSNDMRDGQPLAQQHWFAGFGCTGGNVSPQLAWKNAPAGTRSFA

VTVRDPDAPTGSGWWHWTVVNIASSVFSLPAGAGDKNSATLPGGAVQGRNDFGYAGFGGACPPAGDKPHR

YRFTVWALDVPTLPVDAGASGALVGYLLHSHALASAQLTAMAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043005.1\_2111 [locus\_tag=BN49\_RS12040] [protein=AraC family transcriptional regulator] [protein\_id=WP\_046043005.1] [location=2185055..2185843] [gbkey=CDS]

MESIHFQHNALTAAEITTRRLCRLHRVRLFSPALCRVKRGSKVIVQGESRVLATPQQLIVLPADVELEVI

NQPENGLFCSDLLSLTPELLTRFKTRYLSEPPPGRLTSLCAPVTTELAFMWQSVLQAVREGLSVALQQHQ

TMGLLLALHEAGYAGPLLVERQQDLSAQVRQLIMLSPAQAWSVSRVAKMLFLGESTLRRRLQQESQSFRQ

IVEEVRMAHALGQLQSTSRPIGEIAQNSGYQSGSRFTARFRQHYGLLPKHVR

>lcl|NZ\_FO834906.1\_prot\_WP\_004150835.1\_2112 [gene=yccX] [locus\_tag=BN49\_RS12045] [protein=acylphosphatase] [protein\_id=WP\_004150835.1] [location=2185892..2186173] [gbkey=CDS]

MASICTMAWVYGSVQGVGFRYSTQREALQLGVTGYARNLDDGGVEVLACGEAEQVEKLIAWLKAGGPRSA

RVDRVLTEPHQPTRSWDKFAILY

>lcl|NZ\_FO834906.1\_prot\_WP\_002898457.1\_2113 [gene=tusE] [locus\_tag=BN49\_RS12050] [protein=sulfurtransferase TusE] [protein\_id=WP\_002898457.1] [location=complement(2186170..2186499)] [gbkey=CDS]

MFIFEGNEIETDSEGYLKDTTQWSEAMAEVIAAQEGITLAVEHWEVVRFVREFYLEFNTSPAIRMLVKAM

ANKFGEEKGNSRYLYRLFPKGPAKQATKIAGLPKPVKCI

>lcl|NZ\_FO834906.1\_prot\_WP\_002898458.1\_2114 [gene=yccA] [locus\_tag=BN49\_RS12055] [protein=FtsH protease modulator YccA] [protein\_id=WP\_002898458.1] [location=complement(2186588..2187247)] [gbkey=CDS]

MDRIITSSRDRSSLLSTHKVLRNTYFLLSLTLAFSAITATASTVLMLPSPGLILTLVGMYGLMFLTYKTA

NKPTGIISAFAFTGFLGYILGPMLNAYLSAGMGDLIGLALGGTALVFFCCSAYVLTTRKDMSFLGGMLMA

GVVVVLIGMVANLFLQLPALHLAISAVFILISSGAILFETSNIIRGGETNYIRATVSLYVSLYNIFVSLL

SILGFASRD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529816.1\_2115 [locus\_tag=BN49\_RS12060] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016529816.1] [location=2187518..2189170] [gbkey=CDS]

MTLHKKNHITRTLLAVSMLAMSGGALAAQVPPGTQLAEKQELVRNNGSEPASLDPHKVESDVEFNIISDL

FEGLVNVSPAGAIQPRLAERWENKDNLLWTFHLRPGLTWSDGTAITAQDIVWSWQRLVSPATASPYASYP

GNMHIANAREIALGQKGPETLGVKALNDTTLQVILTQPNAAFLAMLAHPSLVPIDKVLVERYADKWTRPE

HIVTSGPYKLSQWVVNERLVAERNAKYWDNAHTVINKVTYLPISSEAADVNRYKTGEIDIVYTVPINQFA

QLQKTMGDQLDVSPQLATYYYEFNTTRPPFNDARVRRALNMALDKDIIAGKVLGQGQRPAWLIGQPDIGG

VTLHNPDYASWPREKRIAEAKKLLAQAGYDESHPLVFTLLYNTSESHQRIAIAASSMWKKNLGVEAKLQN

QEWKTMLDTMHTHNFDAVRYAWIADYDDAATFLNTFRTGDSENTSQYSNPAYDEALRNAAKASDVATRGK

YYQQAEDLLAQDVPAIPVYHYVRTHLVKPWVGGFTPDKLGYYYTKDMYIKKHPSASGDGR

>lcl|NZ\_FO834906.1\_prot\_WP\_227504846.1\_2116 [locus\_tag=BN49\_RS31425] [protein=cyclic diguanylate phosphodiesterase] [protein\_id=WP\_227504846.1] [location=complement(2189599..2190336)] [gbkey=CDS]

MRKYLNVYTSEEEKLRYAITQGYIVPYYQPLVNGKTGEIYGVEILARWQNSTTPARSPAEFIPLAERTGL

IIPLTRSLMAQVNAQMRPHFSKLPDGFHIGLNISVSYINAPTFIDDCLHYQRGFEGKAVKLMLEITEQEP

LLLNGAVVDKLNTLHSRGFSVALDNFGTGYSGLSCRHELVFDYIKIDQSFVGRVTGEAPTSKLLDCVIEM

ARTLSLRIIAEGVETEAQRDYLNRQNIHLLQGYYF

>lcl|NZ\_FO834906.1\_prot\_2117 [locus\_tag=BN49\_RS31430] [protein=hypothetical protein] [pseudo=true] [partial=3'] [location=complement(<2190454..2190672)] [gbkey=CDS]

MMVNKRPVLIYQTRLAPIRVIVTISDIHLRDALYSDTDNNGLALWVQNQMIARYGDVKPLAADPHQEVFT

SPA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529818.1\_2118 [locus\_tag=BN49\_RS12075] [protein=hypothetical protein] [protein\_id=WP\_016529818.1] [location=2190737..2190925] [gbkey=CDS]

MPVNDEHASKKYHQRQGKGNHSQPVDEETALFLGDRTVSQPAWQPGAMVRLTVSGKARVFSG

>lcl|NZ\_FO834906.1\_prot\_WP\_004224047.1\_2119 [locus\_tag=BN49\_RS12080] [protein=PDR/VanB family oxidoreductase] [protein\_id=WP\_004224047.1] [location=complement(2191095..2192060)] [gbkey=CDS]

MSDYQMFEAVVRDVEQITPLVKRFTLVSPTGAPLPAFSGGSHIIVQMQDGEQRYSNAYSLMSSPLDTTSW

QIAVRLESPSKGGSRFMHQRVRPGDTLTVSTPNNLFAIEPQARKHLLIAGGIGITPFLSHIPELEQRQAD

WQLHYCFHDADSNAFVDTLRAAPWRDRVNVHVSALGSRLDLPRLFADLEPGTHVYTCGPAALNEAVKAAA

ERHQVPASQLHFEQFILEDKSGEAFTLVLARSGREFTVPQDMTILQVIENNKAAKVECLCREGVCGTCET

MILEGEADHRDQYYSEEEKASQQSMLICCSRAKGGRLVLDL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043007.1\_2120 [locus\_tag=BN49\_RS12085] [protein=NAD-dependent succinate-semialdehyde dehydrogenase] [protein\_id=WP\_046043007.1] [location=complement(2192118..2193566)] [gbkey=CDS]

MSVFHSDLFRQQALIAGSWRDAADGTTLAVSNPSTGATLGQIPNMGRAEAQQAVDAAAAALPNWRALTAA

QRAALLKNWHRLILENKTALAQIMTAEQGKPLAEAEGEIAYAASFIEWFAEQGKRANGEIIPSPGADKRL

MVIRQGVGVCAAITPCNFPAAMITRKAGPALAAGCTMVIKPANETPFTALAMAELANQAGIPQGVINVVT

GQSREIGAVFTGDERVRKLSFTGSTEVGRVLMRQCAESIKKLSLELGGNAPFIVFDDADIDKAVEGALIA

KFRNAGQTCVCVNRFYIHRAIYDQFCDKFVARVAALKVGDGSESDVQIGPLINADAGRKVQSLLDDALSR

GATLLTGGKAHPLGGNFFTPTVIGDVQPGSLLLQEEIFGPVAALVKFDDEQQVIKQANNTIYGLASYFYS

NDAARIWRVSEQLEYGMVGINTGLISNEVAPFGGVKQSGLGREGSEHGIEDYLEMKYLCQGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002898571.1\_2121 [locus\_tag=BN49\_RS12090] [protein=ring-hydroxylating oxygenase subunit alpha] [protein\_id=WP\_002898571.1] [location=complement(2193585..2194709)] [gbkey=CDS]

MSNLSPDFTLPINFCANPQDAWTIPARFYTDSQAFEHEKERIFANSWICVAHGSEVARPNDYITREIIGE

NIVIVRGRDNILRAFYNVCPHRGHQLLSGEGKAKNVITCPYHAWAFKLDGNLAHARNCENVANFDSEKAT

LVPVRLEEYAGFVFINMNPEAESVETQLPGLQDKVLEACPDVHDLKLAARFTTLTPANWKNIVDNYLECY

HCGPAHPGFSDSVQVDRYWHTMHGKWTLQYGFAKPSEQSFKFEEGTDAAFHGFWLWPCTMFNVTPIKGMM

TVIYEFPVDEETTLQNYDIYFTNEELTDDQKALIEWYRDVFRPEDLRLVESVQKGLKSRGYRGQGRIMAD

NSGSGISEHGIAHFHNLVAQVFQP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531255.1\_2122 [locus\_tag=BN49\_RS12095] [protein=BCCT family transporter] [protein\_id=WP\_016531255.1] [location=complement(2194746..2196353)] [gbkey=CDS]

MLSNVKKKDVPLIAISLAAIVFIAATLSLFPQQTAQAADSIFNGVTRLLGSTVQVLVLLALGLVLYLATS

KYGNIRLGEGKVEYSTLSWLFMFICAGLGSSTLYWGVAEWAYYYQTPGLNIAPQSPKALEYSIPYSFFHW

GVSAWATYTLASLIMAYHFHVRKNKGLSLSGIVSAITGVNPQGFWGRLVDLMFLIATVGALTISLVVTAA

TFTRGLSALTGLPDNFTVQAFVILLSGGIFCMSSWIGINNGLQRLSKMVGWGAFLLPLVVLLVGPTEFIT

NNVINAVGLTTQNFLQMSLFTDPLGDGAFTRNWTVFYWLWWISYTPGVAMFVTRVSRGRKIKEVIWGLLL

GSTTGCWFFFGVMESYAMHQFVNGVINVPQVMQTLGGETAVQQVLMSLPAGKLFLAAYLFVMIVFLASHM

DAVAYTMAATSTRNLREGEDPDRGMRLFWCVVITLIPLSILFTGASLETMKTTVVLTALPFLAILLIKTG

GFVRWLKQDYAHVPVHQIETHTPEPIIKAETLPVGAVLKGDGQSL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531254.1\_2123 [locus\_tag=BN49\_RS12100] [protein=tartrate dehydrogenase] [protein\_id=WP\_016531254.1] [location=complement(2196859..2197944)] [gbkey=CDS]

MKKTCRIAAIPGDGIGKEVLPEGIRVLQAAAQRWDLSLSFEQMEWASCEYYAHYGKMMPDDWREQLQGFD

AIYFGAVGWPDTVPDHISLWGSLLKFRREFDQYVNLRPVRLFPGVPCPLAGKKAGDIDFYVVRENTEGEY

SALGGRANEGTEHEVVIQESVFTRRGVDRILRYAFELAKSRPRKTLTSATKSNGLAISMPYWDERVEEMA

KNYPEIRWDKQHIDILCARFVLQPERFDVVVGSNLFGDILSDLGPACTGTIGIAPSANLNPERNFPSLFE

PVHGSAPDIYGKNIANPIATVWAGAMMLDFLGNGDERYHAAHDGILAAIEQTIACGPKTPDMKGSASTQQ

VSDAICKAILA

>lcl|NZ\_FO834906.1\_prot\_WP\_004221441.1\_2124 [locus\_tag=BN49\_RS12105] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_004221441.1] [location=2198027..2198989] [gbkey=CDS]

MKHKTQIMNNLPLLNDLRVFMLVARRAGFAAAAEELGVSPAFVSKRVSLLEQTLNVMLLHRTTRRVTITE

EGERIYEWAQRILQDVDEMMDELSDVRQVPQGTLRIISSFGFGRRVVAPALSALALQYPQLELRFDVQDR

LVDLVNEGVDLDIRVGDDIAPNLIARQLAANHRVLCASPQFLARHAPPKQLSDLAALPCLVIKERDHPFG

VWQLHSKEGQHAIKVTGPLSSNHGEIVHQWCLDGQGIALRSWWDVRENIASGHLVQVLPDYWQPANVWAV

YVSRLATSAKIRTTVEFLRHYFQLHYPQHEPTASAVGRGD

>lcl|NZ\_FO834906.1\_prot\_WP\_002898585.1\_2125 [locus\_tag=BN49\_RS12110] [protein=FAD-binding oxidoreductase] [protein\_id=WP\_002898585.1] [location=complement(2198986..2200266)] [gbkey=CDS]

MTEHTTSYYAASANKYEPFPTLEGSINCDVCVVGGGYTGLSSALHLAEMGYDVVVLEGARIGFGASGRNG

GQLVNSYSRDIDVIEKNYGPDAAKMLGSMMFEGGDIIRERIQRYQIQCDYRPGGLFVAMNHKQLETLEEQ

KANWERYGNTQLELLDREAIRREVDSDRYVGALLDHSGGHIHPLNLAIGEADAIRLNGGRVYEQSPVTRI

QHTSPAVVSTARGQVTARYVIVAGNAYLGDKLEPELAKRSMPCGTQVVTTAPLSEEVARSLIPKNYCVED

CNYLLDYYRLTGDNRLLYGGGVVYGARDPDDVERLIMPKLLKTFPQLQGVKIDYRWTGNFLLTLSRMPQF

GRLDNNIYYMQGYSGHGVTCTHLAGRLISELLRGDAERFDAFAKLPHYPFPGGRSLRIPFTAMGAAYYSL

RDRLGV

>lcl|NZ\_FO834906.1\_prot\_WP\_004214498.1\_2126 [gene=puuC] [locus\_tag=BN49\_RS12115] [protein=aldehyde dehydrogenase PuuC] [protein\_id=WP\_004214498.1] [location=complement(2200269..2201756)] [gbkey=CDS]

MNFQHLAYWQEKAKNLAIETRLFINGEYCAAADNTTFETIDPAAQQTLAQVARGKKADVERAVKAARQAF

DNGDWSQASPAQRKAILTRFADLMEAHREELALLETLDTGKPIRHSLRDDIPGAARAIRWYAEALDKVYG

EVAPTGSNELAMIVREPIGVIAAVVPWNFPLLLACWKLGPALAAGNSVILKPSEKSPLTALRLAGLAKEA

GLPDGVLNVVSGFGHEAGQALALHPDVEVITFTGSTRTGKQLLKDAGDSNMKRVWLEAGGKSANIVFADC

PDLQQAVRATAGGIFYNQGQVCIAGTRLLLEESIADEFLARLKAEAQHWQPGNPLDPDTTMGMLIDNTHA

DNVHSFIRGGESQSTLFLDGRKNPWPAAVGPTIFVDVDPASTLSREEIFGPVLVVTRFKSEEEALKLAND

SDYGLGAAVWTRDLSRAHRMSRRLKAGSVFVNNYNDGDMTVPFGGYKQSGNGRDKSLHALEKFTELKTIW

IALES

>lcl|NZ\_FO834906.1\_prot\_WP\_002898590.1\_2127 [gene=puuR] [locus\_tag=BN49\_RS12120] [protein=HTH-type transcriptional regulator PuuR] [protein\_id=WP\_002898590.1] [location=complement(2202077..2202634)] [gbkey=CDS]

MSDDGLAPGKRLSEIRQQLGLSQRRAAELSGLTHSAISTIEQDKVSPAISTLQKLLKVYGLSLSEFFSEP

EKPDEPQVVINQDDLIEMGSQGVSMKLVHNGNPNRTLAMIFETYQPGTTTGERIKHQGEEIGTILEGEIV

LTINGQSYHLVAGQSYAINTGIPHSFSNTSAGICRIISAHTPTTF

>lcl|NZ\_FO834906.1\_prot\_WP\_020802183.1\_2128 [gene=puuD] [locus\_tag=BN49\_RS12125] [protein=gamma-glutamyl-gamma-aminobutyrate hydrolase] [protein\_id=WP\_020802183.1] [location=complement(2202660..2203412)] [gbkey=CDS]

MYKPVIGVVMCRNRLKGHQTQTLQEKYLNAIVNAGGLPIALPHALAEPELLNAVVDKLDGIYLPGSPSNV

QPHLYGENGDEPDADPGRDLLSMALINAALERRIPIFAICRGLQELVVATGGTLYRRLFEQPELLEHRED

PELPVEQQYAPSHQVEVQEGGLLSQLIPGCNTFWVNSLHGQGAKTLSPQLRVEARAPDGLVEAVSVNDHP

FALGVQWHPEWNSSEYALSRMLFDGFITACQGHHAEKRRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898595.1\_2129 [locus\_tag=BN49\_RS12130] [protein=glutamine synthetase family protein] [protein\_id=WP\_002898595.1] [location=2203638..2205059] [gbkey=CDS]

METNIVEVENFVQQTEERRVSAFAKEVKRYLETYPDTQYVDVLLTDLNGCFRGKRIPVAGLSKLEKGCYF

PASVFAMDILGNVVEEAGLGQEMGEPDRSCIPVPGTLTPSAADPQSIAQVQLTMVDEDGAPFDVEPRNVL

NRLWQQLRQRGLFPVVAVELEFYLLDRKRDAEGYLQPPCAPGTDDRNTQSQVYSVDNLNHFADVLNDIDE

LAKLQLIPADGAVAEASPGQFEINLHHTDNVLDACDDALALKRLVRLMAEKHKMHATFMAKPYEEHAGSG

MHIHISMLNNKGENVLVDGDGEDSALLKRALAGMIDLMPASMALLAPNVNSYRRFQPGMYVPTQASWGHN

NRTVALRIPCGERQNHRVEYRVAGADANPYLVMAAIFAGILHGLDNPQLPLQEEVEGNGLEQEGLPFPIR

QSDALWEFMQNDHLRERLGERFCHVFHACKHDELLQFERLITETEIEWMLKNA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531253.1\_2130 [locus\_tag=BN49\_RS12135] [protein=APC family permease] [protein\_id=WP\_016531253.1] [location=2205413..2206804] [gbkey=CDS]

MAINPPAHNAAQAGRPRLRKSLKLWQVVMMGLAYLTPMTVFDTFGIVSGISNGHVPASYLLALAGVLFTA

ISYGKLVRQFPEAGSAYTYAQKSISPHVGFMVGWSSLLDYLFLPMINVLLAKIYLSALFPEVPPWVWVVT

FVAILTAANLKSVNLVANFNTLFVLVQISIMVVFVILVVQGLHKGEGVGTVWSLQPFISQNAHLIPIITG

ATIVCFSFLGFDAVTTLSEETPDAARVIPKAIFLTAMYGGIIFIVASFFMQLFFPDIHRFKDPDAALPEI

ALYVGGKLFQSIFLCTTFVNTLASGLASHASVSRLLYVMGRDNVFPERIFGYVHPKWRTPALNVIMVGIV

ALSALFFDLVTATALINFGALVAFTFVNLSVFNHFWRRKGYNKTWKDRLHYLLLPMVGALTVGVLWINIE

ATSLTLGLVWAALGLLYLTYLTRRFRKPPPQFDAAKAEQAWES

>lcl|NZ\_FO834906.1\_prot\_WP\_002898600.1\_2131 [locus\_tag=BN49\_RS30395] [protein=small membrane protein] [protein\_id=WP\_002898600.1] [location=complement(2206923..2207045)] [gbkey=CDS]

MSGLILFIVAVALLGVAIYSLVSYLKERRASQLPVHKKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004214502.1\_2132 [locus\_tag=BN49\_RS12145] [protein=hypothetical protein] [protein\_id=WP\_004214502.1] [location=2207302..2207523] [gbkey=CDS]

MYKKTLSLLGVALVLSAFASQAESERQASRERIVEQVLKPCEGKKAGDKVVITDRRGGEHEAICTLTAVP

LPE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531252.1\_2133 [locus\_tag=BN49\_RS12150] [protein=SDR family oxidoreductase] [protein\_id=WP\_016531252.1] [location=complement(2207544..2208332)] [gbkey=CDS]

MTQPSHTAFITGASSGIGAIYAERLAARGYNLILAARREDRLQALADQLQARYAIQASILKADLSEEHGI

AAVEQRLQQDPAIDLFINNAGTAKLAGFLASTPREHQAIHTLNTTALLRLSYAALAAFTPRRRGTLINIA

SILALHTLPGSAVYSASKAWVLSFTRGLQEEFADSGVRIQAVLPAATATDLWPTSGVALDTLPSGTVMTT

EDLVDAALRGLEMGEQVTLPPVHDLGLWETFEQSRVALFTSARTGQPAPRYR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531251.1\_2134 [locus\_tag=BN49\_RS12155] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_016531251.1] [location=complement(2208448..2208897)] [gbkey=CDS]

MKRTRLENSCCPIARSLDVIGDWWSLLIVRDALRGVRRFSEFQKNLGIAKNMLAGRLKMLVDEGILRLQP

ASDGSAWQEYVLTDKGRALQTVLVALSQWADDHLFDPDEPATRLIDRQQRQSLRKLVLQAADGRELAPAD

ITIAIPLND

>lcl|NZ\_FO834906.1\_prot\_2135 [gene=agp] [locus\_tag=BN49\_RS12160] [protein=bifunctional glucose-1-phosphatase/inositol phosphatase] [pseudo=true] [location=2209050..2210297] [gbkey=CDS]

MKKRLLAAAVAGAVMLSAGAQAQDTAAPEGYQLQQVLIMSRHNLRAPLANNGSVLEQSTAKAWPQWDVPG

GQLTTKGGVLEVYMGHYMREWLAQQKLVTSGECPPENAVYAYANSLQRTVATAQFFITGAFPGCGIPVHH

QPQMGTMDPTFNPVITDDSPAFREKALQAMEKERQGMQLTESYKLLETMIDYRNSPSCKEKKVCSLSEGK

DTFSAGYQQEPGVSGPLKVGNSLVDAFTLQYYEGFPKDQVAWGEIASDKQW\*VLSKLKNGYQDSLFTSVA

VAQNVAKPLVKYIDNALVGEGASKAKVTLLVGHDSNIASLLTALDFKPYQLPGQYERTPIGGKLLFQRWH

DSAGNRDLMKIEYVYQSTEQLRNADALTLQAPPQRITLALNGCPVDDQGFCPLETFKKVINEAAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002898701.1\_2136 [locus\_tag=BN49\_RS12165] [protein=YccJ family protein] [protein\_id=WP\_002898701.1] [location=complement(2210366..2210593)] [gbkey=CDS]

MPTQEAKAHRVGEWASLRNTSPEIAEAIFEVAHYDEKLAEQIWEEGSDEVLALAFAKTDKDSLFWGEQTI

ERKNV

>lcl|NZ\_FO834906.1\_prot\_WP\_002898704.1\_2137 [gene=wrbA] [locus\_tag=BN49\_RS12170] [protein=NAD(P)H:quinone oxidoreductase] [protein\_id=WP\_002898704.1] [location=complement(2210614..2211210)] [gbkey=CDS]

MAKILVLYYSMYGHIETMAHAVADGANRVDGVEVVVKRVPETMQAEAFAKAGGKTQNAPVATPQELAEYD

AIIFGTPTRFGNMSGQMRTFLDQTGGLWASGALYGKIASVFSSTGTGGGQEQTITSTWTTLAHHGMIIVP

IGYGAQELFDISQVRGGTPYGATTIAGGDGSRQPSEEELAIARYQGEHVAKLAVKLHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004224058.1\_2138 [locus\_tag=BN49\_RS30975] [protein=hypothetical protein] [protein\_id=WP\_004224058.1] [location=complement(2211427..2211558)] [gbkey=CDS]

MTAADGGECNIQKQSRAKKASSRREQLLTDSAGEEKIVSKNVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002898708.1\_2139 [locus\_tag=BN49\_RS12180] [protein=general stress protein] [protein\_id=WP\_002898708.1] [location=2211646..2211819] [gbkey=CDS]

MANHRGGSGNFAEDRERASEAGRKGGQHSGGNFKNDPQRASEAGKKGGKNSHGSRES

>lcl|NZ\_FO834906.1\_prot\_WP\_004183619.1\_2140 [locus\_tag=BN49\_RS12185] [protein=DMT family transporter] [protein\_id=WP\_004183619.1] [location=2211984..2212922] [gbkey=CDS]

MSSLKFSVSRQEALLIMITMFWGGTFLAVQYAVSLSGPLFFVGLRFATAALAVGLLSLRTLRGLTWLEVK

AGVAIGVAIALGYGLQTWGLQTISSSKSAFITAMYVPLVPLLQWLCLGRMPGVMSCVGIVLAFIGLILLA

GPENNLLALGVGEMITLASAVAIAAEIILISAWAGKVDVRRVTVVQLATASLVAFAAMKPAGESVPSLTP

ALLGVALGLGIFSAIIQVTMNWAQRSVSPTRATLIYTGEPVWAGIFGRLAGERLPLLALLGCVLILAGVL

VSELKWKRKSPPQVSTNDDAQPLTDLADRREP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043011.1\_2141 [gene=rutG] [locus\_tag=BN49\_RS12190] [protein=pyrimidine utilization transport protein G] [protein\_id=WP\_046043011.1] [location=complement(2213329..2214651)] [gbkey=CDS]

MALFDFPRWKLTSPAAESGVVAPDERLSAGQTLVMGVQHAVAMFGATVLMPLLMGLDPNLSILMSGVGTL

LFFVVTGGRVPSYLGSSAASVGVVIAITGFNGQGLNPHLSVALGGIIACGLVYTLIGLVVMKIGTRWIER

LMPPVVTGAVVMAIGLNLAPIAVRSVSASAFDSWMAVLTVLCIGIVAVFTRGMLQRLLILVGLIVACALY

ALLANGLGLGKPLDFSPLAQAAWFGLPHFTTPSFNGQAMMLIAPVAVILVAENLGHLKAVAGMTGRNMDP

YMGRAFVGDGLATMLSGSVGGSGVTTYAENIGVMAVTKVYSTLVFVAAALIAMLLGFSPKFGALIHTIPG

PVIGGASIVVFGLIAVAGARIWVQNRVDLSQNSNLIMVSVTLVLGAGDFALSLGGFTLGGIGTATFGAIL

LHALLHRGTREAKEARVTPV

>lcl|NZ\_FO834906.1\_prot\_WP\_004176611.1\_2142 [gene=rutF] [locus\_tag=BN49\_RS12195] [protein=pyrimidine utilization flavin reductase protein F] [protein\_id=WP\_004176611.1] [location=complement(2214673..2215167)] [gbkey=CDS]

MELTDKASFRDAMAHVGAAVNIITTDGPAGRAGFTASAVCSVTDTPPTLLVCLNRSASVWPVFSEHHTLC

VNTLAAGQEALSTLFGGKTAMDERFAAADWQTGATGCPRLEAALVSFDCRIDQRVSVGTHDILFCHVVAI

TRHPEPRGLMWFDRGYHTLMRPAC

>lcl|NZ\_FO834906.1\_prot\_WP\_004141442.1\_2143 [locus\_tag=BN49\_RS12200] [protein=malonic semialdehyde reductase] [protein\_id=WP\_004141442.1] [location=complement(2215178..2215768)] [gbkey=CDS]

MNDAINHTACETLFTQARTHNGWLDKPVSDAQLQAVWDLMKMGPTSANCSPARIVFVRSAEGKEKLRPTL

SSGNLQKTMQAPVTAIVAWDSAFYDRLPTLFPHGDARSWFTSSPQLAEETAFRNSSLQAAYLIFACRARG

LDTGPMSGFDREKVDAAFFADNGWKSNLLVNIGYGDPGKLYGRLPRLSFDEACLLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004179289.1\_2144 [gene=rutD] [locus\_tag=BN49\_RS12205] [protein=pyrimidine utilization protein D] [protein\_id=WP\_004179289.1] [location=complement(2215765..2216568)] [gbkey=CDS]

MMRLNIAPAPWPGAPVVVLSAGLGGGGGYWLAQRAALEEQYQLVSYDHNGTGENAGPLPADYSLATMAGE

LFSALQAAGIARFALVGHALGALIGLQLALDRPEAVSALALVNGWLSLSPHTRRCFQVRERLLHAGGAQA

WVEAQPLFLYPAEWMAARLPRLEAEDALAISHFQGKENLLKRLQALKQADFSRRASAIACPTLIISAADD

LLVPASCSRVLQTAIPGSQLVEMPWGGHACNVTDADTFNTILRDGLSAMLPVARETR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898877.1\_2145 [gene=rutC] [locus\_tag=BN49\_RS12210] [protein=pyrimidine utilization protein C] [protein\_id=WP\_002898877.1] [location=complement(2216565..2216957)] [gbkey=CDS]

MPKQVIIPPGTTAPIAPFVPGTLADGVVYVSGTLPFDKQNNVVHIGDPKAQTRHVLETIRSVIETAGGSM

ADVTFNSIFITDWTNYAAINEVYAEFFPGDKPARFCIQCGLVKPDALVEIASVAHIGTPT

>lcl|NZ\_FO834906.1\_prot\_WP\_004224061.1\_2146 [gene=rutB] [locus\_tag=BN49\_RS12215] [protein=pyrimidine utilization protein B] [protein\_id=WP\_004224061.1] [location=complement(2216950..2217660)] [gbkey=CDS]

MITLPARPESLTFAPQQSALIVVDMQNAYASQGGYLDLAGFDVSATRPVIDNINTAVAAARAAGMLIIWF

QNGWDDQYVEAGGPGSPNYHKSNALKTMRQRPELQGKLLAKGGWDYQLVDELTPQEGDIVLPKPRYSGFF

NTPLDSILRSRGIRHLVFTGIATNVCVESTLRDGFFLEYFGIVLEDATHQAGPAFAQQAALFNIETFFGW

VSDVESFCHALSPATPLALAKEKRYA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043013.1\_2147 [gene=rutA] [locus\_tag=BN49\_RS12220] [protein=pyrimidine utilization protein A] [protein\_id=WP\_046043013.1] [location=complement(2217660..2218751)] [gbkey=CDS]

MKIGVFVPIGNNGWLISTHAPQYMPTFELNKAIVQKAEHYHFDFALSMIKLRGFGGKTEFWDHNLESFTL

MAGLAAVTSKIQIYATAATLTLPPAIVARMASTIDSISGGRFGVNLVTGRQKPEYDQMGMWPGDDYFASR

YDYLTEYVQVLRDLWGTGRSDFKGDYFTMNDCRVSPRPSQPMKVICAGQSDAGMAFSAQHADYNFCFGKG

VNTPTAFAPTAARMMQAAEKTGRDVGSYVLFMVIADETDEAARAKWEHYKAGADEEALAWLTEQSQKDTR

SGSDTNVRQMADPTSAVNINMGTLVGSYASVARMLDEVASVPGTDGVLLTFDDFLAGIDAFGERIQPLMR

CRNHIASVTREVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898883.1\_2148 [gene=rutR] [locus\_tag=BN49\_RS12225] [protein=HTH-type transcriptional regulator RutR] [protein\_id=WP\_002898883.1] [location=2219036..2219674] [gbkey=CDS]

MAQGAVKKSGKRSQAVSAKKEAILAAALEAFSQFGIHGTRLEQVAERAGVSKTNLLYYYPSKEALYVAVL

QQILAIWLAPLKAFREDISPLVAIREYIRLKLEVSRDHPQASKLFCLEMLQGAPLLMGELTGDLKALVDE

KSAIVSGWIDRGKLAPVDPQHLIFMIWATTQHYADFATQVEAVTGATLQDAAFFEQTVDNVQRMIIEGIR

VR

>lcl|NZ\_FO834906.1\_prot\_WP\_002898886.1\_2149 [locus\_tag=BN49\_RS12230] [protein=lysozyme inhibitor LprI family protein] [protein\_id=WP\_002898886.1] [location=complement(2219671..2220066)] [gbkey=CDS]

MKRTLFAVMALLASGAALADECSSANTQTEMNQCAAAQYQAADKKLNDTWQQALQRAVGKQQTLLKQAQQ

AWIALRDADCAFLASGAEGGSMQPMLVSQCMTDKSVERESFLASLLQCEDGDQSCPLPPAN

>lcl|NZ\_FO834906.1\_prot\_WP\_004183621.1\_2150 [gene=putA] [locus\_tag=BN49\_RS12235] [protein=trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase] [protein\_id=WP\_004183621.1] [location=complement(2220252..2224214)] [gbkey=CDS]

MGTTTMGVKLDDATRERIKSAASRIDRTPHWLIKQAIFNYLEKLENDETLPELPALLSGAANESDDASEP

TEEPYQPFLEFAEQILPQSVSRAAITAAWRRPETDAVPMLLEQARLPQPLGEQAHKLAYQLAEKLRNQKT

ASGRAGMVQSLLQEFSLSSQEGVALMCLAEALLRIPDKATRDALIRDKISNGNWQSHIGRSPSLFVNAAT

WGLLFTGKLVSTHNETSLSRSLNRIIGKSGEPLIRKGVDMAMRLMGEQFVTGETIAEALANARKLEEKGF

RYSYDMLGEAALTAADAQAYMVSYQQAIHAIGKASNGRGIYEGPGISIKLSALHPRYSRAQYDRVMEELY

PRLKSLTLLARQYDIGINIDAEEADRLEISLDLLEKLCFEPELAGWNGIGFVIQAYQKRCPFVIDYLIDL

ATRSRRRLMIRLVKGAYWDSEIKRAQMEGLEGYPVYTRKVYTDVSYLACAKKLLAVPNLIYPQFATHNAH

TLAAIYQLAGQNYYPGQYEFQCLHGMGEPLYEQVVGKVADGKLNRPCRIYAPVGTHETLLAYLVRRLLEN

GANTSFVNRIADNTLPLDELVADPVSAVEKLAQQEGQAGLPHPKIPLPRDLYGSGRSNSAGLDLANEHRL

ASLSSSLLNSALHKWQALPMLEQPVAEGEMQPVVNPAEPKDIVGYVREASDAEVQQALTSAINNAPIWFA

TPPQERAAILERAAVLMESQMPTLMGILVREAGKTFSNAIAEVREAVDFLHYYAGQVRDDFDNETHRPLG

PVVCISPWNFPLAIFTGQIAAALAAGNSVLAKPAEQTPLIAAQGVAILLEAGVPPGVIQLLPGRGETVGA

ALTSDERVRGVMFTGSTEVATLLQRNIASRLDPQGRPTPLIAETGGMNAMIVDSSALTEQVVIDVLASAF

DSAGQRCSALRVLCLQEEVADHTLTMLRGAMSECRMGNPGRLTTDIGPVIDAEAKENIERHIQAMRAKGR

TVYQAVRENSEDAREWRHGTFVPPTLIELDSFDELKKEVFGPVLHVVRYNRNELDKLVEQINASGYGLTL

GVHTRIDETIAQVTGSAKVGNLYVNRNMVGAVVGVQPFGGEGLSGTGPKAGGPLYLYRLLSSRPQDAVGV

TFARQDAERPLDAQLKTLLEKPLQALQQWAAGRPELQALCQQYSEQAQSGTQRLLPGPTGERNTLTLMPR

ERVLCVADNEQDALIQLAAVLAVGCEVLWPDSALQRDLAKKLPREVSERIRFAKAEQLPGQAFDAVIYHG

DSDQLRELCEQVAARDGAIVSVQGFARGETNLLLERLYIERSLSVNTAAAGGNASLMTIG

>lcl|NZ\_FO834906.1\_prot\_WP\_004147889.1\_2151 [gene=putP] [locus\_tag=BN49\_RS12240] [protein=sodium/proline symporter PutP] [protein\_id=WP\_004147889.1] [location=2224636..2226144] [gbkey=CDS]

MAISTPMLVTFIVYIFGMVLIGFIAWRSTKNFDDYILGGRSLGPFVTALSAGASDMSGWLLMGLPGAIFL

SGISESWIAIGLTLGAWINWKLVAGRLRVHTEVNNNALTLPDYFTGRFEDKSRVLRIISALVILLFFTIY

CASGIVAGARLFESTFGMSYETALWAGAAATIIYTFVGGFLAVSWTDTVQASLMIFALILTPVIVIISVG

GFGDSLEVIKQKSIENIDMLKGLNFVAIISLMGWGLGYFGQPHILARFMAADSHHSIVHARRISMTWMIL

CLGGAVAVGFFGIAYFNNNPSLAGAVNQNAERVFIELAQILFNPWIAGILLSAILAAVMSTLSCQLLVCS

SAITEDLYKAFLRKNAGQKELVWVGRMMVLVVALVAIALAANPENRVLGLVSYAWAGFGAAFGPVVLFSV

MWSRMTRNGALAGMVIGALTVIVWKQFGWLGLYEIIPGFVFGSIGIVVFSLLDKAPSASMQQRFAEADAH

YHTPPPVRATAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150827.1\_2152 [locus\_tag=BN49\_RS12245] [protein=DUF3574 domain-containing protein] [protein\_id=WP\_004150827.1] [location=2226279..2226713] [gbkey=CDS]

MTFRQGAMALVLAGLLSGCVAGGSSSTSAPKPGVCPADKSMVQTTLYFGLSRPAGKDITAEEWQQFVDRD

VTPRFRDGLTVFDAHGQWLGQNGQVVREQSKALMVIHGHDAQSEAGIEALRQGYKSRFAQESVMRVDQPV

CVQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002898911.1\_2153 [locus\_tag=BN49\_RS12250] [protein=nucleoside transporter] [protein\_id=WP\_002898911.1] [location=complement(2226745..2227929)] [gbkey=CDS]

MTAFFHFLLALAVILALAWLVSYDRQKIRIRYILQLIIIEIALAFFFLHAESGLWLVKNISGFFASLLGF

AAEGTNFVFGGMSEKGLAFIFLGVLCPIVFISALIGILQHWRILPIFIRVIGTLLSKVNGMGKLESFNAV

SSLILGQSENFIAYKGVLGDLSSRRLFTMAATAMSTVSLSIVGAYMTMLDAKYVVAALILNMFSTFIVLS

VINPTRPGSEQEIKLEKLHESQSFFEMLGEYILAGFKVAMIILAMLIGFIALISAINALFATLFGLSFQQ

ILGYVFYPLAWLIGIPLSDALNAGSIMATKLVANEFVAMIELQKIAASMTPRGLGILSVFLVSFANFASI

GIIAGAIKGLNEPQGNIVSRFGLRLVYSATLVSLLSASFAGLVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002898913.1\_2154 [locus\_tag=BN49\_RS12255] [protein=FTR1 family protein] [protein\_id=WP\_002898913.1] [location=2228200..2229030] [gbkey=CDS]

MFVPFLIMLREGLEAALIVSLIASYLKRTQRGNWIGVMWIGVILAAALCLGLGIFINETTGEFPQREQEL

FEGIVAVIAVVILTWMVFWMRNVSRNVKQQLEQAVDKALQRGNHHGWALVMMVFFAVAREGLESVFFLLA

AFQQDVGIWPPLGALLGLATAIVLGFLIYWGGIRLNLGVFFKWTSLFILLVAAGLAAGAIRAFHEAGLWN

LFQDTAFDLSNVLSTHTLFGTLLEGIFGYQETPSVSEVAVYLLYLIPALVLFALPPRNNTTASRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004157740.1\_2155 [locus\_tag=BN49\_RS12260] [protein=iron uptake system protein EfeO] [protein\_id=WP\_004157740.1] [location=2229082..2230209] [gbkey=CDS]

MMIHFRRNALRVTVAALLSSAFGAQAADIPQVKVTVNDKQCEPMQVTVNAGKTQFIIQNHSQKALEWEIL

KGVMVVEERENIAPGFTQKLTANLQPGEYDMTCGLLTNPKGKLIVTGAATKDAAKADAVLSLGDAITAYK

AYVTAETAQLVSGTKAFTDAVKAGDIEKAKALYAPTRQHYERIEPIAELFSDLDGSIDAREDDFEKKAED

PKFTGFHRLEKALFGDNSVKGMEKYADQLNSDVLELQKRISELAFPPSKVVGGAAGLIEEVAASKISGEE

DRYSHTDLWDFQANIDGAQKIVDLLRPQLQKENSALLAKVDANFKKVDSILSKYRTKDGFETYDKLTTAD

RNALKGPITTLAEDLAQLRGILGLD

>lcl|NZ\_FO834906.1\_prot\_WP\_004147893.1\_2156 [gene=efeB] [locus\_tag=BN49\_RS12265] [protein=iron uptake transporter deferrochelatase/peroxidase subunit] [protein\_id=WP\_004147893.1] [location=2230214..2231497] [gbkey=CDS]

MAQQKPHDVNEPSRRRLLKGIGALGGALAITGGCPVAHAAKAESSPGTLTPDARQEKQPFYGRHQAGILT

PQQASMMLVAFDVLAADKADLERLFRLLTQRIAFLTQGGPAPDTPNPRLPPMDSGILGPWIAPDNLTITV

SVGHSLFDERFGLADKAPKKLQPMTRFPNDSLDAALCHGDLLLQICANTQDTVIHALRDVIKHTPDLLSV

RWKREGFISDSAARSKGKETPINLLGFKDGTANPASHDSALMDKVVWVTADQDEPAWTVGGSYQAARIIQ

FHVEFWDRTPLKEQQTIFGRDKHTGAPLGMKNEHDTPDYSKDPNGEVIALDSHIRLANPRTPETQSSLMM

RRGYSYSLGVTNAGQLDMGLLFVCYQHDLEKGFLTVQKRLNGEALEEYVKPIGGGYFFVLPGVVDEKHYL

GESLLQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898923.1\_2157 [gene=phoH] [locus\_tag=BN49\_RS12270] [protein=phosphate starvation-inducible protein PhoH] [protein\_id=WP\_002898923.1] [location=2232002..2232790] [gbkey=CDS]

MGRQKAVIKARREAKRVLRRDSRSHKQREEESVTSLVQMSGVEAIGMARDSRDTSPIEARNEAQAHYLNA

IDNKQLIFATGEAGCGKTWISAAKAAEALIHKDVDRIIVTRPVLQADEDLGFLPGDIAEKFAPYFRPVYD

VLVKRLGASFMQYCLRPEIGKVEIAPFAYMRGRTFENAVVILDEAQNVTAAQMKMFLTRLGENVTVIVNG

DITQCDLPSGVRSGLSDALARFEEDEMIGIVRFTTDDCVRSALCQRTLKAYY

>lcl|NZ\_FO834906.1\_prot\_WP\_002898927.1\_2158 [locus\_tag=BN49\_RS12280] [protein=isochorismatase family protein] [protein\_id=WP\_002898927.1] [location=complement(2233405..2234082)] [gbkey=CDS]

MSTPANFNGARPVIDVNDTAMLLIDHQSGLFQTVGDMPMPELRARAAALAKMASLAGIPVITTASVPQGP

NGPLIPEIHENAPHAKYIARKGEINAWDNPEFVAAVKATGRKTLIIAGTITSVCMAFPAIAAVADGYKVF

AVIDASGTYSKMAQEITLARVVQAGVVPMDTAAVASELQRTWNRPDAAEWAEVYTKVFPAYQLLIESYSK

AQDVVKNNEQLDSQR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531957.1\_2159 [locus\_tag=BN49\_RS12285] [protein=pirin family protein] [protein\_id=WP\_016531957.1] [location=complement(2234101..2234961)] [gbkey=CDS]

MKQITGVYTAPAQHWVGDGFPVRSMFSYQTHGQQLSPFLLLDYAGPYTFPAGSEKRGVGEHPHRGFETVT

IVYAGEVEHRDSTGRGGVIGPGDVQWMTAGAGILHEEFHSEAFTRSGGELKMIQLWVNLPAKDKMATPGY

QRITAGTIPTVALADGAGQVRVIAGQYDDVSGPAHTFSPLNVWDLQLNQGHDLTLRQPEGWSTALVVLEG

EVIINGSESAREGQLAVLSQAGDAVHLEATAPAKVLLMAGEPLQEPIVGYGPFVMNNKTQIAEAVRDFNS

GRFGQI

>lcl|NZ\_FO834906.1\_prot\_WP\_016531956.1\_2160 [locus\_tag=BN49\_RS12290] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016531956.1] [location=2235076..2235981] [gbkey=CDS]

MQDLNDFAWFVQVVDHGGFAAAGRALDQPKSKLSRRIAQLEERLGVRLIQRTTRQFAVTEVGQTFYQHCK

AMLIEAEAAQQAVETLRAEPRGSVRITCPVTLLHVHIGPMLARFMARYPGVTLHLEATNRRVDVVGEGID

VAIRVRPRPIEDSDLVMRVLADRGHRLVASPDLISRLGRPQAPSELSAWPGLSLGANKHQHKWQLTGPGG

ARAEVYFTPRMVTTDMLALREAAMAGVGVVPLPLLMVRDQLASGELEVVLDEWQPRREVIHAAFASRRGL

LPSVRALVDYLSEEYQRMEED

>lcl|NZ\_FO834906.1\_prot\_WP\_004224069.1\_2161 [locus\_tag=BN49\_RS12295] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_004224069.1] [location=complement(2236172..2236744)] [gbkey=CDS]

MLKKTETYHKLITAAAACFAEKGFSATSVREISTRAGISQGAMYTYFKSKDELVKAIVLEEQNSALTAHN

ATYAGSYFDRLCAQVTSCISEIGYPITHQLWVEIMAESARNPELRKTYISSDDIMRKSFARLIQEGIAAG

EFRRDINLEEITIIIFALIDGLIARQAINTTFSFKDDLPMFFDVMAKLLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176596.1\_2162 [locus\_tag=BN49\_RS12300] [protein=arginase family protein] [protein\_id=WP\_004176596.1] [location=complement(2236839..2237702)] [gbkey=CDS]

MTSKTLRLIFPQWQGGNNPPYYLGSQLLSFLSPEAKGPVEIVPVELPTTEPLPRINDITAKPSLIRQLNN

AAALIEKHDPNSIVILGGDCLVSLAPFAHLLDKFGDKLGVLWIDSHPDVQTAEQYPNAHAHVLGALMGTG

DNDLVAHVKTKLNPSKIMIAGIHAPLPYEAEYLTRHNITTLAPEQVKSGADEVLEWIAKEKIAYLAIHID

LDVLDPSLFRSILFAKPGRGKHDFGDVAEGKLTIEDVLNLIAAATTKAVPVGLTIAEHLPWDMLNLKNML

SELPLLK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531955.1\_2163 [gene=ghrA] [locus\_tag=BN49\_RS12310] [protein=glyoxylate/hydroxypyruvate reductase GhrA] [protein\_id=WP\_016531955.1] [location=2238586..2239524] [gbkey=CDS]

MEIIFYHPTFDTQYWICELEKQLPGARVREWKAGDNRPADYALVWHPPVEMLQGRALKAVFALGAGVDSI

LSKLRDHPDMLPLSIPLFRLEDTGMGRQMQEYAVSQVLHWFRRFDDYQALKLASRWQPLPEYRADEFTVG

IMGAGVLGTKVAESLQPWGFPLRVWSRSRKSWPQVQSFAGQAELGEFLQGTRVLINLLPNTAETAGIINQ

TLLAQLPDESYVLNLARGVHVVEEDLLAALNSGKLKGAMLDVFSREPLPQESPLWAHPRVAMTPHVAAVT

RPMEAITYIAETISRLERGEPVSGQVDRQRGY

>lcl|NZ\_FO834906.1\_prot\_WP\_004140764.1\_2164 [locus\_tag=BN49\_RS12315] [protein=phosphatase] [protein\_id=WP\_004140764.1] [location=2239613..2240350] [gbkey=CDS]

MYPVDLHMHTVASTHAYSTLHDYIAEAKRKGIKLFAITDHGPDMADAPHYWHFVNMRIWPRLVDGVGILR

GIESNIKNIEGEIDCSGPMLTSLDLIIAGFHEPVFPPQDRDTHTQAMIAAMASGKVHMISHPGNPKFPVD

IPAIAEAAARYQVALEINNSSFVSSRVGSEDNCRAIAAAVRDAGGWVALGSDSHTAFTLGEFTECRKILD

AVDFPEERILNVSPRRLLNFLESRGMPAIPEFADL

>lcl|NZ\_FO834906.1\_prot\_WP\_004140758.1\_2165 [locus\_tag=BN49\_RS12320] [protein=molecular chaperone] [protein\_id=WP\_004140758.1] [location=2240373..2240927] [gbkey=CDS]

MNEFSILCRVLGSLYYRQPQDPLLVPLFTLIREGKLAASWPLEQDELLARLQKSCEMQSLATDYNALFVG

EACSVPPYRSAWVEGSSEAEVRAFLSEHGIPTGEGPADHLGSLLLAASWLEDHAAEDQSETLELLFADYI

LPWCGTMLGKVEAHAHTPFWRTMAPLTRDAIAAMWDELQEEDEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016531954.1\_2166 [locus\_tag=BN49\_RS12325] [protein=DUF1097 domain-containing protein] [protein\_id=WP\_016531954.1] [location=2241031..2241513] [gbkey=CDS]

MNILFAIALTTGILSGIWGWVAVALGLLSWAGFLGCTAYFACPQGGLKGLAISSCTVMSGVAWALVIIHG

SALAPQVQILSYMMTGVVAFLMCIQARRTLLSFVPGTFIGACATFAADGDWRLVITSLALGLVFGYAMKN

SGLWLAARADKHKLFVNDNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176593.1\_2167 [gene=ymdB] [locus\_tag=BN49\_RS12330] [protein=O-acetyl-ADP-ribose deacetylase] [protein\_id=WP\_004176593.1] [location=2241663..2242190] [gbkey=CDS]

MAVKPEVILGDITTLDVDVIVNAANPSLLGGGGVDGAIHRAAGPALLAACKQVLQQQGECPPGHAVITIA

GNLPASAVIHTVGPVWHGGDRMEAQTLADAYKNSLQLASANNYRSIAFPAISTGVYGYPKEEAAAIAVRT

VTAFLTRYNPLERVLFVCFDEETAAIYRRLLASYP

>lcl|NZ\_FO834906.1\_prot\_WP\_004179313.1\_2168 [locus\_tag=BN49\_RS12335] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_004179313.1] [location=2242257..2242850] [gbkey=CDS]

MSEGKVQQKQQARRAEIVVAAQKCFAEKGLHGASVADIAREAGLSVGQLYRIFASKEAIIEAIVSEIVNA

RVGEMIDENHNLARKAAVLAGRIPTSAATKSDNYLLMEINAEASRNPRLREILMQADRRLKEEGGRLSQR

YHPGLSDARRNAASELIAVLTEGAAYRCELSASTPVDKADLEALYNMIFDRLFDEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004140754.1\_2169 [gene=mdoC] [locus\_tag=BN49\_RS12340] [protein=glucans biosynthesis protein MdoC] [protein\_id=WP\_004140754.1] [location=complement(2242885..2244045)] [gbkey=CDS]

MNNTPVQREYFFDSIRAWLMLLGIPFHISLIYSSHSWHVNSAEPSWWLTLFNDFIHAFRMQVFFVISGYF

SYMLFLRYPLKKWWKVRVERVGIPLLTAIPLLTLPQFIMLQYVNGKAENWHTLSGYDKFNTLAWELISHL

WFLLVLVVLTSLGVVLFKWLTRRPAGGASAFGDTVTMGQLTMIFLALGVLYALIRRSLFLIYPPLLSNGL

FNFVVMQTLFYLPFFVLGAQTFINPRLKAMFTTPSPWCCAAALLGFIAYRLNQQYGSGDGWMYETESVIT

MVLGLWMVNVVFSLGHRLLNFQSARVTYFVNASLFIYLVHHPLTLLYGAWITPVIKSNTLGFIGGLVFVV

GIALILYEIHLRIPLLRFLFSGKPMNKPAKTPASAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004140751.1\_2170 [gene=mdoG] [locus\_tag=BN49\_RS12345] [protein=glucans biosynthesis protein MdoG] [protein\_id=WP\_004140751.1] [location=2244297..2245850] [gbkey=CDS]

MKHKPQMMKMRWLSAAVMLSLCTSSAWAFSIDDVAKEAKTLAGKGYEAPKSNLPSAFRDMKYADYQQIQF

NHDKAYWNNQKTPFKLEFYHQGMYFDTPVTINEVTATSVRKIKYSPDYFNFGNVQHDKDTVKDLGFAGFK

VLYPINSKDKNDEIVSMLGASYFRVLGQGQVYGLSARGLAIDTALPSGEEFPRFREFWIERPKATDKRLT

IYALLDSPRATGAYRFVIMPGRDTVVDVQSKVYLRDKVGKLGVAPLTSMFLFGSNQPSPALNYRPALHDS

NGLSILAGNGEWIWRPLNNPKHLAVSSYAMENPQGFGLLQRGRQFSRFEDLDDRYDLRPSAWITPKGEWG

KGKIELVEIPTNDETNDNIVTYWTPDQLPEPGKEMNFKYTITFSRDEDKLHAPDNAYVMQTRRSTGDVKQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_002898967.1\_2171 [gene=mdoH] [locus\_tag=BN49\_RS12350] [protein=glucans biosynthesis glucosyltransferase MdoH] [protein\_id=WP\_002898967.1] [location=2245843..2248371] [gbkey=CDS]

MNKITKYIDALPLSDAEKSALPDTSLQAVHQALDDDHQTFAREDDSPLGSVKARLAHSWPDSLSGDQLVK

DDEGRTQLHAMPKAKRSSMIPDPWRTNPVGRFWDRLRGRDVTPRYLSRLTQEERESEQKWRTVGTIRRYI

LLLLTLSQTVVATWYMKTILPYQGWALINPADMVGQNLWISFMQLLPYVLQSGILILFAVLFCWVSAGFW

TALMGFLQLLIGRDKYSISASTVGDEPLNPAHRTALIMPICNEDVDRVFAGLRATWESVKATGNAAHFDV

YILSDSYNPDICVAEQKAWMELIAEVQGEGQIFYRRRRRRVKRKSGNIDDFCRRWGSQYSYMVVLDADSV

MTGECLSSLVRLMEANPNAGIIQSSPRASGMDTLYARCQQFATRVYGPLFTAGLHFWQLGESHYWGHNAI

IRVKPFIEHCALAPLPGEGNFAGSILSHDFVEAALMRRAGWGVWIAYDLPGSYEELPPNLLDELKRDRRW

CQGNLMNFRLFLVRGMHPVHRAVFLTGVMSYLSAPLWFMFLALSTALQVVHALTEPQYFLQPRQLFPVWP

QWRPELAIALFASTMVLLFLPKLLSIILVWCKGPKEYGGFIRVTLSLLLEVLFSVLLAPVRMLFHTVFVV

SAFLGWEVVWNSPQRDDDSTPWGEAFMRHGSQLLLGLVWAVGMAWLDLRFLFWLAPIVVSLILSPFVSAI

SSRATVGLRTKRWKLFLIPEEYSPPQVLKDTDAYLTMNRQRSLDDGFMHAVFNPSFNALATAMATARHRQ

GHILEIARERHVEQALNETPDKLNRDRRLVLLSDPVTMSRLHYRVWAAPEKYSSWVNAYQQLALNPLALK

TK

>lcl|NZ\_FO834906.1\_prot\_WP\_002898978.1\_2172 [locus\_tag=BN49\_RS12355] [protein=YceK/YidQ family lipoprotein] [protein\_id=WP\_002898978.1] [location=2248438..2248665] [gbkey=CDS]

MRILPIIAMALLLSGCGSIISRTVPGQGHGNQYYPGVQWDVRDSAWRYLTILDLPFSLVFDTLLLPLDAS

HGPYN

>lcl|NZ\_FO834906.1\_prot\_WP\_002898981.1\_2173 [locus\_tag=BN49\_RS12360] [protein=MysB family protein] [protein\_id=WP\_002898981.1] [location=complement(2248666..2249052)] [gbkey=CDS]

MPKDSMFYATLEEAIDAAREEFLANNPDSDEESANVEQLNIQKYVLQDGDIAWQAEFFADEEEQGECLPM

LSGEAAQSVFDGDYDEIELRQEWLEENTLHEWDEGEFQLEPSLDTEEGQTAADEWDER

>lcl|NZ\_FO834906.1\_prot\_WP\_004224072.1\_2174 [gene=mdtG] [locus\_tag=BN49\_RS12365] [protein=multidrug efflux MFS transporter MdtG] [protein\_id=WP\_004224072.1] [location=complement(2249144..2250370)] [gbkey=CDS]

MSSAETPINWKQNLTVTWLGCFLTGAAFSLVMPFLPLYVEQLGVTGHSALNMWSGLVFSITFLFSAIASP

FWGGLADRKGRKIMLLRSALGMAIVMMLMGMAQNIWQFLLLRALLGLLGGFIPNANALIATQIPRHKSGW

ALGTLSTGAVSGALLGPLAGGFLADHWGLRTVFFMTAAVLFICFLFTLFLIRENFVPIARKEMLSAREVF

SSLQNPKLVLSLFVTSLIIQVATGSIAPILTLYVRDLAGNVSNIAFISGMIASVPGIAALMSAPRLGKLG

DRIGPEKILIVALIISVLLLIPMSFVQTPLQLGILRFLLGAADGALLPAVQTLLVYNSTSQISGRIFSYN

QSFRDIGNVTGPLIGASVSANYGFRAVFLVTAGVVLFNAIYSTLSLRRPAADTSHSVN

>lcl|NZ\_FO834906.1\_prot\_WP\_004150825.1\_2175 [locus\_tag=BN49\_RS12370] [protein=LpxL/LpxP family Kdo(2)-lipid IV(A) lauroyl/palmitoleoyl acyltransferasee] [protein\_id=WP\_004150825.1] [location=complement(2250542..2251462)] [gbkey=CDS]

MTHLPKFSPALLHPRYWLLWLGIGLLWLVVQLPYPLIYRLGNAIGRLAMRFMKRRAKIAYRNLELCFPEK

SEQERHRMVVMNFESVGMGLMETGMAWFWPVRRIARWTDTIGFEHIRDVQAQQRGILLIGIHFLTLEMGA

RMFGMNEPGIGVYRPNDNPVIDWLQTWGRLRSNKDMIDRKDLKGMIRALKKGEVVWYAPDHDYGPTASVF

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IMMAPEQYMWLHRRFKTRPEGMPSRY

>lcl|NZ\_FO834906.1\_prot\_WP\_002898987.1\_2176 [locus\_tag=BN49\_RS12380] [protein=rhodanese-related sulfurtransferase] [protein\_id=WP\_002898987.1] [location=2251668..2252732] [gbkey=CDS]

MPVLHNRISNETLKAQMLAETEPRTTISFYKYFTIVDPQATRDALWVALTQLKVFGRIYLAREGINAQIS

VPQSNVEALREFLYGFDPALAGLRFNIAVEDDGKSFWVLRLKVRDRIVADGIDDPSFDASNVGEYLKAAE

VNAMLDDPDAVFIDMRNHYEYEVGHFENALEIPADTFRDQLPKAVEMMQDHKDKKIVMYCTGGIRCEKAS

AWMKHNGFNKVWHIEGGIIEYARRAREQGLPVRFIGKNFVFDERMGERISNDVIAHCHQCGAPCDTHTNC

LNDGCHLLFIQCPSCAEKFAGCCSEACMEEHKLPEEEQRKLRAGRENGNKIFNKSRGRLNTKLGILDPEP

SEKP

>lcl|NZ\_FO834906.1\_prot\_WP\_016530426.1\_2177 [locus\_tag=BN49\_RS12385] [protein=YceO family protein] [protein\_id=WP\_016530426.1] [location=complement(2252718..2252831)] [gbkey=CDS]

MRRLFNMLVNNVREHFMIYLALWLLLTIIDLVWLWFF

>lcl|NZ\_FO834906.1\_prot\_WP\_046043018.1\_2178 [gene=solA] [locus\_tag=BN49\_RS12390] [protein=N-methyl-L-tryptophan oxidase] [protein\_id=WP\_046043018.1] [location=complement(2252903..2254021)] [gbkey=CDS]

MQYDLIIIGSGSVGAAAGYYARRAGLNVLMTDAHQPPHQEGSHHGSSRLIRHAYGEGEKYVPLVLRAQQL

WDELAEISGEAVFERTGVINLGPASSAFLANVAASARAFQLEVEELDAQAVMQRWPEIRLPDDYRAIFEP

ASGVLRSELAVETWIRLAREAGCAQLFNCPVSAIHHHADGITIDTLDGEYHGKKLLVSAGTWVTRLLPDL

PIQPVRKVFAWYQADGRYSSKNHFPAFTGELPNGDQYYGFPAEDNELKIGKHNGGQPISTPQERVAFGAV

ASDGSESFPFLRNVLPGIGGCLHGASCTYDNTVDEDFIIDTLPGRPDTLLITGLSGHGFKFAPVLGEIAS

QFAQDEAPSFNLAPFSLARFNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002898992.1\_2179 [gene=bssS] [locus\_tag=BN49\_RS12395] [protein=biofilm formation regulator BssS] [protein\_id=WP\_002898992.1] [location=complement(2254147..2254401)] [gbkey=CDS]

MEKNNEVIQTHPLVGWDISTVDSYDALMLRLHYQNPTQENSNDAEIGQTLWLTTDVARQFISILEAGIAK

IESGEYQENEYRRH

>lcl|NZ\_FO834906.1\_prot\_WP\_004140729.1\_2180 [gene=dinI] [locus\_tag=BN49\_RS12400] [protein=DNA damage-inducible protein I] [protein\_id=WP\_004140729.1] [location=complement(2254704..2254955)] [gbkey=CDS]

MRIEVSIAKTTALPNGALEALNNELSRRIAEQFPAIDSQVSVRYASGNQLSVFGALKEDKDRISEILQET

WESADDWFVHDLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176586.1\_2181 [gene=pyrC] [locus\_tag=BN49\_RS12405] [protein=dihydroorotase] [protein\_id=WP\_004176586.1] [location=complement(2255028..2256074)] [gbkey=CDS]

MTAQSQVLKIRRPDDWHIHLRDDDMLKTVVPYTSEFYGRAIVMPNLVPPVTTVAAAIAYRQRIMDAVPAG

HDFTPLMTCYLTDSLDPAELERGFNEGVFTAAKLYPANATTNSSHGVTSTDAIMPVLERMEKLGMPLLVH

GEVTHAEIDIFDREARFIETVMEPLRQRLPGLKVVFEHITTKDAAEYVRDGNELLAATITPQHLMFNRNH

MLVGGIRPHLYCLPVLKRNIHQQALRELVASGFSRAFLGTDSAPHARHRKEASCGCAGCFNAPTALGSYA

TVFEEMNALQHFEAFCSLNGPRFYGLPVNESYVELVREETTVVDSIALPNDTLVPFLAGETVRWTVKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004150824.1\_2182 [locus\_tag=BN49\_RS12410] [protein=lipoprotein] [protein\_id=WP\_004150824.1] [location=complement(2256200..2256760)] [gbkey=CDS]

MKKILIAAALIVSGLLSGCNQLTQYTVSEQEINQALQKRNHFAKDIGLKGVADAHIELQNLTSAIGREEP

GKVTLSGIANVDLNSLFGTQKATIDLKLKALPTFDREKGAIFLQEMEVVDAKVAPEKLQSVIQALLPYLN

QSLRSYFSQQPAYVLREDASTGEALAKKYAKGIEVKPGEIVIPFTN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530423.1\_2183 [gene=mdtH] [locus\_tag=BN49\_RS12415] [protein=multidrug efflux MFS transporter MdtH] [protein\_id=WP\_016530423.1] [location=complement(2256874..2258082)] [gbkey=CDS]

MSRVSQARSLGKYFPLVDNMLVVLGFFVVFPLISIRFVDQMGWAALMVGIALGLRQLVQQGLGIFGGAIA

DRFGAKPMIVTGMLMRAGGFAAMAVAHEPWVLWFSCILSGLGGTLFDPPRAALVVKLVRPHQRGRFFSIL

MMQDSAGAVIGAPLGSWLLQYDFRLVCSAGAALFIACAAFNAWYLPAWKLSTVKTPIREGLGRVLRDKRF

VTYVLTLTGYYMLAVQVMLMLPIMVNDIAGSPAAVKWMYAIEATISLTLLYPIARWSEKRFRLEHRLMAG

LLVMTLAMLPIGMTSSLQQLFTLICLFYIGSIIAEPARETLGASLADARARSSYMGFSRLGLAFGGALGY

AGGGWLFDAGKAVGQPELPWLMLGAIGVITFLALWWQFSPKRSASGMLEPRT

>lcl|NZ\_FO834906.1\_prot\_WP\_016530422.1\_2184 [gene=rimJ] [locus\_tag=BN49\_RS12420] [protein=ribosomal protein S5-alanine N-acetyltransferase] [protein\_id=WP\_016530422.1] [location=2258312..2258896] [gbkey=CDS]

MFGYRSNVPKVRLTTDRLVVRLVHDRDAWRLADYYAENKAFLKPWEPVRDDSHCYPSGWQARLSMIAEFH

KQGAAFYFALLDPEEKEIIGVANFSNVVRGSFHACYLGYSIGEKWQGQGLMFEALTSAIRYMQRTQHIHR

IMANYMPHNQRSGALLARLGFEKEGYAKDYLLIDGQWRDHVLTALTTPDWSAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179323.1\_2185 [locus\_tag=BN49\_RS12425] [protein=YceH family protein] [protein\_id=WP\_004179323.1] [location=2258906..2259559] [gbkey=CDS]

MKYQLTAHEARVIGCLLEKQVTTPEQYPLSVNAVVTACNQKTNREPVMSLSESEVQALLDTLVKRHYLRT

VSGFGNRVTKYEQRFCNSEFGDLKLSAGEVAVVTTLLLRGAQTPGELRSRAQRMYEFSDMAEVESVLEGL

TTREDGPFVARLPREPGKRESRYMHLFCDDMDTLITTVEALAPLDDDGDLRARVEALEGEVAELKARLDS

LLHHLGD

>lcl|NZ\_FO834906.1\_prot\_WP\_004140718.1\_2186 [locus\_tag=BN49\_RS12430] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_004140718.1] [location=2259575..2260486] [gbkey=CDS]

MRIGVVGLGSIAQKAWLPVLGAAESWTLQAAWSPGKEKALRICETWRMPYADSLDALAAQCDAVFVHTST

ASHYEVVNHLLNAGVHVCVDKPLADKLSEAETLVELAARRRLTLMVGFNRRFAPLYRELKGRLGEAASLR

MDKHRSDSVGNDLRFTLLDDYLHVVDTALWLADGQARLRGGALKITPQGEMLYAEHQFSSPRLQVTTSMH

RRAGSQREWVQAVTDGGLYAVSEMREWQEECGHGVVQRPVAGWQTTLEQRGFVGCARHFIECVQNQTVPE

TAGEQALLAQRIVEKLWRDAISE

>lcl|NZ\_FO834906.1\_prot\_WP\_002899104.1\_2187 [gene=murJ] [locus\_tag=BN49\_RS12435] [protein=murein biosynthesis integral membrane protein MurJ] [protein\_id=WP\_002899104.1] [location=2260598..2262133] [gbkey=CDS]

MNLLKSLAAVSSMTMFSRVLGFARDAIVARIFGAGMATDAFFVAFKLPNLLRRIFAEGAFSQAFVPILAE

YKSKQGEDATRVFVSYVSGLLTLALAIVTVIGMLAAPWVITITAPGFADTADKFALTTQLLRITFPYILL

ISLASLVGAILNTWNRFSVPAFAPTFLNVSMIGFALFAAPYFHPPVLALAWAVTVGGVLQLAYQLPHLKK

IGMLVLPRINLKDAGAMRVVKQMGPAILGVSVSQISLIINTIFASFLVSGSVSWMYYADRLMEFPSGVLG

VALGTILLPSLSKSFASGNHDEYCRLMDWGLRLCFLLALPSAVALGILAKPLTVALFQYGKFSAFDAAMT

QRALVAYSVGLMGLIVVKVLAPGFYSRQDIKTPVKIAIITLIMTQVMNLAFIGPLKHAGLSLSIGLAACL

NAALLYWQLRKQKIFTPQPGWLAFLLRLIIAVLVMAAALLGVMHLMPEWSLGTMPFRLMRLLAVVIAGVV

AYFATLLVLGFRVKEFVRRTA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043021.1\_2188 [locus\_tag=BN49\_RS12440] [protein=MFS transporter] [protein\_id=WP\_046043021.1] [location=complement(2262188..2263372)] [gbkey=CDS]

MTPTSLSTRDAGWIIFILALGAGFSVASIYYAQPLLPLMGANLHLTVEGMGLVPTLTQAGYALGILFLLP

LGDRHDRRRLILVKSALLALLLLLCSLTGQLSSLLVVSLLIGMAATMAQDIVPAGKQGKMVGTVMTGLLL

GILLSRTVSGVVGAVFGWRVMYQAAAVSVALIGLVMWRVLPRFAVHSTLSYPQLMASMAHLWQRYPALRR

AALAQGALSIAFSAFWSTLAVMLSEHYHMGSAVAGGFGIAGALAAPLAGGLADKFGAGKVTQMGAALVTL

SFALMFMLPLLPVHAQLALIALSAIGFDLGLQSSLVAHQNLVYGLEPRARGRLNALLFTVVFIGMSLGSV

LGSKLYVLAGWNGVVTLTVITGALALAIRLLENARILAAERSAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004218670.1\_2189 [locus\_tag=BN49\_RS12445] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004218670.1] [location=2263389..2264417] [gbkey=CDS]

MRWGYFSLNATGAVAGLVVKRLYVARIGKRKMKRQERIDRIELMRTYIRIVEAGSLSAAAGQMDTTQATV

SRRLQSLEGLLGVKLILRTTHAMKLTDDGERCYRHARQVVDAWLALEDDLRIADDRPVGVLRVRAPHAFG

QQQLLAPLVAFLQRHPQLSVEWMLNDNTVDFLSDNIDCAIRVGAEVDPATVSVLLAEVPRCVVASPELLA

KYPPLTSLEALSGLPWIAINTFYQHEVRLRHQASGQIVSTAITPCLSTDSLYVARNTALAGLGVAMVSSW

TVVEDIAAGRLIELFPQWRPASLPVHLVYPWARYYPTRLRKFLDLMREIMPDLAGMQRPQSA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043023.1\_2190 [gene=rne] [locus\_tag=BN49\_RS12450] [protein=ribonuclease E] [protein\_id=WP\_046043023.1] [location=complement(2264456..2267689)] [gbkey=CDS]

MKRMLINATQQEELRVALVDGQRLYDLDIESPGHEQKKANIYKGKITRIEPSLEAAFVDYGAERHGFLPL

KEIAREYFPANYNAHGRPNIKDVLREGQEVIVQIDKEERGNKGAALTTFISLAGSYLVLMPNNPRAGGIS

RRIEGDDRTELKEALASLELPDGMGLIVRTAGVGKSAEALQWDLSFRLKHWEAIQKAAESRPAPFLIHQE

SNVIVRAFRDYLRQDIGEILIDNPKVLELARQHIAALGRPDFSSKIKLYTGEIPLFSHYQIESQIESAFQ

REVRLPSGGSIVIDSTEALTAIDINSARATRGGDIEETAFNTNLEAADEIARQLRLRDLGGLIVIDFIDM

TPVRHQRAVENRLREAVRQDRARIQISHISRFGLLEMSRQRLSPSLGESSHHVCPRCSGTGTVRDNESLS

LSILRLIEEEALKENTKEVHAIVPVPIASYLLNEKRAAVSAIESRQGDVRVIIVPNDEMQTPHYSVLRVR

KGEETSTLSYLLPKLHEEEMALPGDDEPAERKRPEQPALAAFVMPDAPPAPMLEEPAAAPVAAAAPVAAA

APAQPGLLSRFFSALKNIFSGAEEAKPAEVQVEKKAEEKPERQQERRKPRANNRRDRNDRRDNRDNRDNR

DNRDNRDTRADNAEGREPRESREENRRNRREKPSQNVEARDVRQTSGDDAEKAKSRDEQQPRRERTRRRS

DDKRQAQQEAKAQTREEPVVQETEQEERVQTLPRRKPRQLAQKVRVESAVVEPVAEIVPEAVVAEVIAPH

SEPVKAELPAGVESVADQDENGESREANGMPRRSRRSPRHLRVSGQRRRRYRDERYPTQSPMPLTVACAS

PEMASGKVWIRYPVVRPQDQQPEEVQVQDASVAKTVEAVAAPVAVVETVTAAPVTVEPATMEPVTAEPVV

VEPVAAAEPLVVDAAEVVAPAAVEPAPQEPVTEAPAVEAPQAIAPVTLDAEPVVVEPEAVETTPVVAAPV

ETIAPAAETVEQAPVTEAAPAEPVKAEPPVSKPVVVAGHRHATAPMTRAPAPDYVPEAPRHSTWVRPPFA

FEGKGAAGGHSATHKATAEPTRPQPVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002899271.1\_2191 [gene=rluC] [locus\_tag=BN49\_RS12455] [protein=23S rRNA pseudouridine(955/2504/2580) synthase RluC] [protein\_id=WP\_002899271.1] [location=2268389..2269342] [gbkey=CDS]

MKTETPTVKMVAIAADEAGQRIDNFLRTQLKGVPKSMIYRILRKGEVRVNKKRVKPEYKLEAGDEVRIPP

VRVAEREEEAVSPHLQKVAALSEVILYEDDHILVLNKPSGTAVHGGSGLSFGVIEGLRALRPEARFLELV

HRLDRDTSGVLLVAKKRSALRSLHEQLRDKGMQKDYLALVRGQWQSHTKVVQAPLLKNILQSGERIVRVS

QEGKPSETRFKVEERYEFATLVRCSPVTGRTHQIRVHTQYAGHPIAFDDRYGDREFDKQLSATGLNRLFL

HAAALKFTHPGSGEVMRVEAPLDNQLKHCLQVLRKSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002899273.1\_2192 [locus\_tag=BN49\_RS12460] [protein=Maf-like protein] [protein\_id=WP\_002899273.1] [location=complement(2269380..2269964)] [gbkey=CDS]

MSDLILASTSPWRRMLLEKLGLPFECAAPDVDETPRPDESARQLVTRLAQAKAQSLATRFPNHLIIGSDQ

VCVLDGEITGKPHTEENARRQLRKASGSIITFYTGLALYNSASGHLQTECEPFDVHFRHLSDKEIEGYVR

KENPLQCAGSFKSEGLGITLFERLEGRDPNTLVGLPLIALCQMLRRENYNPLLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002899276.1\_2193 [gene=yceD] [locus\_tag=BN49\_RS12465] [protein=23S rRNA accumulation protein YceD] [protein\_id=WP\_002899276.1] [location=2270106..2270627] [gbkey=CDS]

MQKVKLPLTLDPVRTAQKRLDYEGIYARDQVERVTDSVVSVDSDVECSMSFAIDNQRLAVITGDAKVTVT

LECQRCGKPFSHHVHTTYCFSPVRNDEQAEALPEAYEPIEVNEFGEIDLQAMVEDEIILSLPVVPVHDSE

HCEVSDADMVFGELPEEAQKPNPFAVLASLKRK

>lcl|NZ\_FO834906.1\_prot\_WP\_000290724.1\_2194 [gene=rpmF] [locus\_tag=BN49\_RS12470] [protein=50S ribosomal protein L32] [protein\_id=WP\_000290724.1] [location=2270644..2270817] [gbkey=CDS]

MAVQQNKPTRSKRGMRRSHDALTAVTSLSVDKTSGEKHLRHHITADGFYRGRKVIAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004224085.1\_2195 [gene=plsX] [locus\_tag=BN49\_RS12475] [protein=phosphate acyltransferase PlsX] [protein\_id=WP\_004224085.1] [location=2271021..2272118] [gbkey=CDS]

MTRLTLALDVMGGDFGPSVTVPAALQALNSNSQLTLLLVGDPDAITPLLAKADFEQRSRLQIIPAQSVIA

SDARPAQAIRSSRGSSMRVALELVKEGRAQACVSAGNTGALMGLAKLLLKPIEGIERPALVTVLPHQQKG

KTVVLDLGANVDCDSTMLVQFAVMGAVLAEEVVGIANPRVALLNIGEEEMKGLGSIRDAAAVLKTLPSLN

YIGYLEANELLTGKTDVLVCDGFTGNVTLKTMEGVVRMFLSLLKSQGEGKKRSWWLLLLKRWLQKSLARR

FSHLNPDQYNGACLLGLRGSVIKSHGAANQRAFSVAIEQAVQAVQRQIPQRIAARLESLYPAGFELPESD

SDVNARQQSGTNGHD

>lcl|NZ\_FO834906.1\_prot\_WP\_002899288.1\_2196 [locus\_tag=BN49\_RS12480] [protein=ketoacyl-ACP synthase III] [protein\_id=WP\_002899288.1] [location=2272172..2273125] [gbkey=CDS]

MYTKIIGTGSYLPEQVRTNADLEKMVETSDEWIVTRTGIRERRIAAAHETVATMGFEAAKQALAMAGVSA

EQIGLIIVATTSGTHAFPSSACQIQSMLGVKGCPAFDVAAACAGFTYALSVADQYVKNGAVDYALVVGAD

VLARTCDPADRGTIIIFGDGAGAVVLGASEEPGIISTHLHADGSYGELLTLPNADRVDPENPIYLTMAGN

EVFKVAVTELAHIVDETLAANNLERSALDWLVPHQANLRIISATAKKLGMSMDNVVVTLDRHGNTSAASV

PCALDEAVRDGRIQRGQLILLEAFGGGFTWGSALVRF

>lcl|NZ\_FO834906.1\_prot\_WP\_009308402.1\_2197 [gene=fabD] [locus\_tag=BN49\_RS12485] [protein=ACP S-malonyltransferase] [protein\_id=WP\_009308402.1] [location=2273141..2274070] [gbkey=CDS]

MTQFAFVFPGQGSQAVGMLAEMAAAWPVIEETFGEASAALGYDLWALTQQGPAEELNKTWQTQPALLAAS

VALYRVWQQQGGKAPALLAGHSLGEYSALVCAGVIGFADAVRLVELRGKFMQEAVPEGTGAMSAIIGLDD

AAIAKACEESAEGQVVSPVNYNSPGQVVIAGHKEAVERAGAACKAAGAKRALPLPVSVPSHCALMKPAAE

KLAVELQKITFNAPTIPVVNNVDVKCETAPDAIRDALVRQLYSPVQWTKTVEFMATEGVSHLYEVGPGKV

LTGLTKRIVDTLTASALNEPAAMSAALEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002899294.1\_2198 [gene=fabG] [locus\_tag=BN49\_RS12490] [protein=3-oxoacyl-ACP reductase FabG] [protein\_id=WP\_002899294.1] [location=2274083..2274817] [gbkey=CDS]

MSFEGKIALVTGASRGIGRAIAETLVARGAKVIGTATSESGAQAISDYLGANGKGLMLNVTDPASIESVL

ENVRAEFGEVDILVNNAGITRDNLLMRMKDDEWNDIIETNLSSVFRLSKAVMRAMMKKRHGRIITIGSVV

GTMGNAGQANYAAAKAGLIGFSKSLAREVASRGITVNVVAPGFIETDMTRALTDEQRAGTLAAVPAGRLG

TPNEIASAVAFLASDEASYITGETLHVNGGMYMV

>lcl|NZ\_FO834906.1\_prot\_WP\_000103754.1\_2199 [gene=acpP] [locus\_tag=BN49\_RS12495] [protein=acyl carrier protein] [protein\_id=WP\_000103754.1] [location=2275028..2275264] [gbkey=CDS]

MSTIEERVKKIIGEQLGVKQEEVTNNASFVEDLGADSLDTVELVMALEEEFDTEIPDEEAEKITTVQAAI

DYINGHQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002900666.1\_2200 [gene=fabF] [locus\_tag=BN49\_RS12500] [protein=beta-ketoacyl-ACP synthase II] [protein\_id=WP\_002900666.1] [location=2275354..2276595] [gbkey=CDS]

MSKRRVVVTGLGMLSPVGNTVESTWKALLAGQSGISLIDHFDTSAYATKFAGLVKDFNCDDIISRKEQRK

MDAFIQYGIVAGVQAMQDSGLEVTEENATRIGAAIGSGIGGLGLIEENHSSLVNGGPRKISPFFVPSTIV

NMVAGHLTIMFGLRGPSISIATACTSGVHNIGQAARIIAYGDADAMVAGGAEKASTPLGVGGFGAARALS

TRNDNPQAASRPWDKDRDGFVLGDGAGMVVLEEYEHAKKRGAKIYAEIVGFGMSSDAYHMTSPPEDGAGA

ALAMVNAIRDAGIEPGQIGYVNAHGTSTPAGDKAEAQAVKSVFGDAASRVLVSSTKSMTGHLLGAAGAVE

SIYSILALRDQAVPPTINLDNPDEGCDLDFVPHEARQVSGMEYTLCNSFGFGGTNGSLIFKKV

>lcl|NZ\_FO834906.1\_prot\_WP\_002900669.1\_2201 [gene=pabC] [locus\_tag=BN49\_RS12505] [protein=aminodeoxychorismate lyase] [protein\_id=WP\_002900669.1] [location=2276721..2277530] [gbkey=CDS]

MFLINGVVQDTLAANDRATQFGDGCFTTARIQQGQVALLDAHLQRLQTTCEKLHIPFNDWLTLSEEMQRL

ARPHAQGVLKVTLTRGVGGRGYSTAGCVSPTRILSFSPFPAHYARWREEGITLTQSPVPLGRNSWLAGLK

HLNRLEQVLIRSHLEQTDADEALVLDSDGWLTECCAANLFWRQGRDVFTPRLDYAGVNGIMRQRCIAQLA

PSTFRVVEVTARPETLREADEVLICNALMPLVPVRRWEETTWSSRELYHFLAPLCELSG

>lcl|NZ\_FO834906.1\_prot\_WP\_020864845.1\_2202 [gene=yceG] [locus\_tag=BN49\_RS12510] [protein=cell division protein YceG] [protein\_id=WP\_020864845.1] [location=2277532..2278554] [gbkey=CDS]

MKKMLRFILLLVVLLGIAAAAGMWKVRQLADSKLLIKEETIFTLEAGTGRLALGQDLYREKVINRPRVFQ

WLLRVEPELSHFKAGTYRFTPQMTVREMLQLLASGKEAQFPLRFVEGMRVSDYLRQLRDAPYVKHTLGDD

SYATVAKALGLEHADWVEGWFWPDTWMYTANTSDIAILKRAHQKMVAEVAKVWEGRMENLPYADQNQLLT

MASIIEKETAVAEERDRVASVFINRLRIGMRLQTDPTVIYGMGAGYTGKLTRKDLETPTAYNTYTISGLP

PGPIAVPGEASLKAAAHPAKTPYLYFVADGKGGHTFTTNLVSHNRAVQDYLKVLKEKNAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002900674.1\_2203 [gene=tmk] [locus\_tag=BN49\_RS12515] [protein=dTMP kinase] [protein\_id=WP\_002900674.1] [location=2278544..2279185] [gbkey=CDS]

MRSNYIVIEGLEGAGKTTARQLVVETLQSAGIHDMVFTREPGGTILAEKLRSLVLDIQSTGDEVINDKAE

VLMFYAARVQLVETVIKPALARGQWVIGDRHDLSTQAYQGGGRGIDRTMLATLRDAVLGDFRPNLTLYLD

VTPEVGLQRARARGELDRIEQESMNFFNRTRARYLELAAADPSIRTVDATQPLDAVARDIRATIAQWMAE

QAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004147932.1\_2204 [gene=holB] [locus\_tag=BN49\_RS12520] [protein=DNA polymerase III subunit delta'] [protein\_id=WP\_004147932.1] [location=2279182..2280186] [gbkey=CDS]

MKWYPWLRPSFEQLVGSYQAGRGHHALLLQSLNGMGGEALIYALCRFLMCRQPEGHKSCGHCHSCQLMQA

GTHPDYYALSPEKGKSALGIDAVRDVNEKLYEHARLGGAKVVWISDAALLTDAAANALLKTLEEPPENTW

FFLACEEPARLLTTLRSRCRLHHLAPPSEPYALAWLEREVSLPQESLLTALRLCASAPAAALELLQEPLW

TARQQLCQALAATLASGDWLALLPILNHEQAAVRLHWLASLLVDAQKRQQGITLVSNPDVWPLLEQLAHS

LPAARLQAIAHDVCTCREQLLNVVGVNRELLLTERLLRWEHYLQPGTVLPVSHL

>lcl|NZ\_FO834906.1\_prot\_WP\_004140680.1\_2205 [locus\_tag=BN49\_RS12525] [protein=metal-dependent hydrolase] [protein\_id=WP\_004140680.1] [location=2280197..2280991] [gbkey=CDS]

MFLVDSHCHLDGLDYQTLHKNVDDVLAKAAARDVKFCLAVATTLPGYRSMRELVGTRDNVVFSCGVHPLN

QDEPWEVETLRALAAEEGVVAMGETGLDYFYTPETKAQQQSSFRDHIRIGRELNKPVIVHTRDARADTLA

ILREEKVTDCGGVLHCFTEDRETAGKLLDMGFYISFSGIVTFRNAEQLRDAARYVPLDRLLVETDSPYLA

PVPHRGKENQPALVRDVAEYMAVLKGVSLEQLAQQTTDNFATLFHIDPARLQPA

>lcl|NZ\_FO834906.1\_prot\_WP\_002900680.1\_2206 [gene=ptsG] [locus\_tag=BN49\_RS12530] [protein=PTS glucose transporter subunit IIBC] [protein\_id=WP\_002900680.1] [location=2281288..2282721] [gbkey=CDS]

MFKNAFANLQKVGKSLMLPVSVLPIAGILLGVGSANFSWLPAVVSHVMAEAGGSVFANMPLIFAIGVALG

FTNNDGVSALAAVVAYGIMVKTMAVVAPLVLHLPADEIAAKHLADTGVLGGIISGAIAAYMFNRFYRIKL

PEYLGFFAGKRFVPIISGLAAIFTGVILSFIWPPIGSAIQTFSQWAAYQNPVVAFGIYGFIERCLVPFGL

HHIWNVPFQMQIGEYTNAAGQVFHGDIPRYMAGDPTAGKLSGGFLFKMYGLPAAAIAIWHSAKPENRAKV

GGIMISAALTSFLTGITEPIEFSFMFVAPILYVIHAILAGLAFPICILLGMRDGTSFSHGLIDFIVLSGN

SSKLWLFPIVGICYAIVYYVIFRVLIKALDLKTPGREDTTEESKAGATSEMAPALVAAFGGKENITNLDA

CITRLRVSVADVAKVDQAGLKKLGAAGVVVAGSGVQAIFGTKSDNLKTEMDEYIRNS

>lcl|NZ\_FO834906.1\_prot\_WP\_002900681.1\_2207 [gene=hinT] [locus\_tag=BN49\_RS12535] [protein=purine nucleoside phosphoramidase] [protein\_id=WP\_002900681.1] [location=2282983..2283339] [gbkey=CDS]

MAEETIFSKIIRREIPSDIVYQDELVTAFRDISPQAPTHILIVPNVLIPTVNDVTAEHELALGRMMTVAA

KIARDEGLADDGYRLIVNCNRHGGQEVYHIHMHLLGGRPLGPMLAHKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002900683.1\_2208 [locus\_tag=BN49\_RS12540] [protein=YcfL family protein] [protein\_id=WP\_002900683.1] [location=2283344..2283718] [gbkey=CDS]

MLRTLLGACLAAGLLAGCSSHPEIPVSDQQALVMESSVLAAGISASEPAVVATEIQATASSTLYNERQQP

VTVHYRFFWYDARGLEMHPLDAPRTIVVPARSSVTLYGSANILGAHKARLYLYL

>lcl|NZ\_FO834906.1\_prot\_WP\_074424848.1\_2209 [gene=lpoB] [locus\_tag=BN49\_RS12545] [protein=penicillin-binding protein activator LpoB] [protein\_id=WP\_074424848.1] [location=2283740..2284360] [gbkey=CDS]

MCRYALITALAIFLAGCAGLREQPAPVEEAKPQPQPTVPTVPAVPSVPAQPGPIEHQDQQSGQPAPRVRH

YDWNGAVQPLVGQMLQASGVNAGSILLVDSVNNRTNGSLNAGEATTALRSALAGNGKFTLVSAQQLAVAK

QQLGLSPQDSLGSRSKAMGIARNVGAQYVLYSNATGNVNAPELKMQLMLVQTGEIIWSGKGAVQQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043029.1\_2210 [gene=thiK] [locus\_tag=BN49\_RS12550] [protein=thiamine kinase] [protein\_id=WP\_046043029.1] [location=2284341..2285168] [gbkey=CDS]

MLFSNNKLTRDELLSRFFPHYHPVASLSQSGLSGGSVIISDGDRRHVLRQPHDPSAGTYYFRRQYHALRR

LPARLAPTPLFYSPCWMVVEYCTGEVKSELPASPQLSGLLYDLHQQPRFGWRVSLTPLLAQYWQRCDPAR

RKPRWLRWHQRLRRQGEPRPLRLAPLHMDVHAGNIIHNESGLRLIDWEYAGDGDIALELAAVWITPGERR

RLVEAYARRAAIDAQLLWRQVVLWRPWVLLLMAGWYEMRWRQSGDRQFITLADETWCQLDNERKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004147935.1\_2211 [gene=nagZ] [locus\_tag=BN49\_RS12555] [protein=beta-N-acetylhexosaminidase] [protein\_id=WP\_004147935.1] [location=2285192..2286202] [gbkey=CDS]

MLDVEGYELDAEEREILAHPLVGGLILFTRNYHDPAQLRELVRQIRDASRNHLVVAVDQEGGRVQRFREG

FTRLPAAQSFAALLGMEEGGKLAAEAGWLMASEMIAMDIDISFAPVLDVGHISAAIGERSYHEDPQKALT

MARHFIDGMHAAGMKTTGKHFPGHGAVTADSHKETPFDPRAASVIRDHDMAVFKSLIAEQRLDAIMPAHV

IYPELDPRPASGSAYWLKTVLRGELGFDGVIFSDDLSMEGAAIMGSYAERGQASLDAGCDMILVCNNRKG

AVSVLDNLSPIKAERVTKLYHKGSFSRQELRDSARWKTVSAQLEQLHARWQEAKSA

>lcl|NZ\_FO834906.1\_prot\_WP\_002900775.1\_2212 [gene=ycfP] [locus\_tag=BN49\_RS12560] [protein=alpha/beta hydrolase YcfP] [protein\_id=WP\_002900775.1] [location=2286238..2286780] [gbkey=CDS]

MIIYLHGFDSNSPGNHEKVMQLQFIDPDVRLISYSTRHPKHDMQHLLKEVDKMLQLTADDRPLICGVGLG

GYWAERIGFLCDIRQAVFNPNLFPHENMEGKIDRPEEYADIATKCVTNFREKNRDRCLVVLSRQDEALDS

QRSADLLHHYYEIIWDEEQTHKFKNISPHLQRLKAFKTLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002900778.1\_2213 [locus\_tag=BN49\_RS12565] [protein=NAD(P)/FAD-dependent oxidoreductase] [protein\_id=WP\_002900778.1] [location=2287026..2288330] [gbkey=CDS]

MTTPLKKIVIVGGGAGGLELATQLGRKLGRHKKAKITLVDRNHSHLWKPLLHEVATGSLDEGVDALSYLA

HARNHGFQFQLGSVVDINREGKTITLGELRNEKGELLVAERKLPYDTLVMALGSTSNDFNTPGVKENCIF

LDNPHQARRFHQEMLNLFLKYSANLGANGKVNIAIVGGGATGVELSAELHNAVKQLHSYGYKGLTNEALN

VTLVEAGERILPALPPRISGAAHNELTKLGVRVLTQTMVTSADAGGLHTKDGEYIEADLMVWAAGIKAPD

FMKEIGGLETNRINQLVVEPTLQTTRDADIFAIGDCASCARPEGGFVPPRAQAAHQMATCALNNILAQMK

GKPLKAYTYKDHGSLVSLSNYSTVGSLMGNLMRGSMMVEGRIARFVYISLYRMHQIALHGYFKTGLMMLV

GRINRIIRPRLKLH

>lcl|NZ\_FO834906.1\_prot\_WP\_002900781.1\_2214 [locus\_tag=BN49\_RS12570] [protein=glycine zipper 2TM domain-containing protein] [protein\_id=WP\_002900781.1] [location=2288525..2289064] [gbkey=CDS]

MNKSMLAGIGIGVAAALGVAAVAGLNVLDRGPQYAQVVSSTPIKETVKTPRQECRNVTVTHRRPVQDENR

IAGSVLGAVAGGVIGHQFGGGHGRSVATVVGALGGGYAGNQIQGAMQDNDTYTTTQQRCKTVYDKSDKML

GYDVTYKIGDQQGKIRMDHDPGSQIPLDNNGQLVLNNKI

>lcl|NZ\_FO834906.1\_prot\_WP\_016531286.1\_2215 [locus\_tag=BN49\_RS12575] [protein=TonB-dependent siderophore receptor] [protein\_id=WP\_016531286.1] [location=complement(2289122..2291311)] [gbkey=CDS]

MKKRLWVLHPLLLASTLPALAAQSDEDSIIVSANRTHRTVAEMAQTTWVIEGQEIEQQVQGGKEFKDVLA

QLIPGIDVSSQGRTNYGMNMRGRAIVVLIDGVRLNSSRTDSRQLDAIDPFNIEHIEVISGATSLYGGGST

GGLINIVTKKGQQDRQVDLEVGSKSGFANSNDHDERVAAAVSGGTDHASGRLSVAYQRFGGWYDGNDDAL

ILDNTQTGLQHSDRLDVMGTGTIEIDDNRQLQLVTQYYKSQGDDDYGLWLGKNMSAVTSGGKAYTTDGLN

SDRIPGTERHLISLQYSDADFFGQNLVSQVYYRDESLTFYPFPTLTKGQVSSFSSSQQDTDQYGAKLTLN

SQPLAGWDLTWGLDADHETFNANQMFFDLPQSMASGGLHNESIYTTGRYPGYSISNVAPFLQSSYDLNDI

FTVSGGVRYQWTENRVDDFVGYAQQQDIANGKARSADAIKGGKTDYDNFLFNAGIVAHLTERQQTWFNFS

QGVELPDPGKYYGIGKYGAAVNGHLPLISSVNVDDSPLQGIKVNSYELGWRYTGDNLRTQLAAYYSTSDK

TIVVNRTDMTIDVQSDKRRIYGVEGAVDYFIPDSDWSVGGNFNVLKSQVQTDGRWQKWDVTLASPSKATA

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LYSPTYGSSSLYEYKGRGRTFGLNYALTF

>lcl|NZ\_FO834906.1\_prot\_WP\_004140642.1\_2216 [locus\_tag=BN49\_RS30985] [protein=hypothetical protein] [protein\_id=WP\_004140642.1] [location=2291380..2291502] [gbkey=CDS]

MRNIWKNSKKDFAHNEYRNQYHLRLSCARKGNKNQSILWG

>lcl|NZ\_FO834906.1\_prot\_WP\_004140640.1\_2217 [locus\_tag=BN49\_RS12585] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_004140640.1] [location=complement(2291555..2292190)] [gbkey=CDS]

MTTDVQSCAKKSRGRPKVFDRDAALDKAMTLFWQHGYEATSLADLVEATGAKAPTLYAEFVNKEGLFRAV

LDRYISRFAAKHEAVLFAEGKSVDRALRDYFTAVATCFTSKETPAGCFIINTSAALAASSTDIANTIKSR

HAMQEQALTQFLQQRQAQGELPAGRDVAQLAQFLNCVLQGMSISAREGADFDKLMQITDTTLRLWPQVLE

S

>lcl|NZ\_FO834906.1\_prot\_WP\_004147941.1\_2218 [locus\_tag=BN49\_RS30990] [protein=hypothetical protein] [protein\_id=WP\_004147941.1] [location=complement(2292187..2292342)] [gbkey=CDS]

MHFYNDRLTIYKMLKFHTYMNYLFLNRQRWPRRSFIFIMAFHQTNIGTTAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002900788.1\_2219 [gene=bhsA] [locus\_tag=BN49\_RS12595] [protein=multiple stress resistance protein BhsA] [protein\_id=WP\_002900788.1] [location=2292440..2292697] [gbkey=CDS]

MKTVNTLAIAAVLSSLSFASFAAVEVQSTPAGQHKVGTISASAGTNLGSLEDQLAQKADEMGATSYRITS

VTGPNTLHGTAVIYK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531285.1\_2220 [locus\_tag=BN49\_RS12600] [protein=L,D-transpeptidase family protein] [protein\_id=WP\_016531285.1] [location=complement(2292826..2293791)] [gbkey=CDS]

MVMRNRFPVTLWLTLVALVAALALPARANTWPLPPPGSRLVGQNQFHVVQDDGGSLEAIAKKYNVGFLAL

LQANPGVDPYVPRAGSVLTIPLQTLLPDAPREGLVINLAELRLYYYPPGKNEVTVYPIGIGQLGGTTITP

TMVTTVSDKRANPTWTPTTNIRARYKAMGIELPAVVPAGPDNPMGHHAIRLAAYGGVYLLHGTNADFGIG

MRGSSGCIRLRDNDIKALYNTISPGTKVNIINTPIKASVEPDGRRLVEVHQPLSEHIDDDPQTLPITLNA

AMTAFKQAPQTDGTVMERAMNYRSGMPIDVTRHADPGPQSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004183645.1\_2221 [gene=mfd] [locus\_tag=BN49\_RS12605] [protein=transcription-repair coupling factor] [protein\_id=WP\_004183645.1] [location=complement(2293949..2297395)] [gbkey=CDS]

MPEQYRYSLPVKAGDQRQLGELTGAACATLVAEMAERHSGPVVLVAPDMQNALRLNDEIRQFTDSMVMGL

ADWETLPYDSFSPHQDIISSRLATLYQLPTMQRGVLIVPVSTLMQRVCPHSFLHGHALVMKKGQRLSRDA

LRDQLEGAGYRHVDQVMEHGEYATRGALLDLFPMGSDQPYRLDFFDDEIDSLRLFDVDSQRTLEEVAAIN

LLPAHEFPTDQTAIELFRSQWRDRFEVKRDAEHIYQQVSKGTLPAGIEYWQPLFFSEPLPPLFSYFPAST

LIVNTGDLEASAERFQNEARARFENRGVDPMRPLLPPELLWLRSDELFSELKKWPRVQLKTERLADKAAN

TNLGYQTLPDLAVQAQNKAPLDNLRRFLESFTGPVIFSVESEGRREALSEMLARIKVAPKHVLRLEEATG

NGRYLMIGAAEHGFIDSQRGLALICESDLLGERVARRRQDSRRTINPDTLIRNLAELHIGQPVVHLEHGV

GRYAGMTTLEAGGITGEYLMLTYANDAKLYVPVSSLHLISRYAGGAEENAPLHKLGGDAWTRARQKAAEK

VRDVAAELLDIYAQRAAKAGFAFKHDREQYQLFCDGFPFETTPDQAQAINAVLSDMCQPLAMDRLVCGDV

GFGKTEVAMRAAFLAVENHKQVAVLVPTTLLAQQHYDNFRDRFANWPVRIEMLSRFRSAKEQAQILEQAA

EGKIDILIGTHKLLQSEVKLRDLGLLIVDEEHRFGVRHKERIKAMRADVDILTLTATPIPRTLNMAMSGM

RDLSIIATPPARRLAVKTFVREYDALVVREAILRETLRGGQVYYLFNDVENIQKAADKLAELVPEARIAI

GHGQMRERELERVMNDFHHQRFNVLVCTTIIETGIDIPTANTIIIERADHFGLAQLHQLRGRVGRSHHQA

YAWLLTPHPKAMTTDAQKRLEAIASLEDLGAGFALATHDLEIRGAGELLGEDQSGQMETIGFSLYMELLE

NAVDALKAGREPSLEDLTSQQTEVELRMPSLLPDDFIPDVNTRLSFYKRIASAKNEQDLEEIKVELIDRF

GRLPDAARNLLDIARLRQQAQKLGIRKLESNEKGGVIEFNEKNNVNPVWLIGLLQKQPQHFRLDGPTRLK

FMQDLEERKTRMDWVRQFMRQLEENAVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004140630.1\_2222 [locus\_tag=BN49\_RS30995] [protein=hypothetical protein] [protein\_id=WP\_004140630.1] [location=2297435..2297566] [gbkey=CDS]

MEGNSLIFNSEIIRDWSGFANPNCHRVLGEERSALSISVKINK

>lcl|NZ\_FO834906.1\_prot\_WP\_002900795.1\_2223 [gene=lolC] [locus\_tag=BN49\_RS12615] [protein=lipoprotein-releasing ABC transporter permease subunit LolC] [protein\_id=WP\_002900795.1] [location=2297700..2298899] [gbkey=CDS]

MYQPAALFIGLRYMRGRAADRFGRFVSWLSTIGITLGVMALVTVLSVMNGFERELQNNILGLMPQAILSA

KQGSVNPQQLPEREAKLNGVTRVAPITTGDVVLQSARSVAVGVMLGIDPAQNDPLTPYLVNVKQSDLQAG

KYNVILGEQLAGQLGVNRGDKIRVMVPSASQFTPMGRVPSQRLFTVIGTFAANSEVDGYQMLTNIDDASR

LMRYPLGNITGWRLWLDQPLQVDTLSQQTLPPGTQWQDWRERKGELFQAVRMEKNMMGLLLSLIVAVAAF

NIITSLGMMVMEKQGEVAILQTQGLTPRQIMAVFMVQGASAGIVGALLGAVLGALLASQLNNLMPIIGAF

LDGAALPVAIEPLQVIVIALVAMVLALLSTLYPSWRAAATQPAEALRYE

>lcl|NZ\_FO834906.1\_prot\_WP\_002900798.1\_2224 [gene=lolD] [locus\_tag=BN49\_RS12620] [protein=lipoprotein-releasing ABC transporter ATP-binding protein LolD] [protein\_id=WP\_002900798.1] [location=2298892..2299593] [gbkey=CDS]

MNKILLQCDNLCKRYQEGNVQTDVLHNVSFSIGEGEMMAIVGTSGSGKSTLLHLLGGLDTPTSGDVIFSG

QPMSKLSTAARADLRNRELGFIYQFHHLLPDFSALENVAMPLLIGKKKPADIERQAKAMLQAVGLEHRSH

HRPSELSGGERQRVAIARALVNKPRLVLADEPTGNLDARNADSIFQLLGELNVAQRTAFLVVTHDLQLAK

RMSRQLEMRDGRLTADLTLMGAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004176565.1\_2225 [gene=lolE] [locus\_tag=BN49\_RS12625] [protein=lipoprotein-releasing ABC transporter permease subunit LolE] [protein\_id=WP\_004176565.1] [location=2299593..2300837] [gbkey=CDS]

MASPLSLLIALRFSRGRRRGGMVSLISVISTIGIALGVAVLIVGLSAMNGFERELNNRVLAVVPHGEIEP

VNQPWNNWQEALAKVQKVKGIVAAAPYINFTGLVESGSNMRAIQVKGVDPQQESQLSALPTFVQNNAWAG

FKAGEQQVILGKGVADALHVKQGDWVSIMIPNADADHQLLQPKRVRLHVTGILQLSGQLDHSFAMIPMQD

AQQYLEMGGSVTGIAIKVTDVFHANKLVRDAGEVTNSYVYIKSWIGTYGYMYRDIQMIRAIMYLAMVLVI

GVACFNIVSTLVMAVKDKSGDIAVLRTLGAKDGLIRAIFVWYGLLAGSVGSLFGVVIGVICALNLTSIIN

GIEYLIGHKFLSGDIYFIDFLPSELHWLDVFYVLVTALLLSLLASWYPARRASRIDPARVLSGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_015958185.1\_2226 [gene=nagK] [locus\_tag=BN49\_RS12630] [protein=N-acetylglucosamine kinase] [protein\_id=WP\_015958185.1] [location=2300886..2301797] [gbkey=CDS]

MYYGFDIGGSKIALGVFNQERRLQWEKRVATPKSSYEDFLQAVEALVREADERFDQQGSVGIGIPGMPET

ADGTLYAANVPAASGRPLRADLSARLGREVRLDNDANCFALSEAWDDEFTQYPLVMGLILGTGVGGGLVL

NGKSITGHSYITGEFGHIRLPVDALEVVGRDFPLLRCGCGQLGCIENYLSGRGFAWLYEHFYQQPLSSPE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004176563.1\_2227 [gene=cobB] [locus\_tag=BN49\_RS12635] [protein=NAD-dependent protein deacylase] [protein\_id=WP\_004176563.1] [location=2301812..2302642] [gbkey=CDS]

MQSRRLHRLSRFRRNKRRLRDRLRQRIFFREDRMKPEAMAKPRVVVLTGAGISAESGIKTFRAADGLWEE

HRVEDVATPEGFARDPALVQAFYNARRRQLQSPEIAPNAAHLALARLEDLLGDHFLLVTQNIDNLHERAG

NRRVIHMHGELLKVRCSWSGQVLEWTGDVTAEDKCHCCQFPAALRPHVVWFGEMPLGMDEIYSALADADI

FIAIGTSGHVYPAAGFVHEARLHGAHTVELNLEPSQVGSEFAEKHYGLASEVVPAFIDKLLQENAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004190955.1\_2228 [locus\_tag=BN49\_RS12640] [protein=hypothetical protein] [protein\_id=WP\_004190955.1] [location=2302733..2303077] [gbkey=CDS]

MHNPLVIEAIMLIAAIIVGVWSQRALPLHADSRPILFLLCLFLGTGSALCLLLDILALLFTGQVATGGVR

IYGPLLLLVVLWKPLNWVVGIIEDFVQRRAEKGKGKGQHDGGQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004140612.1\_2229 [locus\_tag=BN49\_RS12645] [protein=sugar-binding transcriptional regulator] [protein\_id=WP\_004140612.1] [location=complement(2303102..2304064)] [gbkey=CDS]

MIEQDSDYALLTEIAVAYYDQEQTQEEIAKRFGISRIKVGRLLKKARQEGIVEISVKYHPVFSSQIEQQF

ISHFGIKRALIALDHHDEDEQRQQVAALVSNYLAGVLKNDMTVTVGQGRNVAAVANHVGVFPERHCRFIC

GIGGTKRDNQLIDADHISRNLARKFNGFSETLYAPAYVETPELRAAFMQNRLIKATLEQASKADVAIIGL

GDMNENSFMVQLGWFTPQEIATARQEQGVVGDLAGYSFFNIQGKPVDTVMNDRVIGLSLEQLRAIPCVIA

IASESTKATAILGALRTGVIDVLATSASNARSVINMQKAL

>lcl|NZ\_FO834906.1\_prot\_WP\_025368275.1\_2230 [locus\_tag=BN49\_RS12650] [protein=triose-phosphate isomerase] [protein\_id=WP\_025368275.1] [location=complement(2304100..2304894)] [gbkey=CDS]

MTPIWLGTSWKMNKPLSQAMAWCETLAARMPEGCHPAIQPFVIPPFTAIQPVSHFLQTHQLPLLTGAQNM

HEADQGAWTGEISAAMLAETGATLVELGHSERRAAFNESDAAINRKVHSALGHGLRPLICIGDSAEEKRW

QVSRESVVRQMKIALYGLSHQQALRTLIAYEPVWAIGEHGTPASPQEAGVIHQALRQALCELFGHETGTR

IPLLYGGSVTLQNAVELLRQQEINGLFIGRAAWDAQGYCDIVQRVTQEFILQAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004179336.1\_2231 [gene=pdxA] [locus\_tag=BN49\_RS12655] [protein=4-hydroxythreonine-4-phosphate dehydrogenase PdxA] [protein\_id=WP\_004179336.1] [location=2305137..2306144] [gbkey=CDS]

MSAEKKPVVAITIGDPAGIGPEITVATMMDKSVYDECKPFLIGSVPIISRAMKIMGCDFAIHKIAHPQEA

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GHTEIYQVETQSDYGLTMFHVHNLRVFFVSRHMALKAACDYANKARVLACVQQIHHEFTALNIKNPRIAV

AALNPHGSDNGLFGHEEADNLIPAVKAAQEMGINAIGPVPADSVFHLGKQGRYDAILSLYHDQGHIACKT

LDFERSITITFGLPFMRSSVDHGTAFDIAGTGKAGTVSMLESTLVAARYWKMKHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530227.1\_2232 [locus\_tag=BN49\_RS12660] [protein=four-carbon acid sugar kinase family protein] [protein\_id=WP\_016530227.1] [location=2306180..2307898] [gbkey=CDS]

MEKHLLISKGCKGWGGPLTITPGQGKKIAYITGGIRPPVVDRLSELTGWPSIDVFKNGEPPAEEIGLMVI

DCGGTLRCGLYPKRGIPTINLHPTGKSGPLAEFIHEGIYVSGVTPACIEMVWPQGEGGKLGIVADDLTGA

TTVGVLLARSGLKTAAFFDTESFARNEVEYPAMVVSSDSRLLPKAEAQHKVSAAVKQLQARGAHYFTKRI

DTTLRGGIGFEIDAMLEQLPQETVAVVVPAMPQSRRILVGGYSVIDSVALSRTDVARDVRTPVTESWVPG

LLAAQTHHQVGHIALTSVMKGEGQIQQDLQEQQQRGVRVIVVDAITVDDVDAIAGAVVALNWNVLAVDPG

PFTERLAVRRGLMREARSSAPASLTADGQRGSILIVAGSATPVTKKQLQYLIANDARVCHIPVDAELLVD

RKNAAEIEVNRVVQHARQCVPAQHNALFVFESALTGRLLNLQEEEQRFGLAHGEAAQNINHGLGSIVREV

LNCASGEIKGLYMTGGDTMVNVLKELGATGIEMIDYVIPQTDMVRIIGGDYAGLICVGKGGLTGPEDIIS

IIVDRIYQEAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004140602.1\_2233 [locus\_tag=BN49\_RS12665] [protein=2-keto-3-deoxygluconate permease] [protein\_id=WP\_004140602.1] [location=2307991..2309010] [gbkey=CDS]

MNINILEKMNKVPGGLIIIPLLVAILINTFAPQVLSIGGPTTALFKVGSSAMMGIFLLICGTSINIRQAG

LPLYKGAVLLFLKCLAGALAVWVAGTLFGPSGFLGISTLALIACLTSSNSSLYIALCSNYGDASDAGAIS

VFCIKDGPFVTMMVLGVSGLANIPFAALLSMLIPLLIGMLWGNLDERFKQLCAAAQPLVIIIMSFAIGAN

SSINTVFTAGLSGILLGIISALTGIVFYFIYNLFLKKKSALGAALGTTAASSALTPAMVAQADPSLAMYV

DAATAQLATASIITMITAPILVAWFDKRLKKRAPAAEPLKEVKSEESVTLSSPAAKGHK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140600.1\_2234 [locus\_tag=BN49\_RS12670] [protein=PTS glucitol/sorbitol transporter subunit IIA] [protein\_id=WP\_004140600.1] [location=2309012..2309386] [gbkey=CDS]

MSVPLYSLRITAVGEYVEYSLRELRLILFSDAVPDDIASYCAVHQASELTAELSPGQQMKLNDKNYRVTA

VGRVATANLRQLGHITLNFDGADIAELPGTVHLYGEPPQIIQPGDQISFYPNCH

>lcl|NZ\_FO834906.1\_prot\_WP\_004179338.1\_2235 [gene=rpiB] [locus\_tag=BN49\_RS12675] [protein=ribose 5-phosphate isomerase B] [protein\_id=WP\_004179338.1] [location=2309415..2309873] [gbkey=CDS]

MKTIAIGADDAAYAFRDSIVAYLNGLGINVADYSSDKRQGSTVYPDVAHAVAMSIKQGEHERGILICGTG

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RIDYYEHQHARD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043034.1\_2236 [gene=tal] [locus\_tag=BN49\_RS12680] [protein=transaldolase] [protein\_id=WP\_046043034.1] [location=2309904..2310854] [gbkey=CDS]

MSQLDELKKYTTVVADTGDIESIKKFAPQDATTNPSLVLKAAQLPQYQPLIADAIGKARRQGGSAETQLI

NACDQVAVDIGSEVLRHVPGRISTEVDARFAWDRGMCVAKARKLIQLYEKNGIGPERILIKLAATWEGIR

AAEELEQSGINCNLTLLFSFVQARACAEAGVFLISPFVGRIYDWYQKHQPQSAYQVDSDPGVVSVRQIYQ

YYKSHGYDTVVMGASFRRIEQIQALAGCDRLTISPALLDELAASEGVLTRQLTPGSVTETRPSPMTQAEF

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>lcl|NZ\_FO834906.1\_prot\_WP\_023279547.1\_2237 [gene=tkt] [locus\_tag=BN49\_RS12685] [protein=transketolase] [protein\_id=WP\_023279547.1] [location=2310874..2312877] [gbkey=CDS]

MKTTKTIRCQCANALRALSMDAVQKAKSGHPGAPMGMADIAEVLWRDFLNHNPNNPAWADRDRFVLSNGH

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FNRPGHDIVDHYTYAFMGDGCMMEGISHEVCSLAGTLKLGKLVAFYDDNGISIDGHVEGWFTDDTAKRFE

AYGWHVVRGVDGHDADAIKRAVEEARAVTDKPSLLMCKTIIGFGSPNKAGTHDSHGAPLGDAEIALTREA

LGWKHAPFDIPSDIYAQWDAKEAGQAKEAAWNEKFAAYAKAFPQEAAEFTRRMKGEMPSDFDAKANEFIA

KLQANPAKIASRKASQNAIEAFGPLLPEFLGGSADLAPSNLTLWSGSKPINEDAAGNYIHYGVREFGMTA

IANGIALHGGFLPYTSTFLMFVEYARNAVRMAALMKQRQVMVYTHDSIGLGEDGPTHQPVEQVASLRVTP

NMSTWRPCDQVESAIAWKYGVERQDGPTALILSRQNLAQQERTAEQLANVARGGYVLKDCAGQPELIFIA

TGSEVELAVAAWDKLTAEGVKARVVSMPSTDAFDKQDAAYRESVLPKAVTARVAVEAGIADYWFKYVGLN

GAIVGMTTFGESAPAEQLFEEYGFTVDNVVAKAKALL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043036.1\_2238 [locus\_tag=BN49\_RS12690] [protein=long-chain fatty acid--CoA ligase] [protein\_id=WP\_046043036.1] [location=2313115..2314755] [gbkey=CDS]

MPSPMIYQDLTTAALLGHAAQYHSETEIVSVSTGGEKERSCWGEVASRAQRLASALASLGLPPGLPPGAR

CATLAWNNRRHLEIYFAVASGGWVTHTVNPRLSVDHLRYILNDAADEVLFFDQTFLPLVAQLLPQLPTVK

HVVLMESRSEAALSQLPSLLFYDDLLQQGMADYRWPQLNELTPASLCYTSGTTGRPKGVLNTHRSLVLHA

LSGNQPDAAGISAKDSLLPVVPMFHVNAWGTPFIAAMVGARLVLPGPHLDGDSLLQLLAAEKVTVGFGVP

VIWAGLLAAMRRTEVRLPEFKRALVGGSALPPSMAEAFQRDYGIALTHAWGMTETSPIGTINTPLSKHDA

LPAQEQQKQRAGQGRPIFGIELQVVDVDGEPLPRDGQSQGYLQVRGHWVVEQYYGQDASALTAAGWFDTG

DIGTLDANGYLVISDRAKDIIKSGGEWISTVELENIAIAHPGVRSAAAIAARHPRWDERPVLLCVRAEGG

EVEETDLLSWFEKRVPKWQIPDRVIFVDALPVSATGKVLKNQLRQAYGEILMSEGK

>lcl|NZ\_FO834906.1\_prot\_WP\_009484094.1\_2239 [locus\_tag=BN49\_RS12695] [protein=aldehyde dehydrogenase family protein] [protein\_id=WP\_009484094.1] [location=2314752..2316476] [gbkey=CDS]

MSHARPGLTTCSQYDAALHALSAARQRWAETSVNRRLALLRQIKDALAGIAPAWVAAAAAAKGLPAGDPL

AGEEWLAGPCALMVGCNGLIATLEQLEEKTFLRRIPLRTLADGRLALRVVPGTLWDRLLLSGVRAEIWMQ

PGVTRAHLDRYAARAYDIPPAARQGKLALVLGAGNVASIAPLDVLHKLFIENQVCLLKLNPVNDYLHDLL

AQALAPLIAMDALRIVTGDARAGAWLTTHPAVDEIHITGSRETHDVIVWGEGETARQRRAAGTPLNPRRV

TSELGGVSPTIIVPGPWSEADIAFQAQQLATQKMNNGGFNCVASQVLILQQGWEPATALLNQLYRLIAAN

TRPDYYPGAENRLTDFRLRARQPLEIARGDALPLIVANTDDDPGFCQQEVFGPGLSVTRLEADSAESFLR

QAIGYANQRLQGTLGANIVIHPRTRKAIGRKRFNALIAELRYGTVAINCWSGVAFLLAPCPWGAFPGHTL

DDIQSGRGKVHNSFMLEKTERTVIEAPFRPFPRSLWHGELTLMPLPPWFITHRGQEAVAQRLVDFYHRPR

WRKLPALLWRALRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004213081.1\_2240 [gene=potD] [locus\_tag=BN49\_RS12700] [protein=spermidine/putrescine ABC transporter substrate-binding protein PotD] [protein\_id=WP\_004213081.1] [location=complement(2316523..2317569)] [gbkey=CDS]

MKKWSRHLLAAGALAIGMGAAHADDSKTLYFYNWTEYVPPGLLEQFTKETGIKVIYSTYESNETMYAKLK

TYKDGAYDLVVPSTYFVDKMRKEGMLQKIDKSKLTNFSNLDPQMLNKPFDPNNDYSIPYIWGATAIGVNS

EAIDPKTITSWADLWKPEYKSSLLLTDDAREVFQMALRKLGYSGNTTDPKEIEAAYNELKKLMPNVAAFN

SDNPANPYMEGEVNLGMVWNGSAYVARQAGTPLEVIWPKEGGIFWMDSLSIPANAKNVDGALKLINFLLR

PDVAKQVAETIGYPTPNLAARKMLSPAVANDKSLYPDAATIEKGEWQNDVGSASAIYEEYYQKLKAGR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529719.1\_2241 [gene=potC] [locus\_tag=BN49\_RS12705] [protein=spermidine/putrescine ABC transporter permease PotC] [protein\_id=WP\_016529719.1] [location=complement(2317566..2318351)] [gbkey=CDS]

MIGRLLRGGFMTAIYAYLYIPIIILIVNSFNRSRFGINWQGFTTDWYSLLMNNDSLLQAAQHSLTMAVLS

ATFATLIGSLTAVALYRYRFRGKPFVSGMLFVVMMSPDIVMAISLLVLFMLIGVQLGFWSLLFSHITFCL

PFVVVTVYSRLKGFDVRMLEAAKDLGASEMTILRKIILPLALPAVAAGWLLSFTLSMDDVVVSSFVTGPG

YEILPLKIYSMVKVGVSPEVNALATILLVLSLVMVIASQLIARDKSQGTLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004150812.1\_2242 [gene=potB] [locus\_tag=BN49\_RS12710] [protein=spermidine/putrescine ABC transporter permease PotB] [protein\_id=WP\_004150812.1] [location=complement(2318348..2319205)] [gbkey=CDS]

MKNTSKFQNVVIATIVGWLVLFVFLPNLMIIATSFLTRDDANFVKLVFTLDNYSRLLDPLYYDVLLHSLN

MALLATLACLALGYPFAWFLARLPQKVRPLLLFLLIVPFWTNSLIRIYGLKIFLSTKGYLNEFLLWLGVI

DTPIRIMFTPSAVIIGLVYILLPFMVMPLYSSIEKLDRPLLEAAKDLGASKLQTFIRIIIPLTMPGIIAG

CLLVMLPAMGLFYVSDLMGGAKNLLIGNVIKSQFLNIRDWPFGAATSITLTLVMGLMLLIYWRAARLLNK

KVELE

>lcl|NZ\_FO834906.1\_prot\_WP\_004147966.1\_2243 [gene=potA] [locus\_tag=BN49\_RS12715] [protein=spermidine/putrescine ABC transporter ATP-binding protein PotA] [protein\_id=WP\_004147966.1] [location=complement(2319189..2320325)] [gbkey=CDS]

MGQSQKLNIQPRSRSPLVHLAGIRKSFDGKTVIDNLNLTINNGEFLTLLGPSGCGKTTVLRLIAGLENVD

SGRIHLEDHDITHVPAENRHVNTVFQSYALFPHMTVFENVAFGLRMQKTPAAEITPRVMDALKMVQLEAF

AQRKPHQLSGGQQQRVAIARAVVNKPRLLLLDESLSALDYKLRKQMQNELKALQRKLGITFVFVTHDQEE

ALTMSDRIVVMRDGKIEQDGTPREIYEEPKNLFVASFIGEINIFDATVIERLDEQRVRARVEGRECNITV

NFAVEAGQRLHVLLRPEDLRVDEIHHNSDADGLIGYVRERNYKGMTLESVVELENGKMVMVSEFFNEDDP

DFDHSLDQKMSINWVESWEVVLADEEHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004150810.1\_2244 [gene=pepT] [locus\_tag=BN49\_RS12720] [protein=peptidase T] [protein\_id=WP\_004150810.1] [location=2320584..2321816] [gbkey=CDS]

MDKLLERFLQYVSLDTQSKPGVRQVPSTEGQWKLLRLLQAQLEEMGLVKVTLSEKGTVMGTLPANVEGDI

PAIGFISHVDTSPDFSGKNVNPQIVENYRGGDIALGIGDEVLSPVMFPVLHQLLGQTLITTDGKTLLGAD

DKAGIAEIMTALATLQAKNIPHGDIRVAFTPDEEVGKGAKHFDVEAFDARWAYTVDGGGVGELEFENFNA

ASVTIKIVGNNVHPGTAKGVMVNALSLAARIHAEVPADEAPETTEGYEGFYHLTSMKGSVDRAEMHYIIR

DFDRKHFEARKRKMMEIAKKVGKGLHPDCYIELVIEDSYYNMHEQVIAHPHVVDIARQAMVDCDIEPQMK

PIRGGTDGAQLSFMGLPCPNLFTGGYNYHGKHEFVTLEGMEKAVQVIVRIAELTAARKGH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529718.1\_2245 [locus\_tag=BN49\_RS12725] [protein=transposase] [protein\_id=WP\_016529718.1] [location=2322217..2322708] [gbkey=CDS]

MSDYRRSYIPGGCWFFTVNLQNRRSDLLTRHIVHLRAATASVKSKKPFLINAWVVLPEHMHCIWTLPEGD

TDYSGRWRDIKKMFTRALAQRHIWQPRFWEHAIRNEEDYRRHMDYVYINPVKHGHVRRVQDWPYSTFHRD

VRRGWYPPDWAGEVSEFDAGERR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176560.1\_2246 [locus\_tag=BN49\_RS12730] [protein=cupin domain-containing protein] [protein\_id=WP\_004176560.1] [location=complement(2322964..2324085)] [gbkey=CDS]

MDYQLTLNWPDFIERYWQKRPVVLKRGFANFIDPLSPDELAGLAMESEVDSRLVSHQDGKWQVSHGPFES

YDHLSENNWSLLVQAVNHWHEPSAALMHPFRALPDWRIDDLMISFSVPGGGVGPHLDQYDVFIIQGTGRR

RWRVGEKVPMKQHCPHPDLLQVDPFEAIIDEEMEPGDILYIPPGFPHEGYSLENSLNYSVGYRAPNAREL

FSGFADYVLQRELGSQRYADPDVPSRDHPADILPTELDRLREMMLGLINQPEHFKQWFGEFITQSRHELD

VAPPEPPYQPDEIYDALQQGDTLERLGGLRVLRIDGEVFVNGEKINSPHRPALDALATHLTLRADHFGDA

LEDPSFLAMLAALVNSGYWFFGD

>lcl|NZ\_FO834906.1\_prot\_WP\_004147969.1\_2247 [gene=phoQ] [locus\_tag=BN49\_RS12735] [protein=two-component system sensor histidine kinase PhoQ] [protein\_id=WP\_004147969.1] [location=complement(2324171..2325637)] [gbkey=CDS]

MKGLLRHIFPLSLRVRFLLATAGVVLVLSLAYGMVALVGYSVSFDKTTFRLLRGESNLFYMLARWENGAI

DVDIPENLNMESPTVTLIYDEQGKLLWAQRDVPWLAKRIQPEWLKRNGFHEIEADVDSSSMLLRNNHEIQ

EQLDAIREQGDDSEMTHSVAINLYPATSKMPQLSIVVVDTIPVELKRSYMVWSWFVYVLAANLLLVIPLL

WVAAWWSLRPIESLAKEVRELEEHHREKLNPNTTRELTRLVSNLNRLVRSERERYDKYRTTLTDLTHSLK

TPLAVMQSTLRSLRGEKISVDEAEPVMLEQISRISQQIGYYLHRASMRSGGTLLSRELHPIAPLLDSLTS

ALNKVYQRKGVNISLDISPEITFVGEQNDFMEVMGNVLDNACKYCLEFVEVSVRQTTDSHLHILVEDDGP

GIPQSQRRAVFDRGQRADTLRPGQGVGLSVAREIVEQYDGEIIAGESLLGGACMEVVFGRQQMEDKQS

>lcl|NZ\_FO834906.1\_prot\_WP\_004150807.1\_2248 [gene=phoP] [locus\_tag=BN49\_RS12740] [protein=two-component system response regulator PhoP] [protein\_id=WP\_004150807.1] [location=complement(2325637..2326308)] [gbkey=CDS]

MRVLVVEDNALLRHHLKVQLQELGHQVDAAEDAREADYYLGEHLPDIAIVDLGLPDEDGLSLIRRWRSHD

VSLPVLVLTAREGWQDKVEVLSAGADDYVTKPFHIEEVAARMQALLRRNSGLASQVISLPPFQVDLSRRE

LSVNDQPIKLTAFEYTIMETLIRNRGKVVSKDSLMLQLYPDAELRESHTIDVLMGRLRKKIQAEYPQDVI

TTVRGQGYLFELR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179353.1\_2249 [locus\_tag=BN49\_RS12745] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004179353.1] [location=2326592..2327398] [gbkey=CDS]

MSQQQSADWVRLAQSPSRTERIEAFFGGHGYEPHRHDTYAIGQTIAGVQSFHYRGGLQHSLPGGTMVLHP

DEIHDGEAGTEAGFHYRMVYIEPALIQKILGGRPLPFIPDGLSADPRLRRAAQPLLKAVTDTFEPLEEED

ALYDLAQTLAVVGGQRSRRQAFDYQAAERAREYIHACFMQDMTLDTLSQVSGRDRWSLSRDFRTLYGTSP

WRYVMMRRLDFCRQRMRAGERLVDIAADAGFADQSHMTRQFISRFGLSPGRWLRAIRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004176558.1\_2250 [locus\_tag=BN49\_RS12750] [protein=cupin domain-containing protein] [protein\_id=WP\_004176558.1] [location=2327482..2327844] [gbkey=CDS]

MYQLVNLAQKFSLFSEQWQPKVVAEMNDYQFKVVRIAGDFIWHSHPETDETLMVVEGVLRVDFRDGHVLV

KAGEMIVVPRGVEHKTSAETEAKLMLIEPRGVLNTGHEGGERTAVNDVWI

>lcl|NZ\_FO834906.1\_prot\_WP\_004176557.1\_2251 [gene=purB] [locus\_tag=BN49\_RS12755] [protein=adenylosuccinate lyase] [protein\_id=WP\_004176557.1] [location=complement(2327899..2329269)] [gbkey=CDS]

MELSSLTAVSPVDGRYGDKVSALRGIFSEFGLLKFRVQVEVRWLQKLAAHAAIKEVPAFAADANGFLDKI

VADFSVEDAERIKTIERTTNHDVKAVEYFLKEKVADVAELHAVSEFIHFACTSEDINNLSHALMLKTARD

EVVLPYWRKLIDAVKDLATQYRDVPLLSRTHGQPATPSTMGKEMANVAYRMERQYRQLNQVEILGKINGA

VGNYNAHIAAYPEVDWHQFSEEFVTSLGIQWNPYTTQIEPHDYIAELFDCIARFNTILIDFDRDVWGYIA

LNHFKQKTIAGEIGSSTMPHKVNPIDFENSEGNLGLANAVMQHLASKLPVSRWQRDLTDSTVLRNLGVGI

GYALIAYQSTLKGISKLELNQDRLLDELDHNWEVLAEPIQTVMRRYGIEKPYEKLKELTRGKRVDAEGMK

QFIDSLALPEEEKVRLKAMTPANYIGRATTMVDELK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140557.1\_2252 [gene=hflD] [locus\_tag=BN49\_RS12760] [protein=high frequency lysogenization protein HflD] [protein\_id=WP\_004140557.1] [location=complement(2329273..2329914)] [gbkey=CDS]

MAKNYYDITLALAGVCQAARLVQQLAHQGHCDSDALHVSLNSIIDLDPESTLAVFGGSEANLRLGLETLL

GVLNTSSRQGLNAELTRYTLSLMVLERKLAASKGAMDTLGNRIAGLHRQLEHFDLQSETLLSAMAGIYVD

VISPLGPRIQVTGSPAVLQSPQVQAKVRSALLAGIRAAVLWHQVGGGRLQLMFSRNRLVNQAKQILAHLT

PEL

>lcl|NZ\_FO834906.1\_prot\_WP\_004150803.1\_2253 [gene=mnmA] [locus\_tag=BN49\_RS12765] [protein=tRNA 2-thiouridine(34) synthase MnmA] [protein\_id=WP\_004150803.1] [location=complement(2329969..2331075)] [gbkey=CDS]

MSESQKKVIVGMSGGVDSSVSAYLLLQQGYKVEGLFMKNWEEDDGEEYCTAAADLADAQAVCDKLGIELH

TVNFAAEYWDNVFELFLEEYKAGRTPNPDILCNKEIKFKAFLEFAAEDLGADYIATGHYVRRADVDGKSQ

LLRGLDGNKDQSYFLYTLSHEQIAQSLFPVGELEKPQVRKIAEELDLITAKKKDSTGICFIGERKFRDFL

GRYLPAQPGKILTVDGEEIGTHQGLMYHTLGQRKGLGIGGTKEGSEDPWYVVDKDVENNILIVAQGHDHP

RLMSVGLIAQQLHWVNREPLQGTLRCTVKTRYRQTDIPCTVTALDEDRIEVRFDEPVAAVTPGQSAVFYL

GEVCLGGGIIEQRLPLQS

>lcl|NZ\_FO834906.1\_prot\_WP\_004150802.1\_2254 [locus\_tag=BN49\_RS12770] [protein=NUDIX hydrolase] [protein\_id=WP\_004150802.1] [location=complement(2331132..2331590)] [gbkey=CDS]

MFKPHVTVACVVHAQDKFLIVEETINGKALWNQPAGHLEANETLLQAAERELWEETGIRATPQHFIRMHQ

WLAPDNTPFLRFLFAIELSDLCATEPHDSDIDRCLWLSAEEILNAPNLRSPLVAESIRCYLQDPRQPLSL

IGAFNWPFTGGE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529797.1\_2255 [gene=rluE] [locus\_tag=BN49\_RS12775] [protein=23S rRNA pseudouridine(2457) synthase RluE] [protein\_id=WP\_016529797.1] [location=complement(2331608..2332258)] [gbkey=CDS]

MRQLIKPENTMQKTSFRKHRVERFSTQQVTRQRKEHQPKTVILFNKPYDVLPQFTDEAGRSTLKDFIPVA

GVYAAGRLDRDSEGLLVLTNDGALQAKLTQPGKRTGKIYYVQVEGEPTPEALTALRDGVTLNDGPTLPAG

VELVEEPVWLWPRNPPIRERKSIPTRWLKITLYEGRNRQVRRMTAHVGFPTLRLIRYAMGGYTLDGLANG

DWRKAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150800.1\_2256 [gene=icd] [locus\_tag=BN49\_RS12780] [protein=NADP-dependent isocitrate dehydrogenase] [protein\_id=WP\_004150800.1] [location=2332499..2333749] [gbkey=CDS]

MESKVVVPAEGQKITLQNGKLNVPHNPIIPFIEGDGIGVDVTPAMLKVVDAAVEKAYKGERKISWMEVYT

GEKSTHVYGQDVWLPAETLDLIRDYRVAIKGPLTTPVGGGIRSLNVALRQELDLYVCLRPVRYYQGTPSP

VKHPELTDMVIFRENSEDIYAGIEWKADSAEADKVIKFLRDEMGVKKIRFPEHCGIGIKPCSEEGTKRLV

RAAIEYAITNDRDSVTLVHKGNIMKFTEGAFKDWGYQLAREEFGGELIDGGPWVKIKNPNTGKEIVVKDV

IADAFLQQILLRPAEYDVIACMNLNGDYISDALAAQVGGIGIAPGANIGDECALFEATHGTAPKYAGQDK

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>lcl|NZ\_FO834906.1\_prot\_WP\_014228877.1\_2257 [locus\_tag=BN49\_RS12785] [protein=site-specific integrase] [protein\_id=WP\_014228877.1] [location=complement(2333867..2334994)] [gbkey=CDS]

MAARPRKNNISIPNLYPLFSRKVNKVYWRYKHPITGKFHSLGTDEAEATAIAIEANKRLAEQQTRQIMAI

TDRISTSSGKSISTNTWLERYWKIQQERLKSGDIKENTIKQKAKPVSLLKERVGMKLISAVNVRDVAQIL

DEYLAEGQPRMAQVIRSVLIDVFKEAQHAGEVPPGYNPALATKQPRRKITRQRLTLEEWQKIFDIADENH

KYMGNAMLLAIVTGQRLGDISRMKFSDIWDDHLHVEQEKTGSKIAIPLALRCNAINWSLRDVISRCRDYA

VSPYLVHFFRTTSQAERGAQVKPRTLTMNFSKARDSADIDWGQGTPATFHEQRSLSERLYKAQGINTKDL

LGHKTQQQTDRYHDDRGKGWTTVAL

>lcl|NZ\_FO834906.1\_prot\_WP\_012542206.1\_2258 [locus\_tag=BN49\_RS12790] [protein=excisionase] [protein\_id=WP\_012542206.1] [location=complement(2334975..2335220)] [gbkey=CDS]

MLQMLTLEEWANEKYRSNPPSVSTLRNYAKQNMFSPPAKKEGRFWRVREDAELVGTLTTPVVKKSDPVLL

QRILNDGCQTT

>lcl|NZ\_FO834906.1\_prot\_WP\_227504839.1\_2259 [locus\_tag=BN49\_RS27990] [protein=exonuclease] [protein\_id=WP\_227504839.1] [location=complement(2335273..2337069)] [gbkey=CDS]

MSGNIGANPNNEEALFNLAEMSFRTQLLAQYMADERHVYHISIPHRNRLSAMEMDTDNHGVQNLLLTAEN

IPELKKYDMPGLWKFTSAFKSVFPVGKRHELGKQIQFAKLWLETSHIDRGILTKEWAAGNYIISINKTDT

GANAGGGNKTDRNPDYQHSLDTLDIELALATMPMDFDIYNFPASVHRRAKEIVQKKESPFKEWSAALRST

PGILDYSRAAIFALIREASSGITPFPDRLRGYINANLTEHKHDTPSAETLAKAGHIPSAAVTLDAINQAI

AVEDNSAKLETLSSDFKAVGTELVKEAQKQRPDANQVLAAERGEYVEGISDPTDPKWITEDLTKTRKPEV

SKIGDGVFSIEGLVDVTGKVNQKEKTDEVVHQTDAVDIEPGHHNKEEDQPIDYVHVMVDLETMGKKHNAP

IVAIGAVVFDPATGSIGESFYKVVCLESSVNWGAVIDPSTVIWWLKQSSEARSAIVNDDAIPLQDALLQF

REFVSDNVAGGSKKAQVWGNGASFDNSILRSSYDCIAEDYPWEYWNDRDVRTMVELGQAISFDPKTTIPF

EGSRHKALADAIHQARYVSAIWQRIIAGNQVLQKLMQN

>lcl|NZ\_FO834906.1\_prot\_WP\_115217266.1\_2260 [locus\_tag=BN49\_RS12805] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_115217266.1] [location=complement(join(2337054..2337967,2337967..2338282))] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_2261 [locus\_tag=BN49\_RS12815] [protein=exonuclease] [pseudo=true] [partial=3'] [location=complement(<2338373..2338747)] [gbkey=CDS]

MNNYPYLIKAKAKANEAKSLFCWFSAKSDSRAERKILDILEDAEINVGRGASHQLPIRTNWLIVDDLPEE

GVLDDTWCDRYELGGEDGLTWQKIVVPAAAEPQPSSKPENDISPANSDEEDYSNN

>lcl|NZ\_FO834906.1\_prot\_WP\_223168510.1\_2262 [locus\_tag=BN49\_RS12820] [protein=Rrf2 family transcriptional regulator] [protein\_id=WP\_223168510.1] [location=complement(2338889..2339221)] [gbkey=CDS]

MKRVLASVQAAATLNKLYDGSPVSLTAISKESKLSTSYLEQIFKKLRAGNLVISQRGPGGGYSPRGDDIT

VTEVITAVSKLPAHKTFEPILRALDDVRVSQLLRGDSPAP

>lcl|NZ\_FO834906.1\_prot\_WP\_016160636.1\_2263 [locus\_tag=BN49\_RS12825] [protein=DUF1482 family protein] [protein\_id=WP\_016160636.1] [location=complement(2339276..2339470)] [gbkey=CDS]

MNTLFALVISVCALTGECSDVLIGVYPSEASCNSNADEQKVQGQCLPYRNAQNMADDQQPAVSF

>lcl|NZ\_FO834906.1\_prot\_WP\_012542200.1\_2264 [locus\_tag=BN49\_RS12830] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_012542200.1] [location=complement(2340313..2340702)] [gbkey=CDS]

MKNTEELNNQLIARLEEITQRGISKADMARIAGVTPQAVNGWFKKGVISKKSAIALAEAANVSVTWLLGE

KVSEDSGLKPNESKMLRLFRQLPEAEQERMIDTFEVRLKEIDDYVEKYLRGRFKASDTN

>lcl|NZ\_FO834906.1\_prot\_WP\_012542199.1\_2265 [locus\_tag=BN49\_RS29005] [protein=Cro/CI family transcriptional regulator] [protein\_id=WP\_012542199.1] [location=2340804..2341019] [gbkey=CDS]

MTALDNAIRVAGSANKLASTLGVSGMAVSQWKTKGIVPSSRVLQVFNATGVTPHELRPDLYPNPTDGIPK

E

>lcl|NZ\_FO834906.1\_prot\_WP\_014907826.1\_2266 [locus\_tag=BN49\_RS12840] [protein=toxin YdaT family protein] [protein\_id=WP\_014907826.1] [location=2341022..2341576] [gbkey=CDS]

MQTTSFENHTPVMSMQLKTENQYLPRRRDGKKCRAILAAVQEWESSLPGRAQDHVAQLVAEQWEKQNGRG

ISVNKQNLYRYLKNEGGSEKYTSYVIQLSAAIADAMPIEIARKHGLKHGLTETELVANAIKECSEAHQAK

LLGAPLQKLEREIREAAIALFNMLPADAAGPLLASISAVAPQFF

>lcl|NZ\_FO834906.1\_prot\_WP\_016528971.1\_2267 [locus\_tag=BN49\_RS31435] [protein=DnaT-like ssDNA-binding domain-containing protein] [protein\_id=WP\_016528971.1] [location=2341628..2342611] [gbkey=CDS]

MARIRTVKPEFWTDEKVVECSIPARLLFIGLFNFANDMGCLERSPKRLKMQIFPADALDCEPLIQELITH

GLLTEYSVNDVCYLQIKGFLKHQKINRPSASKIPLPPEFTESKAGKEEKRAPNQGGLSEDSVNPHGGLTD

GKGREGKGKGSNPTLYAQERNFPQQPQYLPGVDIPIGKFAMHDLWLPSQDWPRLAATWGIALPEPAYLPT

ELAEFIAYWKSEGKVFTQIQWEQKLARSVISARAKSKPQPATGGKDHAGIQPVNTASRAVQEIQAARERW

EKQNGLAGGGYGMAAMDSHGGNIFESVDPEERGGALGYVDCPDWIDE

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MGEIFSNRWTQKNGAAPSDMWIAQIGSMSEAQITLVCSQCMERCAAGNTWPPDLAEFVALVSASGANPFN

LTSESVMAEYKRWRNESYRYSGSDKYPWKQDVLYHICIEMRRTGVERSLTEGELKKMAENLLTKWTKHLA

NGFSIPPIRRQLAAPRHPAGPTPAQVLMEEYKRRKAAGLTK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528969.1\_2269 [locus\_tag=BN49\_RS12855] [protein=hypothetical protein] [protein\_id=WP\_016528969.1] [location=2343082..2343522] [gbkey=CDS]

MTKQSKTKVTKAQMVLAIVSRTPECVLQDVCDALDLQASTAGNLLRQLHAAGKLHRTHNGCQYVYRVVAG

VEVPDVALPQAATQLSEEDVKKVQDALSLAKTLEDRKLWRRAATVYTSTLGMATTANELWLLAKMRNRCL

RNAARC

>lcl|NZ\_FO834906.1\_prot\_WP\_016528968.1\_2270 [locus\_tag=BN49\_RS12860] [protein=ComF family protein] [protein\_id=WP\_016528968.1] [location=2343901..2344482] [gbkey=CDS]

MEVNIKDIVGNWNRGVVLDKHSKYSVVIGQNEWGHNIYDTTRTEVGEALFQLKYRSDWSQVHPLAQCLYD

EAYPLFEKVGFILPMAASNVRARQPVTEIARALANLAGVPCYDNLLLKAPGGVSLKNLHTKEEKVEAIGN

SFSVNPIITNQGQSNVLVIDDLYHTGASMEAACAALSGYNKISNIYVAALTWR

>lcl|NZ\_FO834906.1\_prot\_WP\_016528967.1\_2271 [locus\_tag=BN49\_RS12865] [protein=hypothetical protein] [protein\_id=WP\_016528967.1] [location=2344485..2345039] [gbkey=CDS]

MTTIFVAGSITIKELDPLIIERLKKIVDKKYRVVVGDANGVDSSVQRALIALNCETTTVFSSSPKPRNNL

GAWPVNVVKTDYKRGTREFYTAKDIQMAEHADCGLMVWDCKSPGTLNNVVELLLRNKYSVVFVNKMRDFI

KVKTPDDIDTLIKMMKTTDLEKAEDKISLSGKLARLKNNQMSLL

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REVSLKDDLTNELHRADILYGQGTGFETVLELQHSPISEEERISRETFYRKGRRMFWLVHIDASSTSSNG

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>lcl|NZ\_FO834906.1\_prot\_WP\_012542186.1\_2273 [locus\_tag=BN49\_RS12875] [protein=DinI family protein] [protein\_id=WP\_012542186.1] [location=2346519..2346752] [gbkey=CDS]

MKVEITIDRQKKLPDGAVPALEKELLRRLDQNFNNCSLVIRRASSDGLTVLGGMDGDKKRVEEILQDTWE

SADDWFC

>lcl|NZ\_FO834906.1\_prot\_WP\_077253592.1\_2274 [locus\_tag=BN49\_RS29010] [protein=hypothetical protein] [protein\_id=WP\_077253592.1] [location=2346764..2347054] [gbkey=CDS]

MAYLVYFEDFAVGKKQETPNTGYAIIRCDDGVIVARLTSFPVCERALMYRRGDTVSFMPLQPDEIVGTLS

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528965.1\_2275 [locus\_tag=BN49\_RS12880] [protein=LexA DNA binding domain-containing protein] [protein\_id=WP\_016528965.1] [location=2347095..2347487] [gbkey=CDS]

MTQTPEVSKSHQTGAPSSSAGLLSSSKLTFRQQEVFDLLVAYINQHSYPPTLSELADMLGVSSSNAVLLH

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MRALLNVDIARHLGIVLLKPSSELMPLFGAGRVLVEMPPASMKKTPSGRLPDARQPLRDDIGIRPFFMKK

AVITAAGGVSALESWLRRQVKNCQWTHSDYHHHELVPFRHSTGVIIACWHCDNELKNQTEQTLDQLVGVN

NADWIIDTARIALGLDAQRSLSLAELCWWAVGAGIGDEITEEMARRSLRIKDDGIKSVYRESEIVPSVPA

TSILSPRLENAIRPTAITTPGKPLVPVNVDPVAPATLFARPKRSRWLSADFISWVKKQPCMCCGQPADDA

HHLIGWGQGGVGTKAHDIFTIPLCRKHHRALHHDPGAFEREYGTQPVLIIKLLDRAYSLGVLS

>lcl|NZ\_FO834906.1\_prot\_WP\_016528963.1\_2277 [locus\_tag=BN49\_RS12890] [protein=antitermination protein from phage origin] [protein\_id=WP\_016528963.1] [location=2348732..2349079] [gbkey=CDS]

MRDMYEIIDRWGAWAASDNSGVDWQPIAAGFKDLLPYGKKTRQQCDDDEGIMIDGCVARLRKYKPEEYEL

IMAHFVLGYSLRTIAKKQKCSDGKVRKELQNALGFIEGVICTLAY

>lcl|NZ\_FO834906.1\_prot\_WP\_016528962.1\_2278 [locus\_tag=BN49\_RS12895] [protein=hypothetical protein] [protein\_id=WP\_016528962.1] [location=complement(2349098..2349982)] [gbkey=CDS]

MALFALMDKSIATRVVRVELDLGASTSVSTIFQQQRLHFQTHHNNHVAFYAGYEPRYDECFEIQNFADAA

LLIDAATRPTAMPVWDPSQISIDNIKALFVGVDAPGNPNIIALQTFNKKQILDTSKSFLATMIGRSTTFS

KAVDVGFNLDDKLVAIIDNNTICFKSFFKLRSVFDMTSYFTAATDQDLDAFSQLPIFSIAQGFDIKNVAD

TVIRNKITLINQTGLLTPQNLALFKAEAVKVGFPLQTVVVGGVEKITMPSSKKEIKSLLDFIEEDIWVSG

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>lcl|NZ\_FO834906.1\_prot\_WP\_023159888.1\_2279 [locus\_tag=BN49\_RS29015] [protein=hypothetical protein] [protein\_id=WP\_023159888.1] [location=complement(2349992..2350504)] [gbkey=CDS]

MNRLARLLLTASSIAPVCATLFFIGFVKETVWLMNYSLYVGLASWCLAIGLVKYADCKMERLTKNINSLS

PANKEVTNYFLSYLFPLLGTDSISENKSYALFFYFSLLFYICFSENYNFNPVLSLHGYKFYEAEDDTGVG

FVLISKSVITDIKNISFNVVQLTDYTYLHV

>lcl|NZ\_FO834906.1\_prot\_WP\_016528961.1\_2280 [locus\_tag=BN49\_RS12900] [protein=class II holin family protein] [protein\_id=WP\_016528961.1] [location=2351457..2351693] [gbkey=CDS]

MYRMDKLTTGIAYGTSAGNAGFWMLQLLDKVSPSQWAAIGVLGSLVFGLLTYLTNLYFKIKDDRRKAARS

GDGKQSET

>lcl|NZ\_FO834906.1\_prot\_WP\_042940377.1\_2281 [locus\_tag=BN49\_RS12905] [protein=lysozyme] [protein\_id=WP\_042940377.1] [location=2351671..2352201] [gbkey=CDS]

MGNRAKLSAAMLALMAAGASAPTLMDQFLDEKEGNSLTAYRDGSQEIWTICRGTTRIDGKPVTQGMKLTK

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>lcl|NZ\_FO834906.1\_prot\_WP\_046044041.1\_2282 [locus\_tag=BN49\_RS12910] [protein=DUF2514 domain-containing protein] [protein\_id=WP\_046044041.1] [location=2352234..2352710] [gbkey=CDS]

MVIAGAFVAGLAWSDRAWEKRWAERDSAESSQEVNAQTAARMIEQGRLIARDEAVKNAQAQTAAARTAAA

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MTCERIYESVRASIPSKG

>lcl|NZ\_FO834906.1\_prot\_WP\_165454527.1\_2283 [locus\_tag=BN49\_RS31000] [protein=hypothetical protein] [protein\_id=WP\_165454527.1] [location=2352792..2352956] [gbkey=CDS]

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QNCRRDGIATKASSVDHIIPKAHGGTDDDFNLESLCWSCH

>lcl|NZ\_FO834906.1\_prot\_WP\_016528957.1\_2285 [locus\_tag=BN49\_RS12920] [protein=hypothetical protein] [protein\_id=WP\_016528957.1] [location=2353254..2353574] [gbkey=CDS]

MLELPLKENSNRENPMKNFKIEYVDGALTVLETDGQSRMNEAVHGIQFEHVQGGRPLLKLTIAHDIAPAP

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528956.1\_2286 [locus\_tag=BN49\_RS12925] [protein=hypothetical protein] [protein\_id=WP\_016528956.1] [location=2353574..2353996] [gbkey=CDS]

MMYQRTDLTLSMFYASSADAEGNKVATLTMQVIDAEAGAVQTSQLLCITDSAKKKTYTVGEQSISNGSDP

LLVAIENYWRQSTDVVVKGLIAEVTDFIAGNINSVSTWIGQFGMKVFENQPLAERLPESVLQADGSTPER

>lcl|NZ\_FO834906.1\_prot\_WP\_016530358.1\_2287 [locus\_tag=BN49\_RS12930] [protein=DUF1441 family protein] [protein\_id=WP\_016530358.1] [location=2354228..2354716] [gbkey=CDS]

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MAKRASARGIRRDVSGILRAPRRMLVADAVAEYMRVPMGAGNSVPWDPNLAPYVIEPMNCLASREYDAVV

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HDRTFRAGNYLKLGWPSVNIMSSSDYKFVALTDYDRFPEDIDGEGDGFSLASKRTTTFMSSGMTLVESSP

GRDILDTKWRQSSPHEAPPTTGVLSLYNRGDRRRLYWPCPHCGEYFQPEVANMTGYRDTTDLVTASEAAY

LQCPACKGKVLPAMKRELNMKSVWLRDGQSIDRDGNITGEGRRSRIASFWMEGPAAAYQTWSQLIYKYLA

AEQEYEKTHSEETLKTVVNTDFGRPYLPRASTEQRKSELLEQRAEDVPKRCVPDGVCFLVATVDVQGGRN

RRFVVQVTGYGSMGERWLVDRYNIRQSLRCDANGESLPIDPASYPEDWDLLLTDVFYKTWRMASDPRRCM

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MSLLDDAIGVISPGWKAARLRSRAMIQAYEAVKPTRTHKARRENRSADQLSKMGAVSLREQARWLDNNHD

LVIGIFDKLEERVVGKSGIIVEPHPKLKNGKIAKKLAADIRQKWGEWSIRPEVTHQFTRPMLERLMLRSW

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GRQLETKRVDAENMLHLKFVRRLHQTRGTSLLSGVLMRLSALKEYEDAELTAARIAAALGMYIKKGDGQS

WDENAGKDDDRELNIQPGIIYDDLLPGEDIGMVKSDRPNPNLETFRNGQLRAVSAGSRLSFSSTARNYNG

TYSAQRQELVESTDGYLILQDWFIGAVTRPMYRAWLKMAVASGQITLPRGLDIESLYTAVYSGPVMPWID

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ASTSESKRKK

>lcl|NZ\_FO834906.1\_prot\_WP\_071609143.1\_2291 [locus\_tag=BN49\_RS12950] [protein=Clp protease ClpP] [protein\_id=WP\_071609143.1] [location=2358480..2360501] [gbkey=CDS]

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LLDKVESVLIPAYAAKTGKTSDEIAAMLEDETWLDGAECLAMGFADQVIPSLQAMACIHSKRIEEFEKMP

NSIRNMVTPPRNSTQREPQQPVPQPQAHQPTAPQPAAVDENAIRAQVYAEQRNRVNGINDLFAMFGGKHQ

ELQNQCIADPDCTVEQAKDVLLAALGKAATPSNKSEQPHIYAGNGNFVSDGIRQALMARAGYENQERDNV

YNGMTLREYARMALTERGIGVASYNPMQMVGLALTHSTSDFGNILLDVANKALLQGWDEAAETFDLWTKK

GQLSDFKTAHRVGMGGFNSLRKVREGAEYKYVTTGDKGETIALATYGEIFSITRQAIINDDLNALTDVPA

KMGRAAKATIGDLVYAILLDNPKLSDGKPLFHADHKNLSSGAISVSSIDDARKLMRLQKEGERSLNIRPA

YMLVPVGLETIASQTIKSASVKGADINAGIINPIQNFAEVIAEARLDDKDPNAWYLAAAKGTDTIEVAYL

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MAKNFVQEGKTIHLVNAGQEPILSGAAVVVGELIAIAITDIPGGDTGDGLTEGVFQLPKLPADEIKAGKK

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>lcl|NZ\_FO834906.1\_prot\_WP\_023342887.1\_2293 [locus\_tag=BN49\_RS12960] [protein=hypothetical protein] [protein\_id=WP\_023342887.1] [location=2360904..2361179] [gbkey=CDS]

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MSLKGLERAIQNLNSLSRLMVPTATAQALNRVAGRTITQGSRKVAKEATVGDNRKKGLPVRLVRQRSRLK

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MSKHTAIRLAVLDQLKTSIPDRVTWFDGRPVFLEEQDLPALAVYLTDAEYTGESLDEDSWQAVLHIEVFL

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MATPNPMAPVKGAGTTLWLYTGTGNPYANPLSDADWQRLAKIKELTPGEMTAESYDDTYLDDENADWTAT

AQGAKSAGDTSLTLAWKPGEEGQKSLVAWFVDGDVRAYKIKYPNGTVDVFKGWCSSLGKAIPAKEVITRT

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MFLKKDEFTHNGATVPITELSALQRITYLEYLAAEEKALSAISDDVDDQKMSAGLVSMSIRAGARLIALS

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MKLAREFGRPDWRAMLAGMTSSELGDWHHFYRERFFQDAQLDAHFSGLLYTISTFLYRDPDITPAHFSLL

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043046.1\_2299 [locus\_tag=BN49\_RS12990] [protein=phage tail tape measure protein] [protein\_id=WP\_046043046.1] [location=2363669..2366812] [gbkey=CDS]

MAQQISDLVINLDVDSATFTEQIARIKGQLSGVANESEKVQTRMRSAAEAQITALKTTCDAGAGAVSDMQ

RRQADAAAGLQNELQRVSKSVDETYQRVTGLNQRYRENDAQAEALARRQDALAESFFRQIDGVRSLSGET

RSLASVQEQFRKARAQGNITQGDYLSLISRTTARQKELQQVEEKANQAREKFLRQLKAQVVEQKLSGTEL

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TQHAAAAVLAQVVGSGVFGGADVERIANVAARLQQATGQAVDETINQFKRLKEDPVNAVATLNESLHFLT

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MAIETFAWRIQAASQPTLKSKDNIRRVQFGDGYAQVSGNGINNETLSYEFSFSGDPDTALEIYKFLRRHK

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MSLHADYQKLEPGDEIRLFEIDGSAFNMGDILYFHGYNIPHTEAEIVAAGGDESKLPAKSIWWQGIEYKA

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QEKRRLFFIDVKHYEDDEKVEFTLSSPFALQGMMIPTRQLHAICSWCIRNQYRSGNGCDYAGTRYFDRNN

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MHEVMMRIELNGPLGKRFGKIHHRLISTTKEAVVALAKTIPGFEKFMITSEDRGLTYAIFQDEKNIGLDD

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MANNIIKGRKGGGSKQRTPTEQPDDLQSVAKAKILLALGEGEFAGGLTGKDIYLDGTPLENADGSQNFSG

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EPAFIPELVSRYSFNQLEMTAIGCTRQSEAHRKGLWGILTNNKDRMVEIDVGLDGRIPQPGYIIALADEL

LAGRVNGGRISAVNGRVITLDRDVDAKPGDRLQLNLPSGISQSRTIQAVNGRRQITVTTAYSETPERECV

WAIESDDLFLQQYRVTGVKENNDATLTITGVAHDPDKFARIDTGAIIDQRPVSVLPAGNQSPPDDIVITS

RSVVNQGISVETMQVNWSAVSGAIAYEAQWRRNDGNWINVPRSSTTSFEVSGIYAGRYLVRVRAINAAEI

SSGWAYSEEKTLTGKVGEPLAPLALATRSLVHGVQVSWEFPTGSGDTLRTELQYSKNQDGSAPMPLSDVA

YPGKSYQQMGLSMGAEFWYRARLVDRLGNESPWTGWVQGMASDNFDDYYENLTDAIKDTAAWEETQRTIS

ETQEGIRNTQQELEQTAEELRQKAADQAKQVSQNIDASAKSITADVNQQIAVLSKSLADGDAALNAQIKT

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MSSLAAGANIQFDSQVIWHFNSQTTEGWTGSAGVPGVSRDGWLRPADSATDPYITSPGGLAVDGAAYRFI

MLRFRKTGKPVWAGEIRWVSAGENFNNTKRYIVAEPEYADGVATLTVRDIPWTGNIDRIRLDLTNQQDAS

NFIEFDWIAVGRPAPGASTAALQDVRSTLSNALTSEAQARSTLAAQMRGSYDGSDLEKVTSGLLYQEKTA

RVTAIQAEVKARESLQTQFNDNKAAVSGELSSLTTEQRAQASRIGGLETSLGKKADATALTSLTQKVEQQ

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VDEVADATRLDFTSAGSYLIALYSCQVKVAADTTITMTPGNRVFDDTGAVFVNGVQVAWGNASWTTVSFD

LKAGWNTVEFLVNQWAGQAYINLGLKLSDKVAEMYSGLGVSALANAAGVLSSNVSQIGNDVVSNSQSITQ

LRNALTQTDANVASKADQTAMNSLTGRVEKTESGLTAANSNITSLSSSLSQQSKRGANLLPDGTFESYAV

GHNLANNRAIVTTDDSHGGNKCIRVTRPNDYNANATDNTDTHIFSGFQVRDNAVFYMECWVKLDSRSTAM

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ALTALTNRVTQTEKDINSTSSSVTNLNNKVDAISVGGTNLIKNSGDMTGWSNVVSDTYRGNAVISTTVKA

GSGYRDLREITLESPLDAGEYVYSFYAKGGVAGQTMTAFFYNPNTTTSIETSQGAKGNNTDGRAQFTLTT

SWARYWVKWKQTPTTGTKRLILCRIESNTSKDQTVYINSPKFEVGNVVSDWNESPSDSASASAVDSLTTK

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VFTVTARGNGNSVTPGVFDESGKNLFTPGRSWALVTFAKHSNGSTVIATSKTYDVFGSANNGATMSADIE

ALASGTYVCVLTFDEPSGNRGKILSALESLGGTSEVVNSLPYRGAYILLGRKGMRPGDGLELRAPTGGDA

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VESQKFTGNKSLQVSRGANNNGNSDKQLGSWQSVREDAKFRFEFWAMMPADQKPSSGWTTLVGINSLNAA

GQNSWQSAVTVSEAALGARDKWVKFTGIASNNGGGRTRAVVWISTRGASGSGTPGYSLYIDDLVITDVTD

AKAAQDASDATASAVSGLTARVTDAEGKITAQAQQQTALATKVDNANSRVDNMAKTLSDSQSTQASLNTS

LQSQIDAQAAANIKNQTTLDNTIKSVASITSTQQTHATALEALATQQTTLTSSVGDLSASVQNTAKTVAA

VNGTVSSLWSMKVETVNGKKVGAGITLGSNGETSDIILYADRFSLFNRNNATAVPVMVAEGNELYIDTAR

IKNSSLTSTKIADGSITNAKIGNEIRSNDFVDGSRGWRIAKDGSSQFNNVIVRGRVEANSGVFRGTVQAD

SFIGDIAVAKSYDSLTFRRNQTVQRNGAYQNRGYSMTVVLACTLVCQTYGTGSGLGYTSDITFNIGGQEV

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MAMYEVGTVTGAASKARVTGATTKWSQVALGILPGSILVVYRSGSADLYAIKSVDSDTQLTLTRNITTAF

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LNALAKLTGGNKLDGSQVITSDNAGFILGKNSDLALLKKQGQGGTIAVGSGTPFRVQRSRATTVSPADTF

DDILVIGTNNQTTLPGDLVVGGGFDNTAKGKLYSQALELSMGTPYIDFHHNKSANDYTARLITTAADQLS

VQGSHLRVDRDLRVGQAADIGSWMQCRYDCVSQQTDFGSPAIGALISGGKVRSRMSGRGGNGDTAGAWGG

FYLEEYVGYNHRVVLYMDGFGRKDAWLFYTGGTISTPKGDVMTTGSDVRLKKDFTESQEGASRRINALGI

CEFNMKGETRRRRGFIAQQAEKVDPIYTFQSGDVEIDGEKINILNVDHTAIIADLVLTVQELTKQVRDLN

KQVQTKEY

>lcl|NZ\_FO834906.1\_prot\_2306 [locus\_tag=BN49\_RS29025] [protein=NADP-dependent isocitrate dehydrogenase] [pseudo=true] [partial=5'] [location=<2379824..2379994] [gbkey=CDS]

ELLLRHMQWFEAADLIVKGMEGAIAAKTVTYDFERLMEGAKLLKCSEFGDAIIANM

>lcl|NZ\_FO834906.1\_prot\_WP\_004224172.1\_2307 [locus\_tag=BN49\_RS13025] [protein=winged helix-turn-helix domain-containing protein] [protein\_id=WP\_004224172.1] [location=complement(2380267..2380980)] [gbkey=CDS]

MNLLKPQQDSEPEEALETAMAMVASALSDSSRVSILCALMDGRAWTATELSTVAEVSASTTSGHLARLLS

NGLVVCLAQGRHRYYRLAGSHIAGLLENLMGVSMQAHKTLLPSTPVNLRYARTCYDHLAGELAVNIYEYM

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>lcl|NZ\_FO834906.1\_prot\_WP\_004190914.1\_2308 [locus\_tag=BN49\_RS13030] [protein=hypothetical protein] [protein\_id=WP\_004190914.1] [location=complement(2380977..2381369)] [gbkey=CDS]

MYDIHVILSNSPGSLGAMGMALGNNGVGLEGGGVFTTPDAGHAHFLVEDGEKARRVLTEAGFTVSNVCRP

LIRKLPQERPGELGDIADTLAHNGINILVQYSDHRNRLILLTDDDARAAEVTKKWAILSE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150797.1\_2309 [locus\_tag=BN49\_RS13035] [protein=antibiotic biosynthesis monooxygenase] [protein\_id=WP\_004150797.1] [location=complement(2381362..2381685)] [gbkey=CDS]

MIAVLFEADALPQAQERYLQLAAGLTPLLSDTPGFIAIERFQSLSTPGKILSLSWWEDEASVANWQQNER

HLAAQREGKASIFSYYRIRVARVFRDYASDRGAQSDV

>lcl|NZ\_FO834906.1\_prot\_WP\_042942835.1\_2310 [locus\_tag=BN49\_RS31005] [protein=hypothetical protein] [protein\_id=WP\_042942835.1] [location=complement(2381805..2381981)] [gbkey=CDS]

MSVKRLSRPYSPSAIAFIDSRSRQGLSPHIAISLKLSQPCALRLPYRMAGVLFYSPSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004140530.1\_2311 [locus\_tag=BN49\_RS13050] [protein=DUF1272 domain-containing protein] [protein\_id=WP\_004140530.1] [location=complement(2382135..2382362)] [gbkey=CDS]

MLELRPNCECCDKDLPPDSPEAFICSFECTFCRDCMTTRLNGHCPNCGGELVRRPVRPEEALRRHPASTL

RRHAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004140529.1\_2312 [locus\_tag=BN49\_RS13055] [protein=glutathione-dependent formaldehyde dehydrogenase] [protein\_id=WP\_004140529.1] [location=complement(2382475..2383668)] [gbkey=CDS]

MKALTYHGPHHVSVDTMPDPALEAADDIILRVTATAICGSDLHLYRGKIPGTHHGDIFGHEFMGEVVEAG

SEVTAVRKGDRVVIPFVIACGDCFFCRLQQYAACESTNSGQGATLNRKGISPPAALFGYSDLYGGIPGGQ

AEYVRVPKANTGPFKVPDTLPDEKVLFLSDILPTAWQAVKNAEVKPGSSVAIFGAGPVGLLCASCARLNG

AEQIFIIDHNDYRLDFAQQRYGAIPINFDHHDDPAQWIIDNTPGHRGVDAVIDAVGFEAKGSLTETVLST

LKIEGSSGKALRQCIAAVRRGGIVSVPGVYAGFIHGFMFGDAFDKGLTFRMGQTHVHAWLPDLLALIEQG

LLTPEEIVTHHMPLEEAARGYQIFEKREEACRKVILVPGMQPGKATL

>lcl|NZ\_FO834906.1\_prot\_WP\_004150795.1\_2313 [locus\_tag=BN49\_RS13065] [protein=general stress protein] [protein\_id=WP\_004150795.1] [location=2384290..2384475] [gbkey=CDS]

MAEHRGGSGNFAEDREKASEAGRKGGQHSGGNFKNDPQRASEAGKKGGQNSHGGGRKSDNS

>lcl|NZ\_FO834906.1\_prot\_WP\_004148027.1\_2314 [locus\_tag=BN49\_RS13070] [protein=ferritin-like domain-containing protein] [protein\_id=WP\_004148027.1] [location=2384566..2385060] [gbkey=CDS]

MNMKSIEDVFIHLLSDTYSAEKQLTRGLAKLARAASSEKLSAAFNAHLEETQGQIERIDQIIEQESNLKI

KRMKCVAMEGLIEEANEVVESTEKNEVRDAALIAAAQKVEHYEIASYGTLVTLAEQLGYKKAAKLLAETL

EEEKQTDVKLTDLAVGNINKKAEK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140514.1\_2315 [locus\_tag=BN49\_RS13075] [protein=ferritin-like domain-containing protein] [protein\_id=WP\_004140514.1] [location=2385087..2385593] [gbkey=CDS]

MNHVEHYHDWLRDAHAMEKQAESMLESMAGRIDNYPDLRARIEQHVNETKRQITVLEEILDRNEISRSVI

KDSMSKMAALGQSIGGMFPSDEIVKGSISGYVFEQFEIACYTSLLAAAEKAGDTASIPAIEAILAEEREM

ADWLIKHIPQTTEQFLLRSDADGVEAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004179357.1\_2316 [locus\_tag=BN49\_RS13080] [protein=manganese catalase family protein] [protein\_id=WP\_004179357.1] [location=2385610..2386497] [gbkey=CDS]

MFRHVKQLQYTVRVAEPNPGLANLLLEQFGGPQGELAAACRYFTQGLSDDDPGRKDMLMDIATEELSHLE

IIGTLVGMLNKGAKGALAEGTESEAELYRSLTANGNDSHITSLLYGGGTPLTNSAGVPWTAAYIDTIGEP

TADLRSNVAAEARAKIVYERLINVTDDPGVKDALAFLMTREAAHQLSFEKALQSIRNNYPPGKLPPISEY

ANTYYNMSEGGEVRGSWNSDKHFDYVKDPQPGVDGGDGSASVGLTPEQEALCKAMLKRTQSDPQGDPLTG

AELGAGKQNTSSSAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140511.1\_2317 [locus\_tag=BN49\_RS13085] [protein=cytochrome ubiquinol oxidase subunit I] [protein\_id=WP\_004140511.1] [location=2386553..2387959] [gbkey=CDS]

MFEFDAFHLARLQFAFTVSFHILFPAITIGLASYLVVLEGMWLRTRDNVWRSLYNFWLKIFAVNFGMGVV

SGLVMSYQFGTNWSGFSQFAGSITGPLLLYEVLTAFFLEAGFLGVMLFGWNKVPPALHFFTTCMVALGTL

VSTFWILASNSWMQTPQGFIIENGHLIPQDWLAIIFNPSFPYRLFHMAIAAFLSSAMFVGASAAWHLLRG

NDSPAIRKMLSMAMWMALLVAPIQAVVGDMHGLNTLEHQPAKIAAIEGHWENRPGEATPLLLFGLPDMEQ

ERTRYGLEIPALGSLILTHSLHKQVPALKDFPKEDRPYSPAVFWSFRIMVGMGVLMIALGICSAWLRYRR

RLYHSRPFQWFALCMGPAGLIALVAGWVTTEMGRQPWVIYGLLRTRDAVSLHSTLQMAISLLVFIVVYCA

VFGVGYYYIFRLIKKGPQPVTELTSQTAGTPARPLSAAEPVRDEENAS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043052.1\_2318 [gene=cydB] [locus\_tag=BN49\_RS13090] [protein=cytochrome d ubiquinol oxidase subunit II] [protein\_id=WP\_046043052.1] [location=2387956..2388966] [gbkey=CDS]

MSIDISVIWFVIIVFATLMYIVMDGFDLGIGMLFSVVHDGEERDVMVNSVAPVWDGNETWLVLGGAGLFG

AFPLAYAVITDALVIPLTAMLIGLIFRGVAFEFRFKAVPPHRIFWDYAFAGGSLLATFSQGIVVGAFING

FAVADRRFAGSTLDWLTPFNLFCGLGLVVAYLLLGTTWLIMKSEGALQQRMRELTRKVLLALMVVIAVVS

VWTPLGWRYVAERWFTLPNFFWFVPVPILVLALSLWIWRLSARPASHARPFILTLGLIFLGFSGLGISVW

PNIIPPHISLWDAAAPPSSQVFMLPGALLIIPVILMYTAWSYYVFRGKVSGSEGYH

>lcl|NZ\_FO834906.1\_prot\_WP\_004140506.1\_2319 [locus\_tag=BN49\_RS13095] [protein=hypothetical protein] [protein\_id=WP\_004140506.1] [location=complement(2389082..2389279)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150791.1\_2320 [locus\_tag=BN49\_RS13100] [protein=DNA-binding protein] [protein\_id=WP\_004150791.1] [location=2389846..2390478] [gbkey=CDS]

MAGRIDYDIEKYQFTEAGETPRLREQWREVYLECRQLRAGAEERLRIALLNVDYVTSFELPFRLLLVRAP

QLIADVRETLQLSRKAAVFNGKRYGCVYSLKQDLQAVPEAFHYRLANRIRRVDATGLTAAPYQQIAREIK

PARERLRQALNAGLPVTALDALFWFGSQRVAADIAQLRRSGMAIVTTEVEVSDNLFNTTRRVPVYRLASE

>lcl|NZ\_FO834906.1\_prot\_WP\_004140501.1\_2321 [locus\_tag=BN49\_RS13105] [protein=hypothetical protein] [protein\_id=WP\_004140501.1] [location=2390518..2390697] [gbkey=CDS]

MTIAPSNQTHSPLATGRGAGSSHALAMSMRSISASGTMYFLFTALYPLRLFCQQGSGKV

>lcl|NZ\_FO834906.1\_prot\_WP\_016532341.1\_2322 [locus\_tag=BN49\_RS13110] [protein=EAL domain-containing protein] [protein\_id=WP\_016532341.1] [location=2391095..2391781] [gbkey=CDS]

MVEENAKNTSYRFVLEPAISDDGSCHSWELLTKDIIAPARNNASAPAFSFSTLTESDKLALFTRQIELLS

VFDFSLVDNKPISLNIDDLLSHFILTDRYLCDFLRSCKHIALEINENFHEFIVGRELTALSTLAALCPVW

LDDFGRGRTSFPLLERFRFDCVKVDKDYFWDKENDPALPGLLQSIHTLTGHVIVEGIETEKQKRLITSAG

DIIGQGRYWKEEYIFLCG

>lcl|NZ\_FO834906.1\_prot\_WP\_004150789.1\_2323 [locus\_tag=BN49\_RS31010] [protein=hypothetical protein] [protein\_id=WP\_004150789.1] [location=complement(2391894..2392058)] [gbkey=CDS]

MPRDPERMAQAGLIDRSGEIFFHQLAQLRGQLLAYVEMAIGALRMGVFTGNDPS

>lcl|NZ\_FO834906.1\_prot\_WP\_016532342.1\_2324 [locus\_tag=BN49\_RS13120] [protein=UbiD family decarboxylase] [protein\_id=WP\_016532342.1] [location=complement(2392092..2393600)] [gbkey=CDS]

MTAPIQDLRDAIALLQQHDNQYLETDHPVDPNAELAGVYRHIGAGGTVKRPTRIGPAMMFNNIKGYPHSR

ILVGMHASRQRAALLLGCEASQLALEVGKAVKKPVAPVVVPASSAPCQEQIFLADDPDFDLRTLLPAPTN

TPIDAGPFFCLGLALASDPDDASLTDVTIHRLCVQGRDELSMFLAAGRHIEVFRQKAEAAGKPLPITINM

GLDPAIYIGACFEAPTMPFGYNELGVAGALRQRPVELVQGVSVPEKAIARAEIVIEGELLPGVRVREDQH

TNSGHAMPEFPGYCGGANPSLPVIKVKAVTMRNNAILQTLVGPGEEHTTLAGLPTEASIWNAVEAAIPGF

LQNVYAHTAGGGKFLGILQVKKRQPADEGRQGQAALLALATYSELKNIILVDEDVDIFDSDDILWAMTTR

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FARLEKNQGSAK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532343.1\_2325 [locus\_tag=BN49\_RS13125] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_016532343.1] [location=2393721..2394611] [gbkey=CDS]

MSLRALRHFVVVAEELHMHRAAERLHIAQPALSQQIKQLEQRLGVVLFSRANRRLTLTAAGEAFLHKTRL

ALEMADQAVLDAQRIARGEQGRLHLGYVSSAMYDSKLPGLLRRLRADWPGIELSLVQGDVQMLYEALLDL

RLDIAIIRAPLASPPDALVVRPFVREKLCLALYQQHPLAGVGALNLASLRTDNWISLDDPQGTGLEQVFM

DACRVAGFTSQVAQRINDVTSMISLVSAGVGVALVPLSARALRLDNVVYIDLQDRLAESELSMVYHRHIR

SAVVRKVISLLNTAER

>lcl|NZ\_FO834906.1\_prot\_WP\_046043054.1\_2326 [locus\_tag=BN49\_RS13130] [protein=diguanylate cyclase] [protein\_id=WP\_046043054.1] [location=complement(2394618..2396402)] [gbkey=CDS]

MRIATITNWAYGITVGLTLASGSAMLMASSADRVERQAVQQRQVFDTLSDEVENDAWALSDLARLYVIKP

SPETLTQYQQLQQTDKSIEQRLGGLKDNGASREELALLQDGLRIANELQDEQQAALAHVARGDAPAAIAV

LYGTAYETELERMQTQIDRFRQMLEHRAAVAIDQATERSRIWRTLSEIMVGLTALMFLFVLGFILKRRVL

YPVVRLSDVVQRLASQDYAVETPHFTQVDEIGDMAQAIRIFRENGLARQRLEQQRDADWAVRELLARMTQ

RLQGCETIEDVIKVAERFAPNIAPTIPGKLYVLDTDPWQMRCVAQWLSPAGETTPFSPDDCWAIRRGLSH

PPVQGEPDITCYHLPETHAGQSLCVPLIAQGEAIGLLTFQNVTAGDAPSRAYLELMAEALGLALANQRLR

SALLEKALFDSLTGLRNRHHLDEALHSQMALSVHTHTPLSCLMIDIDHFKTINDRYGHEAGDLVIKSVAT

IVQRAVRDIGMAFRYGGEEFLVLLPGIDEAGAHQCASEIYTQVRNMTLRDGLTEIGQVDVSIGIASYPQH

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>lcl|NZ\_FO834906.1\_prot\_WP\_004140494.1\_2327 [locus\_tag=BN49\_RS13135] [protein=HD domain-containing protein] [protein\_id=WP\_004140494.1] [location=complement(2396476..2397684)] [gbkey=CDS]

MRIALKSALMLTTRVIQIINPELHRHMQRTALIALTLAQRLELPDERQQTIFCAALLHDIGVLGDKRTIH

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PTRAVVEQFVALHREIDPPLCDILCEVAENANFWQHLHPGHIQRLLEIIGPINTRYLDIHGLKDVCLLIA

KIVDTYSSFTATHSIMVGEIARQLARWMQLPEPTCQQIQIAGYLHDIGKVYIPLSILEKEGELDDEELSQ

VREHSYMTGELLSDYSELGDIINWASNHHEKMDGSGYPLHLEKEHLTLADRIISIADIFTALTEDRPYRK

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MNFRALLAIAFLTMSSLAFSETRLPHIVILATGGTIAGSAASNTQTTGYKAGALGVQTLINAVPEMSKIA

HVEGEQVANIGSENMTSDIILQLSKRVNALLARDDVDGVVITHGTDTLDETPYFLNLTVKSNKPVVFTAA

MRPATAISADGPMNLLEAVTVAADPDARGRGVMVVLNDRIGAARFVTKTNATSLDTFRAPEEGYLGVVVG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004148038.1\_2329 [gene=lpxP] [locus\_tag=BN49\_RS13155] [protein=kdo(2)-lipid IV(A) palmitoleoyltransferase] [protein\_id=WP\_004148038.1] [location=2399691..2400605] [gbkey=CDS]

MACVFNKQLLHPRNWLTWFGLGILWLIVQLPYPLLHFIGTSAGRLSRRFLKRREHIARRNIELCFPDMSP

AARETLIDQNFMSLGMGLIETGMAWFWSDERVKKWFDVEGFANLNHALSGGKGVMVVGVHFMSLELGGRA

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MFAEFGVLNYLTYLVGAVFIILVPGPNTFFVLKTGIAHGVKKGYLAAAGVFIGDAVLMFLAFAGVATLIK

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QS

>lcl|NZ\_FO834906.1\_prot\_WP\_004140489.1\_2331 [locus\_tag=BN49\_RS13165] [protein=DUF2534 family protein] [protein\_id=WP\_004140489.1] [location=2401464..2401727] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531462.1\_2332 [locus\_tag=BN49\_RS30425] [protein=hypothetical protein] [protein\_id=WP\_016531462.1] [location=complement(2401787..2401906)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150782.1\_2334 [locus\_tag=BN49\_RS30435] [protein=YoaK family small membrane protein] [protein\_id=WP\_004150782.1] [location=complement(2402098..2402199)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531463.1\_2335 [locus\_tag=BN49\_RS13180] [protein=sensor domain-containing diguanylate cyclase] [protein\_id=WP\_016531463.1] [location=complement(2402257..2403270)] [gbkey=CDS]

MSDFILARVSQTLAAEQSLETLVRQLLEMLEAVTRMESTYLTRIDTNAQRQQIMFAHNSSEMQIPEGFSV

PWDESLCKRALEDQCTFSNDVANRWHSCIAAQELGIATFLSIPVRLADGSLFGTLCATSRQQQPYNLEGE

QVMGLFAKLISHYVEKDTLVQQLQAANVALELHSSTDELTQLPNRRALFKQLALRFASAGAQQQQVSLIF

IDLDGFKAINDRFGHPCGDSFLVQVGKRLTAVARREDIVGRLGGDEFLIVGSAQQPAAQQAYVTSLRQAL

CGVYFLGEQRIDYEGASFGVVTCDPQSIDVEAALRAADEAMYQDKKSRRQENFIHID

>lcl|NZ\_FO834906.1\_prot\_WP\_016531464.1\_2336 [locus\_tag=BN49\_RS13185] [protein=DUF333 domain-containing protein] [protein\_id=WP\_016531464.1] [location=2403571..2403810] [gbkey=CDS]

MKKLLAILPLVLAGCAQPQPTAPTKTIGMPNPAAVYCQQSGGTRVPVQTPQGISTQCKLPSGETLDEWAL

WRRDHPAKS

>lcl|NZ\_FO834906.1\_prot\_WP\_014343000.1\_2337 [locus\_tag=BN49\_RS13190] [protein=DUF488 family protein] [protein\_id=WP\_014343000.1] [location=complement(2403800..2404138)] [gbkey=CDS]

MYDPQESSDGYRVLVDRLWPRGIKKEALACDEWCKELTPSAELRKAFHGEAIDFAHFSQRYRQELDAHRE

TGLRLAALAQRQPLTLLYAAKNTEQNHARVLAAWLAALPVTI

>lcl|NZ\_FO834906.1\_prot\_WP\_004176547.1\_2338 [locus\_tag=BN49\_RS13195] [protein=DUF523 domain-containing protein] [protein\_id=WP\_004176547.1] [location=complement(2404143..2404652)] [gbkey=CDS]

MKNKLLVSACLMGFQVRYNGSEKAQLAATLSRWQQAGRLVIHCPELAAGLPTPRLPAEILGGTGGDVLAG

RARIVESDGRDVTGHYQLAAWLALSAAREAGCQAALLTDGSPTCGSQFVYDGSFRGRRKAGAGVAADLLR

AHGITVFSDGQIPQLLAWMAQKEQDDDSV

>lcl|NZ\_FO834906.1\_prot\_WP\_004140471.1\_2339 [locus\_tag=BN49\_RS13200] [protein=CTP synthase] [protein\_id=WP\_004140471.1] [location=2404798..2405490] [gbkey=CDS]

MKTPLRLALVGDYHPDIVAHQAIPLAIDDAAAVLEQPVKYDWLATPSIASGEALAEYDAIWVVPGSPYRH

PEGAFTAIRYARENSIPFLGTCGGFQHAVIEYARNVLGWQDAGHAETDSEGRMVIAPLSCSLVETSAVVE

LRANTLIARAYGRESIEEGYHCRYGVSSAFAAELEQGDLRVTGWDEEGEIRAVELVTHPFFVATLFQHER

HALDGRPAPLVQAFLRAAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_171819493.1\_2340 [locus\_tag=BN49\_RS13205] [protein=CynX/NimT family MFS transporter] [protein\_id=WP\_171819493.1] [location=complement(2405522..2406697)] [gbkey=CDS]

MISSTGRRPALLIAGILLIATTLRVVFTGAAPLLDTIRSDYGLTTAQTGLLTTLPLLAFGLVSPLAAGVA

RRFGMERSLLLAMLLICAGIALRSLPSAALLFIGTAVIGCGIALGNVLLPGLIKRDFSQHVARMTGAYSL

TMGGAAALGSALVVPVAMAGFGWRGALLLLMVFPLLALLSWLPQSRRRVETPLTGSGAMHNRGIWRSALA

WQVTLFLGINSLVYYVIIGWLPSILQSMGYSEAQAGSLHGLLQLATAAPGLAIPLILHRLRDQRGIAVLV

ALMCAISAAGLWLLPELAIGWTLLFGFGSGATMILGLTFIGLRASSAHQAAALSGMAQSVGYLLAACGPP

LMGRIHDANGDWHIPLLAVALISLVMAVCGALAGRDREIHP

>lcl|NZ\_FO834906.1\_prot\_WP\_004224197.1\_2341 [locus\_tag=BN49\_RS13210] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004224197.1] [location=2406805..2407599] [gbkey=CDS]

MMIGLGLDGYEPDSGHESAIAFRIRVVEAEQFIPAHSHRKGQLILALHGALTCEVENAMWMVPPQYAVWV

PGQLSHSNRATPGAQVCFLFIEPGAAPMPDRCCTLKISPLVRELILTLAERGGESLAAPATARLVQVLFD

ELPRQPQEHLQLPVSNHPKIRQMVTMMAEDPARWQTLSQWAAVFAMSERNLARLVVRETGLSFRRWRHQL

QLILALQLLIRGQTVQQTAQALGYDSTTAFITMFKKGLGQTPGRYHGSLATTSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002901080.1\_2342 [locus\_tag=BN49\_RS13215] [protein=DUF441 domain-containing protein] [protein\_id=WP\_002901080.1] [location=complement(2407583..2408029)] [gbkey=CDS]

MFDTTLLILLGLAALGFISHNTTVAISILVLIIVRVTPLNAFFPWVEKQGLTVGIIILTIGVMAPIASGT

LPPSTLIHSFMNWKSLLAIAVGVFVSWLGGRGVSLMGSQPHLVAGLLVGTVLGVALFRGVPVGPLIAAGI

ISLFIGKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002901088.1\_2343 [locus\_tag=BN49\_RS13220] [protein=YbaK/prolyl-tRNA synthetase associated domain-containing protein] [protein\_id=WP\_002901088.1] [location=complement(2408146..2408646)] [gbkey=CDS]

MLEAVEGNIHQRLCALLDEHRARYRVMAHEAVGQCEAVSAIRGTALGQGAKALVCKVKGNGVNQHVLAIL

AADRQADLASLARHIGGSKASLASPAEVEALTACVFGAIPPFSFHPALRLVADPLLFERFPQIAFNAGRL

DRSIILDTEDYLHIARPEIATFRRLS

>lcl|NZ\_FO834906.1\_prot\_2344 [locus\_tag=BN49\_RS31440] [protein=hypothetical protein] [pseudo=true] [location=complement(2408742..2408898)] [gbkey=CDS]

MHHPNLITAIINILCRPIETERNKKSLIENENHSFFYLQSSSAPAGLHHSTV

>lcl|NZ\_FO834906.1\_prot\_WP\_004198512.1\_2345 [locus\_tag=BN49\_RS13225] [protein=glycosyltransferase family 9 protein] [protein\_id=WP\_004198512.1] [location=2408893..2410029] [gbkey=CDS]

MHDATMQGSPRKKFNKIRELNRRRNYFTKKVRNALRVGVAKALWDRRRRQPVDLSSAKTVLLMRNEGAVG

DVVVDSALVKCLHQSGYIVDFLLTTSNSQVMRYNPRIRHIYEADPVTSADFLRKFNHNVPRDVINELANN

KYDIIIDPSLFDIPVHRLRLFRQIKAKSVLGFNKWPSIKHYSHSFDFDCQRWHVTKTFELIADYLQLDTR

GLDAYDLAVPGPIMQEVAQYLASLSGKAVVINIFAGHADRSLSQTQLAELLDKLLARHPGSAAILLDHRR

EIRIPLPPEVVINPFNTLHHAMALIAQAELIISPDTSVVHMAAAWNKPLIAVYKDVLLNNRLWAPGYDNA

RQIIVKCGKVHQHRGLVDRIIAALPETL

>lcl|NZ\_FO834906.1\_prot\_WP\_002901096.1\_2346 [locus\_tag=BN49\_RS13230] [protein=DinI family protein] [protein\_id=WP\_002901096.1] [location=complement(2410200..2410442)] [gbkey=CDS]

MFVELIYDKRNFAGLPGAREAILNELTKRMQRIFPEAEVRVKPMMTLPAINTDASKHEKELISRTVQEMF

EEADMWLTEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002901192.1\_2347 [locus\_tag=BN49\_RS13235] [protein=translesion error-prone DNA polymerase V autoproteolytic subunit] [protein\_id=WP\_002901192.1] [location=2410713..2411132] [gbkey=CDS]

MNVYTPVELRQIVSFPFFADLVQCGFPSPAQDYVEKRIDLNELLVQHPSATYFVKAAGDSMIDAGIDEGD

LLVVDSARKAEHGDIVIAAVGGEFTVKKLQLLPRVQLNPMNPAYSPIVVGREETLDIFGVVTYIIKAAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004183665.1\_2348 [locus\_tag=BN49\_RS13240] [protein=Y-family DNA polymerase] [protein\_id=WP\_004183665.1] [location=2411135..2412400] [gbkey=CDS]

MFAHCDVNAFYASCQTAFRPDLKGRPVVVLSNNDGCVIARSAEAKPFVKMGEPYFKQKAAFLRHGVVAFS

SNYELYADMSSRVMATLEELTPRCEIYSIDEAFCDVSGVRHCRDLTDFGREIRATVLQRTHLTLGVGIAP

TKTLAKLANHAAKQWPRQTGGVVDLSCPQRQRKLMALLPVSEVWGIGRRIGKKLEAMGIGTVLQLAESDI

RFIRKHFTVVLERTVRELRGEPCLALEEFAPAKQEIICSRSFGDRITAYEDMRQAICSYAARAAEKLRGE

HQYCRFVSAFVKTSPFALNEPYYGNSASLKLLTPTQDSRDIIAAATSCLDAIWKAGHRYQKAGVMLGDFY

SQGVAQLNLFDELAPRHNSARLMQVLDQLNAKNGRGALYFAGQGIQQQWQMKREMLSPRYTTRYGDLLRV

R

>lcl|NZ\_FO834906.1\_prot\_WP\_023312958.1\_2349 [locus\_tag=BN49\_RS13245] [protein=LysR family transcriptional regulator] [protein\_id=WP\_023312958.1] [location=complement(2412407..2413312)] [gbkey=CDS]

MDRFSALKAFTRVVEAGSFTRAADSLNMPNATLSKTIQQLEAHLGVSLLQRTTRRITVTPEGREYYEKAR

CLLEDLEEIDASFNTARNKPKGHLRIAIGGSTACDVLIPLLADFMTSWPDIRIDLQVADKPADLISGNID

CAIRGGPMEDSTLIARKIGEAALVTCATPGYLQRYGTPASPDELHHGHRLISYLSPASGRAFPFRFTRHG

VSTELKTEPHLGINESNAHIAAGEAGLGIVQTFTYSLKPALASGELVEILSAWRPAPYPFHVVYARHRHV

PPRLRVFIDWLAAVFPAAVQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002901225.1\_2350 [locus\_tag=BN49\_RS13250] [protein=SDR family oxidoreductase] [protein\_id=WP\_002901225.1] [location=2413479..2414228] [gbkey=CDS]

MSKKLADKVALVTGGSAGIGLASAKALAEQGAKVYITGRRQEELDAAVRFIGPAARGIRADAAVLSDLDA

VFATIAEESGRLDVLFANAGGGDMLPLSAITEAHVDRIFATNVRGVVFTVQKALPLLADGASVILTGSTA

AVKGTANFSIYSASKAAVRSLARSWALEVSDRGIRINVVSPGPVRTPGLGGLVAEADRQGLFDALAAGVP

LGRLGEPEEIGRTVVFLASDESSFINAAEIYVDGGLAQI

>lcl|NZ\_FO834906.1\_prot\_WP\_016529622.1\_2351 [locus\_tag=BN49\_RS13255] [protein=MFS transporter] [protein\_id=WP\_016529622.1] [location=complement(2414225..2415442)] [gbkey=CDS]

MKEIALPLHPAPARVWIAVVALGICAFSIVTSELAPVGMLNALAADFHQTESGVGLAVTAYGWVGALAAL

LSGAMPARISRKALLVGLMLILAFSCLAATRSYSMFALMSARMVGALAHGAFWALIGLVAAQLVPPHRLG

LATAIIFGGVSAASVVGVPLASFIATLAGWRLAFMSMALLSLAAAAVLCSTLPPLAAPAPVRLRVYRDIF

RNPLLGGLYGATACIITAHFAAFTYIEPLLINLQGVPATALSGLLLLSGVSGLLGNVIAGKLIDRHLKGL

IFAALLLSGGALALLGAARLAPLPFCFSGLLLALWGAGIAIVFVGLQTWLLRSAGAVAQPASAIYVAIFN

AAIGTGAFVGGQLIASAGLSEMVWLAAGIMVGSTLLIALLKAPLPGQIGAATAGA

>lcl|NZ\_FO834906.1\_prot\_WP\_009309126.1\_2352 [locus\_tag=BN49\_RS13260] [protein=LysR family transcriptional regulator] [protein\_id=WP\_009309126.1] [location=2415618..2416499] [gbkey=CDS]

MTAEFHWDDARIFLAIARAGTLSGAADKMNMGIATVSRRLDRLEQALNVPLFSRHQSGYRLTDDGEALLA

RAEALEYAGLAFGEAAQLQGHVAGVVRLATSDNLATHFILPSLKGLLDHYPELRVEVLSGVQPVNLHRRD

ADLAIRMVKPEAGHLTLKRLGTVGFGVYGAADCLAGADGLSLSEADFVGWPETHQHLPAAQWITRTLRGR

PCKVEANTLVAQVSAVSAGLGLGVLPHFMARASGLQCLQPEIGADQTLWLVMHSDLAGSRRVRVLADHLI

ALFADHQDRLAMP

>lcl|NZ\_FO834906.1\_prot\_WP\_004220356.1\_2353 [locus\_tag=BN49\_RS31015] [protein=hypothetical protein] [protein\_id=WP\_004220356.1] [location=complement(2416570..2416689)] [gbkey=CDS]

MPRWQQHKIILPDGDILSLCSISDCGAALGRILRGEYHC

>lcl|NZ\_FO834906.1\_prot\_WP\_004140435.1\_2354 [locus\_tag=BN49\_RS13270] [protein=hypothetical protein] [protein\_id=WP\_004140435.1] [location=2416757..2417068] [gbkey=CDS]

MIVRTWHGCVPLQHAEGFARHLERTGVEHAQSIAGNRGALVRQENQGEWAHFFLATYWQDLAAVKAFAGE

DYHVAVTYPDDEAFELLSDPYVFQHEVEAVSPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529621.1\_2355 [locus\_tag=BN49\_RS13275] [protein=glutathione peroxidase] [protein\_id=WP\_016529621.1] [location=complement(2417190..2417672)] [gbkey=CDS]

MTPFYQLTATRLRGQPLSMADYAGKVVLVVNTASHCGFTPQYAGLEALYKKYAAQGLVVLGFPCNQFGKQ

EPGGADEIEQTCHVNYGVSFPMFEKVDVNGPAAHPLFRYLKQALPGVLGGRIKWNFTKFLIGRDGTPLTR

FAPFTTPEKMEASIVAALTC

>lcl|NZ\_FO834906.1\_prot\_WP\_004190861.1\_2356 [locus\_tag=BN49\_RS13280] [protein=hypothetical protein] [protein\_id=WP\_004190861.1] [location=2417831..2418394] [gbkey=CDS]

MMKYVLSLVVVAILAGCTSTPNLPPRDTIVAMKPTESGIVASSAKYSYRFVRDGVPQEYQRYKTFYERFH

QQASGVRVNFVVVQHEVTAEYLVVMDQRKLDAGQHSELVNQYHAVQIDNDRLGVLFKATGFWTASDASDL

AAAYQLAHPVVVSINDKTKTISSLGAVALAPLFPFYMMYGCATGPCV

>lcl|NZ\_FO834906.1\_prot\_WP\_004152363.1\_2357 [locus\_tag=BN49\_RS13285] [protein=YeaH/YhbH family protein] [protein\_id=WP\_004152363.1] [location=complement(2418440..2419723)] [gbkey=CDS]

MTWFIDRRLNGKNKSAVNRQRFLRRYKAQIKQSISEAINKRSVTDIESGESVSIPTDDINEPMFHQGRGG

LRNRVHPGNDHFVQNDRIERPQGGGGGGGSGQGQASADGEGKDEFVFQISKDEYLDLLFEDLALPNLKKN

QHRQLNEFKTHRAGFTSNGVPANISVVRSLQNSLARRTAMTAGKRRELRALEEDLEAISRSEPVQLLEEE

RLRKEIAELRAKIERVPFIDTFDLRYKNYEKRPEPSSQAVMFCLMDVSGSMDQATKDMAKRFYILLYLFL

SRTYKNVDVVYIRHHTQAKEVDEHEFFYSQETGGTIVSSALKLMDEVVQARYDPAQWNIYAAQASDGDNW

ADDSPLCHELLAKKILPVVRYYSYIEITRRAHQTLWREYEHLQATFDNFAMQHIRDQEDIYPVFRELFHK

QSSKSEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002901234.1\_2358 [gene=yeaG] [locus\_tag=BN49\_RS13290] [protein=protein kinase YeaG] [protein\_id=WP\_002901234.1] [location=complement(2419809..2421743)] [gbkey=CDS]

MNIFDHYRQRYEAAKDEEFTLQEFLTICRQDRSAYANAAERLLMAIGEPVMVDTALEPRLSRLFSNRVIA

RYPAFEEFYGMEDAIEQIVSYLKHAAQGLEEKKQILYLLGPVGGGKSSLAERLKALMQRVPIYVLSANGE

RSPVNDHPLCLFNPQEDAQILQKEYGIPTRYLGTIMSPWAAKRLHEFGGDITKFRVVKVWPSILEQVAIA

KTEPGDENNQDISALVGKVDIRKLEHYAQNDPDAYGYSGALCRANQGIMEFVEMFKAPIKVLHPLLTATQ

EGNYNGTEGISALPFNGIILAHSNESEWVTFRNNKNNEAFLDRVYIVKVPYCLRISEEIRIYEKLLNNSE

LTHAPCAPGTLETLARFSILSRLKEPENSSIYSKMRVYDGESLKDTDPKAKSYQEYRDYAGVDEGMNGLS

TRFAFKILSRVFNFDHVEVAANPVHLFYVLEQQIEREQFPQEQAERYLEFLKGYLIPKYAEFIGKEIQTA

YLESYSEYGQNIFDRYVTYADFWIQDQEYRDPDTGQLFDRESLNAELEKIEKPAGISNPKDFRNEIVNFV

LRARANNSGRNPNWTSYEKLRTVIEKKMFSNTEELLPVISFNAKTSTDEQKKHDDFVDRMMEKGYTRKQV

RLLCEWYLRVRKSS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043065.1\_2359 [locus\_tag=BN49\_RS13295] [protein=MipA/OmpV family protein] [protein\_id=WP\_046043065.1] [location=2422160..2422906] [gbkey=CDS]

MTKIKLLALGVLIATSASAAHADGKFTLGAGVGVVEHPYKQYDADVYPVPVISYESENFWFHGLGGGYYL

WNDTNDKLSITAYWSPMYFKPGDSDSEQMRRLDKRKSTVMAGLSYVHNTPYGFLRTTIAGDTLDNSNGIN

WDLAWLYRYTNGNLTLTPGIGVEWNSDNQNEYYYGVSQHESRRSGMRSYDPDSSWNPYLELSANYRFLGD

WSVYGVARYTRLSDEITDSPMVDKSWSGLISTGITYTF

>lcl|NZ\_FO834906.1\_prot\_WP\_004176538.1\_2360 [locus\_tag=BN49\_RS13300] [protein=aldo/keto reductase] [protein\_id=WP\_004176538.1] [location=2422998..2423852] [gbkey=CDS]

MVKKTVRFGEQAAVPAIGLGTWYMGEHAAQRQQEVAALRAGIDHGLTVIDTAEMYADGGAEEVVGQAIRG

LRDRVVLVSKVYPWHAGKAAMHRACENSLRRLQTDYLDMYLLHWRGDIPLQETVEAMEKLVAEGKIRRWG

VSNLDTEDMQALWRTADGEHCATNQVLYHLASRGIEYDLLPWCQQHSLPVMAYCPLAQAGRLRDGLFQHS

DIINMANARGITVAQLLLAWVIRHPGVLAIPKAASIEHVVQNAAALDIVLSGEELAQLDRLYPPPQRKTR

LDMV

>lcl|NZ\_FO834906.1\_prot\_WP\_002901240.1\_2361 [locus\_tag=BN49\_RS13305] [protein=D-hexose-6-phosphate mutarotase] [protein\_id=WP\_002901240.1] [location=complement(2423909..2424793)] [gbkey=CDS]

MINKIFALPVNETISPVISRRQLDDLELIVIDHPQVKASVALQGAHLLSWKPAGEEEVLWLSNNTPFKQG

VALRGGVPICWPWFGPSAQQGLPSHGFARNLPWTLEGHDEDDSGVMLTFALQHSAETMKLWPHEFTLYAR

FKLGKTCEIELEAHGEFETTSALHSYFNVGDIAAVKVSGLGERYIDKVNNAEEGVLSNGVQTFPDRTDRV

YLNADSCSVIHDDALNRTIDVVHHHQHNVVAWNPGPALSVSMGDMPDDGYKTFVCVETCCVTQPQKASEE

TPSRLAQTISVKKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002901243.1\_2362 [gene=gapA] [locus\_tag=BN49\_RS13310] [protein=glyceraldehyde-3-phosphate dehydrogenase] [protein\_id=WP\_002901243.1] [location=complement(2424868..2425863)] [gbkey=CDS]

MTIKVGINGFGRIGRIVFRAAQKRSDIEIVAINDLLDAEYMAYMLKYDSTHGRFDGTVEVKDGHLVVNGK

KIRVTAERDPANLKWDEVGVDVVAEATGIFLTDETARKHITAGAKKVVLTGPSKDNTPMFVRGANFDAYA

GQDIVSNASCTTNCLAPLAKVINDNFGIVEGLMTTVHATTATQKTVDGPSHKDWRGGRGAAQNIIPSSTG

AAKAVGKVLPELNGKLTGMAFRVPTPNVSVVDLTVRLEKAASYEEIKKAIKAASEGAMKGVLGYTEDDVV

STDFNGEVCTSVFDAKAGIALNDNFVKLVSWYDNETGYSNKVLDLIAHISK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901246.1\_2363 [gene=msrB] [locus\_tag=BN49\_RS13315] [protein=peptide-methionine (R)-S-oxide reductase MsrB] [protein\_id=WP\_002901246.1] [location=2426202..2426615] [gbkey=CDS]

MANKPTPEELKNGLSEMQFYVTQHHGTEPPFTGRLLHNKKNGVYHCLVCDAPLFNSQTKYDSGCGWPSFY

EPVSAEAIRYLTDNSHGMQRIEIRCGNCDAHLGHVFPDGPQPTGERYCVNSASLSFTDEQNGEQIKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002901249.1\_2364 [locus\_tag=BN49\_RS13320] [protein=YeaC family protein] [protein\_id=WP\_002901249.1] [location=2426659..2426937] [gbkey=CDS]

MDIEQIIDSMTPEVYQRLATAVELGKWPDGVALTPEQKENSLQLVMLWQARYNTDAQHMTIDTSGQMVMK

SKQQLKEDFGIVPKPIATVKLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002901254.1\_2365 [gene=yajD] [locus\_tag=BN49\_RS13325] [protein=HNH nuclease YajD] [protein\_id=WP\_002901254.1] [location=complement(2427032..2427376)] [gbkey=CDS]

MAYIPKNYARLEVGYREKALKLFPWVCGRCSREFVYSNLRELTVHHIDHDHSNNPEDGSNWEMLCLYCHD

HEHSKYTEADQYGSTVVAGEDAQKSVGEATYNPFADLKAMMNKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901255.1\_2366 [locus\_tag=BN49\_RS13330] [protein=glycoside hydrolase family 18 protein] [protein\_id=WP\_002901255.1] [location=complement(2427537..2428790)] [gbkey=CDS]

MKRLPLLAALPLLCASALSAQPLMSVGYFNGGGDVTAGPGGDIDKLDVRQITHLNYSFGLIYNDEKDETN

AALKDPAHLHEIWLSPKVQADLQKLPALRKQNPDLKVLLSVGGWGARGFSGAAATAESRAVFIRSAQKII

QQYGLDGIDLDWEFPVNGAWGLVASQPADRDNFTALLKSLREAVGEQKLVTIAVGANAESPKSWVDVKAV

APVLNYINLMTYDMAYGTQYFNSNLYDSSHWPTVAAADKYSADFVVNNYLAAGLKPSQMNLGIGFYGRVP

KRAVEPGIDWTKADAQNNPVTQPYFGPQQIALFASLGYDLSKDTYVKYNDIVGKLLNDPQKRFTEHWDDE

AKVPWLSVQSAEGKPLFALSYENPRSVAIKADYIKAKGLAGAMFWEYGADDQNQLARQLAESLGIKH

>lcl|NZ\_FO834906.1\_prot\_WP\_004140413.1\_2367 [gene=pncA] [locus\_tag=BN49\_RS13335] [protein=bifunctional nicotinamidase/pyrazinamidase] [protein\_id=WP\_004140413.1] [location=complement(2428961..2429602)] [gbkey=CDS]

MAHRALLLVDLQNDFCAGGALAVPEGDSTVEVANALIDWSLARGEPIVASQDWHPADHGSFASQHQVEPY

TEGELDGLAQTFWPDHCVQHSEGAALHPLLKQQAIAAVFHKGQNRIIDSYSAFFDNGHRQKTELDGWLRG

QGIVELTVLGLATDYCVKFTVLDALALGYAVNVITDGCRGVNLQPQDSSQAFMEMAAAGATLYTLDDWRE

TQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176535.1\_2368 [gene=ansA] [locus\_tag=BN49\_RS13340] [protein=asparaginase] [protein\_id=WP\_004176535.1] [location=complement(2429612..2430631)] [gbkey=CDS]

MQKKSIYVAYTGGTIGMQRSEHGYVPVSGHLQRQLALMPEFHRPEMPDFTIHEYHPLMDSSDMTPEDWQH

IADDIRSHYEEYDGFVILHGTDTMAFTASALSFMLENLGKPVIVTGSQIPLAELRSDGQINLLNALYVAA

NYPINEVALFFNNRLFRGNRTTKAHADGFDAFASPNLAPLLEAGIHIRRLGTPPAPQGSGELIVHPITPQ

PIGVVTIYPGISADVVRNFLRQPVKALILRSYGVGNAPQNGEFIQVLAEASQRGIVVVNLTQCMSGKVNM

GGYATGNALAQAGVISGFDMTVEATLTKLHYLLSQQLDVDAIRAAMQQNLRGELTPDEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043069.1\_2369 [gene=sppA] [locus\_tag=BN49\_RS13345] [protein=signal peptide peptidase SppA] [protein\_id=WP\_046043069.1] [location=complement(2430770..2432623)] [gbkey=CDS]

MRTLWRLIASFFKWTWRILNFIRKLALNAIFLVLVLVCIGIWSQFSSTTSEHAARGALLLDITGVVVDKP

SASSKLGVIGRQLFGASSDRLQENSLFDIVQTIRQAKDDRNITGIVLDLKNFVGGDQPSMQYIGKALREF

RDSGKPVYAVGSSYSQGQYYLASFANKIWLSPQGEVDLHGFATNGLYYKSLLDKLKVSTHVFRVGTYKSA

VEPFIRDDMSPAAREADSRWIGELWQNYLNTIAANRQITAQQLFPGAQGIIDGLRKVGGDTAKYALDNKL

VDELATSTEVEKALTKQFGWSKADNNYRAISYYDYNVKTPSDQGSAIAVIFANGAIMDGEETPGNVGGDT

TAAQIRDARLDPKIKAIVLRVNSPGGSVTASEIIREELAAAKAAGKPVVVSMGGMAASGGYWISTPADYI

VANPSTLTGSIGIFGVINTMENTLRSIGVHTDGVATSPLADVSSTKALPPEVQQLMQLSIENGYQRFITL

VANARKSTPEKIDQIAQGHVWTGEDAKANGLVDSLGDFDDAVAKAAELAKLKTWHLNYYQEEPTFFSMML

DSLTGSVRASLPAAIQAWLPAPVAAAAETVKAESDKLAAFNDPQNRYAFCLTCANIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176531.1\_2370 [locus\_tag=BN49\_RS13350] [protein=NAD(P)H nitroreductase] [protein\_id=WP\_004176531.1] [location=2432789..2433340] [gbkey=CDS]

MDALDLLLNRRSASRLAEPAPAGEQLENILRAGLRAPDHGTLQPWRFFIIADDGRERFSQLLEKGAREAG

QDEKGIEKARNAPFRAPLIITVVARCEDHPKVPRWEQEMSAGCAVMAMQMAALAQGFNGIWRSGALTESP

VVRAGFECREQDKIVGFLYLGTPQLKASTTIALPDTAPFVTRF

>lcl|NZ\_FO834906.1\_prot\_WP\_085955203.1\_2371 [locus\_tag=BN49\_RS30440] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_085955203.1] [location=complement(join(2433460..2434355,2434355..2434823))] [gbkey=CDS]

MAKPKYSPETKLAVVNHYLSGKDGEQSTADLFGIERTSVRRWVRAWQFHGAEGLTAKNNHYSDEFKLVVV

RAVISDRLTMREAAARFNLSAEILVRRWLDVYNDAGAEGLLNMQCGRPGQMTKPKNIPPLTDKELEKLSP

EELRAELRYLRAENAYPKKVESLGSERKKWQKALIISELRHEHALRDLLRAAGMSRSTWYYNMNALKQGD

RYAGLKENIRKIYHYHKGRYGYRRITLALRKQGLRINHKTVQRLMAELSLRSVIRAKKYRAWKGRTGEAA

PNILSRNFGASKANEKWVTDVTEFPVQGKKLYLSSVLDLFNREVIAYSLSERPVMEMVNTMLDGAFPKLR

PGDAPLLHSDQGWHYRMRSYQERLKAHGMTQSMSRKGNCLDNAVMENFFGTLKSECFYLREFRSVSALRK

AVEDYIHYYNNERISLKLKGLSPVEYRTQALRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002901387.1\_2372 [locus\_tag=BN49\_RS13365] [protein=phosphatase PAP2 family protein] [protein\_id=WP\_002901387.1] [location=complement(2435525..2436271)] [gbkey=CDS]

MKKRVLALCLASFFSVNAFALVPPGNDVTTKPDLYYLTNAQAIDSLALLPPPPAVGSIAFLNDQAMYEQG

RLLRNTERGKLAAEDANLSAGGVANAFSSAFGSPITEKDAPQLHKLLTNMIEDAGDLATRSAKEKYMRIR

PFAFYGVSTCNTTEQDKLAKNGSYPSGHTSIGWATALVLAEINPQRQNEILKRGYELGESRVICGYHWQS

DVDAARIVGSAVVATLHTNPAFQQQLQKAKDEFAKRQK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176528.1\_2373 [gene=selD] [locus\_tag=BN49\_RS13370] [protein=selenide, water dikinase SelD] [protein\_id=WP\_004176528.1] [location=2436497..2437540] [gbkey=CDS]

MSEQAIRLTQYSHGAGCGCKISPKVLETILHSEQAKFVDPNLLVGNETSDDAAVYDLGNGTSIVSTTDFF

MPIVDNPFDFGRIAATNAISDIFAMGGKPIMAIAILGWPINTLAPEIAREVVEGGRFACQQAGIALAGGH

SIDAPEPIFGLAVTGVVPTERIKKNSTAQAGCKLYLTKPLGIGVLTTAEKKSLLKPEHQGLATETMCQMN

LAGAAFAAIDGVKAMTDVTGFGLLGHLSEVCRGAGVQAQLRYADIPKLPGVEDYIAAGAVPGGTGRNFAS

YGHLMGEMPTEWRDLLCDPQTSGGLLLAVTPEAEAEVQAAAAEFGIKLAAIGELVTARGGRPMIEIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004148065.1\_2374 [locus\_tag=BN49\_RS13375] [protein=DNA topoisomerase III] [protein\_id=WP\_004148065.1] [location=2437545..2439491] [gbkey=CDS]

MRLFIAEKPSLGRAIADVLPKPHRKGDGYIECGNGQVVTWCIGHLLEQAQPDIYDSRYARWNLNDLPIVP

EKWQLQPKPSVTKQLNVIKRLLGDAEEVIHAGDPDREGQLLVDEVLDYLQLAPEKRQQVQRCLINDLNPQ

AVERAINRLRANSEFVPLCVSALARARADWLYGINMTRAYTLLGRNAGYQGVLSVGRVQTPVLGLVVRRD

EEIENFVAKDFFDVKAHIVTPQEERFVATWVPSEACEPYQDEEGRLLHRPLAEHVVKRIEGQPAIVTGYN

DKRDSEPAPLPFSLSALQIEAAKRFGFSAQNVLDICQKLYETHKLITYPRSDSRYLPEEHFAGRHAVLNA

IAVHAADLLPQPVVDPEIRNRCWDDKKVDAHHAIIPTARSSQVKLTDNEAKVYTLIARQYLMQFCPDAVF

RKCQIDLEIANGKFVAKARFLAEAGWRTLLGSKERDEENDGTPLPVVAKGDELLCERGEVVERQTQPPRH

FTDATLLSAMTGIARFVQDKDLKKILRATDGLGTEATRAGIIELLFKRGFLSKKGRYIHSSEAGRALIHS

LPEMAGRPDMTAHWESVLTQISEKQCRYQDFMQPLVGTLYQLIDQARSTPVRQFRGLVAPGGAKKSFSKG

KGKPKGKKAADDTAPPPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016532564.1\_2375 [locus\_tag=BN49\_RS13380] [protein=NAD(P)H-quinone oxidoreductase] [protein\_id=WP\_016532564.1] [location=2439671..2440651] [gbkey=CDS]

MKYIAISQPGGPEVLQIREGEIPTIGEHEVLIEVKAAGVNRPDILQRQGLYPMPEGVTPVPGLEVAGVVL

KVGAQVTAFTPGDRVCALTNGGGYAEYCAVPAGQTLPIPAGLSFSEAAAIPETFFTVWANVFQLGKLQPG

ESILVHGGASGIGTTAVQLCHALGMTVYATVGQDEKIVALRPYATAINYKTDDFAEKIGQLTNDEGVDVI

LDIVGGPYFNRNLGLLKKDGRLVIIGFMGGRIAHEVDIQTLMLKRATVTGSTMRGRTPAEKQQIAEALRR

HVWPLLEAGKCKPLIYASYPMAEIAEAHACLDSGQHLGKVVITMTS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176526.1\_2376 [gene=gdhA] [locus\_tag=BN49\_RS13385] [protein=NADP-specific glutamate dehydrogenase] [protein\_id=WP\_004176526.1] [location=complement(2440695..2442038)] [gbkey=CDS]

MDQTCTLEGFLTRVQQRDPHQTEFAQAVREVMTTLWPFLEENPRYRQLALLERLVEPERVIQFRVVWVDD

RNQVQVNRAWRVQFNSAIGPYKGGMRFHPSVNLSILKFLGFEQTFKNALTTLPMGGGKGGSDFDPKGKSD

GEVMRFCQALMTELYRHLGPDTDVPAGDIGVGGREVGFMAGMMRKLSNNSACVFTGKGLSFGGSLIRPEA

TGYGLIYFTEAMLKRHGLGFEGARVAVSGSGNVAQYAIEKAMELGARVVTASDSNGTVVDEAGFTKEKLA

RLIDIKERAHGRVADYAREFGLTYLEGQQPWSVPVDIALPCATQNELDVDAARQLIANGVKAVAEGANMP

TTIAATDLFLEAGVLFAPGKAANAGGVATSGLEMAQNAARMGWKAEKVDARLHHIMLDIHHACVQYGGEA

KQTNYVRGANIAGFVKVADAMLAQGVI

>lcl|NZ\_FO834906.1\_prot\_WP\_004176525.1\_2377 [locus\_tag=BN49\_RS13395] [protein=pyrimidine (deoxy)nucleoside triphosphate diphosphatase] [protein\_id=WP\_004176525.1] [location=complement(2442221..2442631)] [gbkey=CDS]

MLKMIDVVAAIIEQDGQILLAQRPPHADQPGMWEFAGGKVEPGESQPQALARELQEEMGIIARPACYIAS

HQREVSGRRIHLHAWWVPHFQGTPLAHYHTQLRWCLPTEALALDLAPADIPLLHAFIAQRPTLSVR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532561.1\_2378 [locus\_tag=BN49\_RS13400] [protein=CDP-alcohol phosphatidyltransferase family protein] [protein\_id=WP\_016532561.1] [location=2442718..2443341] [gbkey=CDS]

MLDSHLHPRLKPLLNAVAGALDRPGISPDGLTLVGFSIGVLALPFLALGWYGAALAAILLNRLLDGLDGA

LARRRGLTDAGGFLDIALDFLFYALVPFGFILADPLNNALAGGWLLFAFIGTGSSFLAFAALAARHQIAN

PGYAHKSLYYLGGLTEGTETILLFFLGCLFPAHFAWLAWLFGALCWLTTATRICSGYQTLKRVTTTA

>lcl|NZ\_FO834906.1\_prot\_2379 [locus\_tag=BN49\_RS13405] [protein=sulfurtransferase] [pseudo=true] [location=complement(2443393..2444672)] [gbkey=CDS]

MKRVSQLTALALLMGLAASTTCAAETMPALTLSHLQQQHGVAIDTRLSAYYNGWPQRANGPEGHEPQALN

LSARWLGAMSDDQLRAWAKQHQLQSDTPIALYGSPEDNVSVAARLKQTGFTRLSTLSDALSQTDRLQKLP

HFEQLVYPQWLHDLQQGTGKCLKPPGERRSSIC\*AISLARAISIPMRWRANRCGIKCPTRS\*RRCWRSTA

SGMTPR\*SSMVATSTPQRGWRRSCCTPGSKTCACLTAAGRPGPTPGCR\*SAACRRRSSRRLISARRSPAS

RS\*CWIPNKPAGCCIVRTPRWSASAHGRSLSAPPAATAISSRRATSLAPAGATPGATPRTWRISITRTAP

CAALTISLPCGASGTFCQASKWRSIAGPAGGPRKPLCMPAPWAGRTSRCTTAAGTNGAATRTIRWPAESA

ARKAVS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043073.1\_2380 [locus\_tag=BN49\_RS13410] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_046043073.1] [location=complement(2444766..2445398)] [gbkey=CDS]

MLTVSYLTLSVRRQPLLREVAFSVAPGEVLTLMGPSGSGKSTLFAWMIGALSGDFRARGELWLNERRCDT

LPTEHRRIGILFQDPLLFDHFSVGQNLQLALPENVRVEARKAAVEEALSRAGLAGFAPRDPATLSGGQRA

RVSLLRALLARPEALLLDEPFSRLDASLRAGFRRWVFEELARQAIPAILVTHDREDCPPTGRCLAMERWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043075.1\_2381 [locus\_tag=BN49\_RS13415] [protein=ABC transporter permease subunit] [protein\_id=WP\_046043075.1] [location=complement(2445398..2446933)] [gbkey=CDS]

MAAPLRYPLILLAWGAMAAIYLPLLPAAGELVGAARSPAHWRALFADPQLSQALAATLVSTLLSVGGALL

IALTIVAALWPSARWRRLASRLPLLLAVPHLALATAALLLFAEGGWLWQRLPFLTPPVDRYGIGLGLTMA

LKESAFVLWVIYGLLGEKRLADQATALKSLGYGRWQCLRWLVLPALLPALGMVLLATTAWSLSAVDVALV

LGPGNPPTLAVLAWQWLSQGDELQQAKGALASLLLMAILGGLALVAWGGWRLQRQYQPDLHGVRHPHPHA

LPGRLLEALLPLSGLLGALLLAGLARSAPPQMDALGNSLGLALAACALGAAVCLLWLACGPARGDGWVWL

PLVLPALPLADGQYRLALYAWLDGDWWTVLWGHLLWVVPWMLFILRPAWRQRDPRLTVVARTLGWGSTRI

FWLLTLPSLTRPLLTALAVGFSVSIAQYLPTLWLGAGRIPTLTSQAVALSSGGEAQTLAAQALWQLLLPA

VCFTLTALLAWLAGRYRRGLR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043077.1\_2382 [locus\_tag=BN49\_RS13420] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_046043077.1] [location=complement(2446906..2448084)] [gbkey=CDS]

MRRLRDYSLCLCLLLLWPLAVNADDSWRQIQTEARGQTVWFNAWGGDPAVNRYLAWVSEEVKRYYAIDLR

IVPVADAADAVKRIQTEAQAGRRQGGSVDLLWINGENFRTLKQANLLLTGWAEALPNWRYVDLQKPVRED

FSVATEGAESPWGSAQLTFIARRGQTPQPPTSPQALLAFARAHPGSVTYPRPPDFTGTALLEQLLIALTD

QPAALRQPPQPATFAAVTAPLWRYLDALHPALWRAGKDFPASPERMDAMLNQGTFRLSLTFNPLHARQKA

ASGELPTDSYSFGFTAGTLGNVHFVTIPANARAVAGAKVVANFLLSPEAQLRKADAAVWGDPSVLDPQRL

PDGQRQALAAALPQDLPPVLAEPHAAWVDALEQEWLRRYGTH

>lcl|NZ\_FO834906.1\_prot\_WP\_004176519.1\_2383 [locus\_tag=BN49\_RS13425] [protein=carboxymuconolactone decarboxylase family protein] [protein\_id=WP\_004176519.1] [location=complement(2448087..2448647)] [gbkey=CDS]

MSLPPLDSVPLILRPQAWLHRRHYGQVLSPIRWWGRIPWLFYLVSLFVGYIERRRSPLDPVLRSLVSARI

AQLCHCEFCIDITSMTLAARSGSQDKLLAVADWRSSTLFSEKERLALAYAEAATQTPPAVDDALRSAMAA

HFDARALTELTALIGLQNLSARFNAAMAIPAQGLCQIPTSSSQNKE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043079.1\_2384 [locus\_tag=BN49\_RS13430] [protein=TVP38/TMEM64 family protein] [protein\_id=WP\_046043079.1] [location=complement(2448644..2449354)] [gbkey=CDS]

MTQPDRRHLRRARLALAVVVAAALAAWLWLPGGRTFLQQSLTALASLDPQQVRGFIAAWGPQAALVSFAL

MILQAIVAPLPAFLITLANAALFGAFWGGALSWFSAMAGAGLCFCIARALGREVVEKLTGRAVLRSADGY

FTRFGPQTILVCRLLPFVPFDPVSYAAGLTSLRFWPFMLATGVGQLPATIVYSWAGSLLTGGTFWLATGL

SLLFALAVVISIAKNIYRERHKRSSP

>lcl|NZ\_FO834906.1\_prot\_WP\_004140389.1\_2385 [locus\_tag=BN49\_RS13435] [protein=TVP38/TMEM64 family protein] [protein\_id=WP\_004140389.1] [location=complement(2449341..2449997)] [gbkey=CDS]

MATLAVISHRVGLHDLLTHLHLLQDTLRHQGAWGYLVYAALFIIATLCLIPGSLLVIAGGMLFGPLTGSL

LSFAAATLASSLSFLIARWLGRDLLQRYVGHTTVFQAIERGIARSGCDFLILTRLVPLFPYNIQNYAYGL

TAIRFWPFTLISAVTTLPGLVIYSVMASELAREGVTLAFALKLSLAGGLLFALVQIGKRFARARRVAACS

EEVRHDPT

>lcl|NZ\_FO834906.1\_prot\_WP\_002901486.1\_2386 [gene=xthA] [locus\_tag=BN49\_RS13440] [protein=exodeoxyribonuclease III] [protein\_id=WP\_002901486.1] [location=complement(2450211..2451017)] [gbkey=CDS]

MKFVSFNINGLRARPHQLAAIVEKHQPDVIGLQETKVHDDMFPLEEVARLGYNVFYHGQKGHYGVALLTK

ETPIAVRRGFPDDGEEAQRRIIMAEIPSPFGNVTVINGYFPQGESRDHETKFPAKAAFYQNLQNYLETEL

NKENPVLIMGDMNISPTDLDIGIGEENRKRWLRTGKCSFLPEEREWMDRLLGWGLVDTWRQANPDNHEHF

SWFDYRSKGFDDNRGLRIDLLLASQPLAQRCVETGIDYEIRGMEKPSDHAPVWATFRP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043081.1\_2387 [locus\_tag=BN49\_RS13445] [protein=aspartate aminotransferase family protein] [protein\_id=WP\_046043081.1] [location=2451456..2452676] [gbkey=CDS]

MSQSITRNHFDEWMMPVYAPAAFIPVRGAGSRLWDQQGKEYIDFAGGIAVNALGHAHPRLVQALTDQAGK

FWHTGNGYTNEPILRLAKMLIDATFADRVFFCNSGAEANEAALKLARKYAHDRFGSEKSGIVAFQNAFHG

RTLFTVSAGGQPAYSRDFAPLPPQIQHAVFNDLESAKALINDQTCAVIVEPVQGEGGVVPASVEFLRGLR

QLCDQHNALLIFDEVQTGVGRTGELYAYMHYGVTPDVLTTAKALGGGFPIGALLATEACASVMTVGTHGT

TYGGNPLAGAVAGELLSIINTPEVLSGVRQRHQWFCERLQAINARYGLFKEIRGLGLLLGCVLNDAWAGK

AKTLSNLAAEEGVMILIAGANVVRFAPALNVSEEEVNSGLDRVERACARFVAGVSS

>lcl|NZ\_FO834906.1\_prot\_WP\_016531407.1\_2388 [gene=astA] [locus\_tag=BN49\_RS13450] [protein=arginine N-succinyltransferase] [protein\_id=WP\_016531407.1] [location=2452673..2453707] [gbkey=CDS]

MMVIRPVEPGDLPGLLKLAAETGGGLTSLPVDEATLAARIARSQQTWRGELPKSEQGYVFVLEESESGAV

VGICAIEVAVGLNDPWYNYRVGTQVHASKELNVYQALPTLFLSNDHTGSSELCTLFLDPQWRKEGNGYLL

SKSRFLFMAAFRERFNEKVVAEMRGVIDEQGYSPFWESLGKRFFAMEFSRADYLCGTGQKAFIAALMPKH

PLYIDFLSPEAQAVIGKVHPQTAPARTVLEKEGFRYLNYIDIFDGGPTLECDIDRVRAIRKSRLVTTEAG

ETSPGGWPLCLVANEQYHQFRALLVHADPDGDTLTLSARELDMLKCHAGDQVRMVRLIPEEKTA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043083.1\_2389 [gene=astD] [locus\_tag=BN49\_RS13455] [protein=succinylglutamate-semialdehyde dehydrogenase] [protein\_id=WP\_046043083.1] [location=2453704..2455182] [gbkey=CDS]

MSLWINGEWQPGRGPGFSKQDPVNLKVVWQGEAADAGQVAEAVAAARQAFPSWARLPFAARQAIVEKFAA

LLEASKAELTAVIGAETGKPRWEAAGEVTAMINKVAISVKAYHVRTGEQHSDLPDGAATLRHRPHGVLAV

FGPYNFPGHLPNGHIVPALLAGNTVVFKPSELTPRSGEAVVKLWQQAGLPAGVLNLVQGGRETGEALSGQ

ADIDGLLFTGSSTTGFHLHRQLAGQPQKILALEMGGNNPLIVDDPRDVDAAVHLTIQSAFITAGQRCTCA

RRLLVRRGEAGDAFLSRLVTVSQRLIPAAWDAEPQPFLGGLISEQAAQKVHQAWLQRVAAGAVTLLEPRL

LQAGTSLLTPGIVDMSDVANVEDEEVFGPLLGVWRYDTFEEAIALANATRFGLSCGLISPEREKFDRLLL

EARAGIVNWNKPLTGAASTAPFGGTGASGNHRPGAWYAADYCAWPMASLESPTLTLPASLSPGLDFLARE

AS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043085.1\_2390 [gene=astB] [locus\_tag=BN49\_RS13460] [protein=N-succinylarginine dihydrolase] [protein\_id=WP\_046043085.1] [location=2455179..2456504] [gbkey=CDS]

MTAREVNFDGLPGLTHHYAGLSFGNEASTRHRYQVSNPQLAAKQGLKKMKALADAGYPQAVIPPQERPNV

PLLRQLGFSGSDEQVVARVAQQEPDLLSAVSSASAMWVANAATVCPSADSLDGLVHLTVANLQDKFHRAS

EAPTTEALLQAIFPDRTRFAIHPALPASAWFGDEGAANHNRLGGEYGAPGAQLFVYGRRRGSEEAPRRYP

ARQTLEASQAVARLNQVNPRQLIFARQHPAAIDTGVFHNDVIAVSNRQVLFCHEQAFADQTALLQQLAQR

VPGFTPLVVPASRVSVAEAVATYLFNSQLVSRADGSMALILPQEAQEHAGVWEYLNELLAGDNPIADLRV

FDLRESMANGGGPACLRLRVVLTAEEYQAVNPHVLMNDTLFATLNDWVDRYYRDRLTQADLADPQLLREG

RDALDRLTQILQLGSVYPFQQ

>lcl|NZ\_FO834906.1\_prot\_2391 [gene=astE] [locus\_tag=BN49\_RS13465] [protein=succinylglutamate desuccinylase] [pseudo=true] [location=2456514..2457469] [gbkey=CDS]

MEHFLALTLAGRLPHHFHGETAHFRWHWLGEGILELTPHARCERGLVLSCAIHGNETAPVEIVDQLVQRL

VREALPLRWRLLVIVGNPPALRANKRYLHSDMNRMFGERWRQFPLSEETQRAQRLEQAVARFYRDHDGPR

WHLDLHTARYIRASACSRPAIRRERRIFFTGWAAPGWRRWCFIASPAGPSPTSAANGSRRWPAPLSWAKR

CRWGKTI\*RSLPPSSGRSPGCWWGIWPLPTP\*RRCATGWYSS\*PAIAMISACIWRIRR\*TSPPSNPARCW

RRRARRGMWWGLRRSMFCFLTRRWRKDCAPA\*CWRNYP

>lcl|NZ\_FO834906.1\_prot\_WP\_004217130.1\_2392 [gene=spy] [locus\_tag=BN49\_RS13475] [protein=ATP-independent periplasmic protein-refolding chaperone Spy] [protein\_id=WP\_004217130.1] [location=2457813..2458298] [gbkey=CDS]

MMKKLTALFVASTLALGAANLAHAADTTTAPSDSKPMMMHHKGGPGQHDMMFKGLNLTDAQKQQIRDIMK

SQRENMKRPSLEERRAMHDLIASDTFDKAKAEAQIDKMEAQHKAMALSRLETQNKIYNILTPEQKKQFNA

NFEKHLTERNAPAGKMPAPAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004176514.1\_2393 [gene=cho] [locus\_tag=BN49\_RS13480] [protein=excinuclease Cho] [protein\_id=WP\_004176514.1] [location=complement(2458386..2459249)] [gbkey=CDS]

MARKQSAPRLEFEAAAIYEYPEHLRPWLEALPKLPGVYQFHGDSDTMPLYIGKSVNLRSRVLSHLRTPEE

AAMLRQSRRITWQRTAGELGALLLEARLIKEQQPLFNKRLRRNKQLCAWLLADDRPQIVYAREVDFSHQQ

HLYGLFANRRAALQMLQSLADEQRLCYGLLGLEPLSRGRACFRSALGRCAGACCGKESVEAHRERLLAQM

SRLQLVCWPWAGPVALEERGPDMTQYHVIHNWLWLGAVESLDQAAELTRLPAGFDQDGYKILCKPLLSGD

YPLHPLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151921.1\_2394 [gene=nadE] [locus\_tag=BN49\_RS13485] [protein=ammonia-dependent NAD(+) synthetase] [protein\_id=WP\_004151921.1] [location=complement(2459350..2460177)] [gbkey=CDS]

MTLQQEIIQALGAKPQIDVAGEIRRSVDFLKSYLQTYPFIKSLVLGISGGQDSTLTGKLCQIAINELRAE

TGDSSLQFIAVRLPYGVQADEQDCQDAIAFIQPDRVLTVNIKAAVLASEQALREAGIELSDFVRGNEKAR

ERMKAQYSIAGMTKGVVVGTDHAAEAITGFFTKYGDGGTDINPIFRLNKRQGKQLLAHLGCPEHLYKKLP

TADLEDDRPSLPDEVALGVTYENIDDYLEGKTLDPSIAKTIEGWYLKTEHKRRPPITVFDDFWKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901544.1\_2395 [gene=osmE] [locus\_tag=BN49\_RS13490] [protein=osmotically-inducible lipoprotein OsmE] [protein\_id=WP\_002901544.1] [location=2460460..2460798] [gbkey=CDS]

MNKSLAGILGVTVALTLLAGCTAYDRTKDQFTQPVVKDVKKGMSRQQVMQIAGKPSTEVTMVHARGTCQT

YILGQRDGKVETYFVALDETGHVMNSGYQTCAEYDTDPRNAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002901547.1\_2396 [gene=chbB] [locus\_tag=BN49\_RS13495] [protein=PTS N,N'-diacetylchitobiose transporter subunit IIB] [protein\_id=WP\_002901547.1] [location=2461077..2461397] [gbkey=CDS]

MEKKHIYLFCSAGMSTSLLVSKMRAQAEKYEVPVIIEAYPETLAGEKGPEADVVLLGPQIAYMLPEIQRL

LPNKPVEVIDSLLYGKVDGLGVLKAAVAAIKKAAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_014907779.1\_2397 [locus\_tag=BN49\_RS31020] [protein=hypothetical protein] [protein\_id=WP\_014907779.1] [location=2461417..2461533] [gbkey=CDS]

MYFDAWRLPVAGRQKIMSLFSRQRVISYIIAVIVYCGF

>lcl|NZ\_FO834906.1\_prot\_WP\_004148091.1\_2398 [gene=chbC] [locus\_tag=BN49\_RS13505] [protein=PTS N,N'-diacetylchitobiose transporter subunit IIC] [protein\_id=WP\_004148091.1] [location=2461545..2462903] [gbkey=CDS]

MSKVIDSLEKVLLPFAVKIGKQPHINAIKNGFIKLMPLTLAGAMFVLINNVFLSFGEGSFFYSMGIRLDA

STIETLNGFKAIGGNVYNGTLGIMSLMAPFFIGSALAEERKVDPMAAGLLAVAAFMTVTPYSVGEAYAVG

ANWLGGQNIISGMIIGLVVAELFTFVIRRNWVIRLPDSVPGSVSRSFSALIPGFLILSIFGIISWALASY

GSNFHQIIMDSISTPLAAMGSVVGWAYVIFNSLLWFFGVHGSLALTALDNGIMTPWALENIALYNQYGSV

DAAIEAGKQFHFWAKPMLDSYILLGGSGATLGLIIAIFIASRRADHRQVAKLALPSGIFQINEPILFGLP

IIMNPVMFIPFVLVQPILAAITLAAYSLGIIPPVTNLAPWTMPTGLGAFFNSNGSVAALLVALFNLGVAT

LVYLPFVVLSNKAQTVIEQEESEEDIANALKF

>lcl|NZ\_FO834906.1\_prot\_WP\_004140356.1\_2399 [gene=chbA] [locus\_tag=BN49\_RS13510] [protein=PTS N,N'-diacetylchitobiose transporter subunit IIA] [protein\_id=WP\_004140356.1] [location=2462957..2463304] [gbkey=CDS]

MFDLDNIDAVETPENDLEEVVMGLIINSGQARSLAYGALKQAKQGDFAAAKAMMEQSRQALSEAHRVQTQ

LIESDEGEGKMKVSLVLVHAQDHLMTSMLARELVAELIELHEKVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002901552.1\_2400 [gene=chbR] [locus\_tag=BN49\_RS13515] [protein=transcriptional regulator ChbR] [protein\_id=WP\_002901552.1] [location=2463332..2464156] [gbkey=CDS]

MMTTEISTAREQQLFNGKNFHVVIYNKTESVSGLHQHDYYEFTVVLTGRYYQEINGKRVLLERGDFVFIP

MGSHHQSFYEFGATRILNVGISRRFFEKHYLPLLPFGLVASQVYAVQSAFLGYVESVIASLNFRETEFDE

FIELVSFYVINRLRHYREEPVADVTPQWLKNTVEAMHDKLKFGEGALENMVRLSGKTQEYLTRATQRYYG

KTPMQIINDIRINFAKKQLEITNYSVTDIAYESGYSSPSLFIKTFKKLTSFTPSSYRKHLTSIN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530008.1\_2401 [locus\_tag=BN49\_RS13520] [protein=6-phospho-beta-glucosidase] [protein\_id=WP\_016530008.1] [location=2464267..2465613] [gbkey=CDS]

MSQKLKVVTIGGGSSYTPELLEGFLKRYHELPVSELWLVDVEEGQEKLDIIHALCQRMVEKAGVPMKVYK

TLDRRAALQGADFVTTQLRVGQLKAREKDERIPLSHGYLGQETNGAGGLFKGLRTIPVIFDIVKDVQEIC

PDAWIINFTNPAGMVTEAVYRHTNFKRFIGVCNIPIGMKMFITDVLQLSSSDELNIDLFGLNHLVFVRDV

LVNGVSRFDELLDGVASGRLTANSVKNIFDLPFSEGLIRSLRLIPCSYLLYYFKPKEMLAIEMGEYYKGG

ARAQVVQKVEKQLFELYKNPDLNVKPKELEQRGGAYYSDAACEVINAIYNDKQTEHYVNIPHHGHVDNIP

ADWAVEMSCTLGRDGAKPTPRITHFDEKVLGLIYTIKGFEVAASQAAISGELNDVLLALNLSPLIHSDRD

AEQLAREMILAHEKWLPNFAATIEKLKS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043086.1\_2402 [gene=chbG] [locus\_tag=BN49\_RS13525] [protein=chitin disaccharide deacetylase] [protein\_id=WP\_046043086.1] [location=2465626..2466384] [gbkey=CDS]

MERVLIVNADDFGLSKGQNYGIIEACRNGVVTSTTALVNGAAIDHAAQLSRSTPELAVGMHFVLTLGEPL

SAMPGLTRYGRLGKWIWQQAEEDSLPLEEIAHELACQYHRFVELFGHEPTHIDSHHHVHMFAQIYPIVAA

FAREKGIALRIDRQVAAQSGLDQQAARSSAGFSSEFYGEAVSEELFLQTLDASIARGERSLEVMCHPAYV

DRIIMGSAYCYPRLDELDVLTSASLKAAVADRGYRLGTYRDV

>lcl|NZ\_FO834906.1\_prot\_WP\_004140344.1\_2403 [gene=katE] [locus\_tag=BN49\_RS13530] [protein=catalase HPII] [protein\_id=WP\_004140344.1] [location=complement(2466442..2468700)] [gbkey=CDS]

MSDKHPNPHQQQAPVHDSEEAQPGLDSLAPDDREWRPTPKPTAPGVEPTAPGSLKAPDTHNSKLDSLEAQ

RKGGEDFPLTTNQGVRIADDQNSLRAGSRGPTLLEDFILREKITHFDHERIPERIVHARGSAAHGYFQPY

KSLAALTKADFLSSADKITPVFVRFSTVQGGAGSADTVRDIRGFATKFYTDEGIFDLVGNNTPVFFIQDA

MKFPDFVHAVKPEPHWAIPQGQSAHDTFWDYVSLQPETLHNVMWAMSDRGIPRSYRTMEGFGIHTFRLIN

AEGKATFVRFHWKPVAGKASLVWDEAQKLTGRDPDFHRRDLWEAIEAGDYPEFELGLQLIPEENEFAFDF

DLLDPTKLIPEALVPVQRVGRMVLNRNPDNFFAENEQAAFHPGHIVPGIDFSNDPLLQGRLFSYTDTQIS

RLGGPNFHEIPINRPTCPYHNFQRDGMHRMDIDTNPANYEPNSINDNWPRETPPAAKRGGFESLAERVDG

EKIRQRSPSFGEYYAQPRLFWLSQTPIEQQHIIDGFSFELSKVVRTWIRERVVDHLAHIDTKLAEAVGAN

LGIELSDDQRNITLPAPVNGVEKDPSLSLYADAEGDVKGRVVAVLLNERTSAQDLVQLLQALQAQGVHSK

LLYSRMGEVIADDGSPLPIAGTFAGSPSLTVDAVVVPGGDLSALSQSGDARYYLLEAYKHLKPILLAGDA

RQLTSVLQVPTQGEEGVIVTDALDTPAADKLLALMTAHRVWSRSPKIAAIPA

>lcl|NZ\_FO834906.1\_prot\_WP\_008807754.1\_2404 [gene=cedA] [locus\_tag=BN49\_RS13535] [protein=cell division activator CedA] [protein\_id=WP\_008807754.1] [location=2468891..2469145] [gbkey=CDS]

MNPFVMKPLRQQNRPVISYVPRVEPAPPEHAVKMDHFRDVWILRGKYVAFLLMGEHFRRSPAFSVPESAQ

RWANQVRQEGEIEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151918.1\_2405 [locus\_tag=BN49\_RS13540] [protein=L-cystine transporter] [protein\_id=WP\_004151918.1] [location=complement(2469205..2470596)] [gbkey=CDS]

MNFPLIANVVVFAVLLFALGQTRHKQWSLARKVLVGLATGVVFGLALQLIYGSDSQVLKDSIQWFNIVGN

GYVQLLQMIVMPLVFASILSAVARLHNASQLGKISFLSIGTLLFTTLIAALVGVLVTNMFGLTAEGLVQG

SAETARLNAIQSNYVGKVADLSVPQLILSFVPKNPFADLTGANPTSIISIVIFSAFLGVAALKLLKEDVE

KGQRVLTAIDTLQGWVMKLVRLVMQLTPYGVLALMTKVVAGSNLQDIIKLGGFVVASYIALGIMFVVHGL

LLAINGVSPLKYFRKVWPVITFAFTSRSSAASIPLNVEAQTRRLGVPESIASFSASFGATIGQNGCAGIY

PAMLAVMVAPTVGINPLDPMWIATLVGIVTVSSAGVAGVGGGATFAALIVLPAMGLPVTLVALLISVEPL

IDMGRTALNVNGSMTAGTLTSQWLRQTDKSIFDSEEEAELAHR

>lcl|NZ\_FO834906.1\_prot\_WP\_002901611.1\_2406 [locus\_tag=BN49\_RS13545] [protein=metal-dependent hydrolase] [protein\_id=WP\_002901611.1] [location=complement(2470732..2471322)] [gbkey=CDS]

MTAEGHLFFSIACAVFAKNAELTPVLAQGDWWHIVPSAVLTCLLPDIDHPKSFLGQRLSWISKPVARAFG

HRGFTHSLLAVFGALTLFYLKVPDSWIVPADALQGLVLGYLSHILADMLTPAGVPLLWPCRWRFRLPILA

PRKGNQLERALCMALFVYAVWMPQTLADNSAIRWSSGVINSLQITFNRFISHQSGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176511.1\_2407 [gene=kduD] [locus\_tag=BN49\_RS13550] [protein=2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase KduD] [protein\_id=WP\_004176511.1] [location=complement(2471414..2472175)] [gbkey=CDS]

MVLNAFDLTGKVAIVTGCDTGLGQGMTLGLAQAGCDIVGINRKIPHDTAAQVLALGRRFHAIQADLSQEN

DMSGLVDQAVAAMGRVDILVNNAGIIRRHDALTFTESDWDAVIDLNLKAVFFLSQAVARQFIRQGEGGKI

INIASMLSFQGGIRVPSYTASKSGVLGLTRLLANEWAGQGINVNAIAPGYMATNNTQALREDEERNQAIL

ERIPAGRWGAPKDLQGPVVFLASSAADYINGYTLAVDGGWLAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004140335.1\_2408 [gene=hxpB] [locus\_tag=BN49\_RS13555] [protein=hexitol phosphatase HxpB] [protein\_id=WP\_004140335.1] [location=complement(2472325..2472993)] [gbkey=CDS]

MSAKRRIEAAIFDMDGLLIDSEPLWDQAEVEVMESLGVDTRRRDELPDLLGLRIDLVVDLWYAQQPWHGV

DRAEATARIIRRAIELVEASRPLLPGVREAVALCKAQGLKVGLASASPLMMLEKVLDMFELRDQFDALAS

AEHLPWSKPHPQVYLNCAAALGVDPQRCVALEDSVNGMIASKAARMRSIVVPEAENSRDPRFALADVKLP

SLLALTAENLLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002901627.1\_2409 [locus\_tag=BN49\_RS13560] [protein=YniB family protein] [protein\_id=WP\_002901627.1] [location=2473182..2473718] [gbkey=CDS]

MTYQQAGRIAVIKRILGWVIFIPAVLSTLISVLKFMYEHSEKKPGIDAVMMDFAHVMIEMMRFNTPFLNF

FWYNSPLPDFHHSLNIGFWIIFILVFVGMALQASGARMARQAKFLREGIEDQLILEQAKGADGLTREQLA

ERIVVPRHTILVQYFPLYVLPVIVIVIGYFFFSLLGFL

>lcl|NZ\_FO834906.1\_prot\_WP\_002901629.1\_2410 [gene=yciA] [locus\_tag=BN49\_RS13565] [protein=acyl-CoA thioester hydrolase YciA] [protein\_id=WP\_002901629.1] [location=complement(2473748..2474146)] [gbkey=CDS]

MTTTDLAPKGEMVLRTLAMPADTNANGDIFGGWLMSQMDIGGAIMAKEIAQGRVVTVRVDGMTFLRPVAV

GDVVCCYARCVKRGNTSVTINIEVWVKKVSSEPIGQRYKATEALFIYVAVDNQGKPRPLPAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004179434.1\_2411 [locus\_tag=BN49\_RS13570] [protein=TonB-dependent siderophore receptor] [protein\_id=WP\_004179434.1] [location=complement(2474246..2476429)] [gbkey=CDS]

MRSPQYSVPTTLALVISSLLAPNAFAEESEQDTETMIVRSTAEEALKQQPGVSIITAEDIAKQPPVNDLS

DIIRKMPGVNLTGNSASGSRGNNRQIDIRGMGPENTLILIDGVPVTSRNAVRYSWRGERDTRGDSNWVPA

EMVERIEVLRGPAAARYGSGAAGGVVNIITKRPTNTWHGSLSFFTNQPENNKEGTTNRANFNLSGPLAGE

ALTMRLYGNINKTEPDAWDINHAQNGSYAAGREGVRNKDINALLSWKMTPQQILDFSYAYSRQGNIYAGD

TQYSNGNLSPNGLVDSLYGHETNRLYRQSWGLTYNGLWDWGQSKAGVYYEKTNNTRLQEGSTGRVEGMIN

SEDYATSRLESWRTTSEFNVPFFWLADQTLTLGMEWNHDQLDDPASMQATNSNGETIPGTSGDPTQRSTK

NSATLTGIYLEDNIEAVPGTNLIPGIRFDYHNQFGSNWSPSLNLSQELGDMFTLKAGIARVFKAPNLYQS

SKGYLLSTRGNGCPNTIAEGSCYLLGNPDLDPEISINKEIGIEFNLNGYAAGVTWFRNDYKNKIVSGTEV

LGYTSSGNNILQWQNGGKAVVEGLEGNLLIPVLRDVLSWRTNATWMLKSESKETGNPLSVIPKYTVNTML

DWQVNDALSANVNWTLYGRQKPRQYAEIRNETGTLATTEVGAYSIVGIGTQYQLNRDIRLNAGISNLFDK

QLYRENAGASTYNEPGRAYYAGVTLSF

>lcl|NZ\_FO834906.1\_prot\_WP\_002901631.1\_2412 [locus\_tag=BN49\_RS13575] [protein=septation protein A] [protein\_id=WP\_002901631.1] [location=complement(2476701..2477240)] [gbkey=CDS]

MKQFLDFLPLVVFFAFYKLYDIYAATTALIVATAVVLIYSWVRYRKVEKMALITFVLVAVFGGLTIFFHN

DEFIKWKVTVIYALFAGALLFSQWVMKKPLIQRMLGKELSLPQQVWSRLNLAWAVFFILCGLANIYIAFW

LPQNIWVNFKVFGLTALTLVFTLLSGIYIYRHMPQDDHH

>lcl|NZ\_FO834906.1\_prot\_WP\_002901632.1\_2413 [locus\_tag=BN49\_RS13580] [protein=envelope biogenesis factor ElyC] [protein\_id=WP\_002901632.1] [location=complement(2477295..2478038)] [gbkey=CDS]

MSITAKSVYRDTGNFFRNQFITILLIALLCAFITVVLGHAFSPSDEQLSILSEGDNLAGSAGLFELVQNM

TPEQQQVLLRASAASTFSGLVGNAILVGGVLLLIQLVSAGHRVSALRAIGASAPVLPKLLLLILFTTFLV

QMGMMLVLVPGVLLAIVLAFAPIMLVQDKMGILGAMRSSMRLAWANLRLVAPAIIGWLVAKTLLLLFASS

FAALTPNVGAVVINTISNLISALLLIYLFRVYMLIRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002901633.1\_2414 [locus\_tag=BN49\_RS13585] [protein=YkgJ family cysteine cluster protein] [protein\_id=WP\_002901633.1] [location=complement(2478064..2478477)] [gbkey=CDS]

MSEINPCMTCGACCAYFRVSFYWAEADDAGGLVPSALTEPLTPFLRCMSGTNQRQSRCAALSGDIGDAVH

CTIYENRPSPCREFAMSGENGEENDACNRARARYGLPPLRPLYKDIPALTGAESATTERFAVQSPAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002901634.1\_2415 [gene=ompW] [locus\_tag=BN49\_RS13590] [protein=outer membrane protein OmpW] [protein\_id=WP\_002901634.1] [location=2478747..2479385] [gbkey=CDS]

MKKLAAAALILGTLSTGSVWAHEAGEFFIRAGTATVRPTEGSDNVLGSLGSFNVSNNTQLGLTFTYMATD

NIGVELLAATPFRHKVGTGPTGTIATVHQLPPTLMAQWYFGDAQSKVRPYVGAGINYTTFFNEDFNDTGK

AAGLSDLSLKDSWGAAGQVGLDYLINRDWLLNMSVWYMDIDTDVKFKAGGVDQKVSTRLDPWVFMFSAGY

RF

>lcl|NZ\_FO834906.1\_prot\_WP\_004140326.1\_2416 [gene=ybiX] [locus\_tag=BN49\_RS13595] [protein=PKHD-type hydroxylase YbiX] [protein\_id=WP\_004140326.1] [location=complement(2479470..2480147)] [gbkey=CDS]

MMYHIPDVLSTDQVAEFTRQLAQAEWVDGRVTVGSQGAAVKQNQQIDTRTPLYARLQAAVLDMLRGHPQF

FSAALPRTISAPLFNRYGPGETYGFHVDGAVRQNGEAGWMRTDLSATLFLCDPESYEGGELVIEDTYGQH

RVKLPAGHLVLYPASSLHCVTPVTRGVRQASFLWIQSMVRDDKQRAMLYDLDRTIQSLKARFGDGEEVLS

LLNMYHNLLRQWTEV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043089.1\_2417 [locus\_tag=BN49\_RS13600] [protein=catecholate siderophore receptor Fiu] [protein\_id=WP\_046043089.1] [location=complement(2480196..2482487)] [gbkey=CDS]

MEKNASLPFGSFNSLALFTGLCLGASPAAGIAAENSVKNSEETLVVEAAPPSLYSPGASADPKFNKPLVD

TTRTITVIPEQVIKDQGVTNLTDALKNVPGVGAFYAGENGSSTTGDAIFMRGVDTSNSIYVDGIRDIGSV

TRDTFNTQQVEVIKGPAGTDYGRSAPSGSINMISKQPRLDSGIDGSASIGSAWSRRGTLDLNQAFSDNAA

FRLNLMGEKTHDAGRDRIENERYGIAPSLAFGLDTPTRLYLNYLHVRQNNTPDGGIPTVGLPGYSAPSPK

YAALNSAGKVDTSNFYGTDSDYDKSTTDSGTLRFEHDLTENTTVRNTTRWSRVKQEYLLTAVMGGANNIT

APDINDVNTWSWSRLVNTKDVSNRILTNQTNITSTFNTGSIGHDVSAGVEFTRENQTNYGVNAKTAPAVN

LYHPVSNLSIGGLDRNGANANGQTDTFGIYAFDTLTLTERIEINGGLRLDNYHTKYDSATACGGSGRGAI

ACPPGQSTGSPVTTVDTAKSGNLVNWKAGALYRLTEQGNVYVNYAISQQPPGGSSFALAASGSGSGNSAN

RTDFKPQKAKSSELGTKWQIFDNRLLLSAALFRTDIENEVAANDDGTWSQYGKKRVEGYELSATGNLTPD

WTIIAGYTQQHATVTEGQNVAQDGSSALAYTPKHAFTLWTQYQATSDLSVGGGVRYVGSLRRGSDGAVGT

PDHTEGYWVADAKLGYRVNRNLDLQLNMYNLFDTDYVASINKSGYRYHPGEPRTFMLTANVHF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529821.1\_2418 [locus\_tag=BN49\_RS13605] [protein=SDR family NAD(P)-dependent oxidoreductase] [protein\_id=WP\_016529821.1] [location=complement(2482796..2483503)] [gbkey=CDS]

MKSDQHNTILIVGASRGLGHAMATTFLQHGWEVIGTVRDLSSHTPLHDLAKTHPLRLRLATLDIRDEAQL

AALQATLPPASLDMLFVNAGTTNRDPSQTIGDVSTEEFYQVMLTNALAPMRVIERLQQAVKPQGLLGVMS

SGQGSLTNNLTGQRELYRGSKAALNMFMRSFAARPSPASHPLVVMAPGWIRTELGGADAPLTIEETIPRL

VNVLLDKRQRPGLEYLDYQGRTVPW

>lcl|NZ\_FO834906.1\_prot\_WP\_004179443.1\_2419 [locus\_tag=BN49\_RS13610] [protein=hypothetical protein] [protein\_id=WP\_004179443.1] [location=2483622..2483894] [gbkey=CDS]

MNDPDFNLLAALDPLPVSTEVITVSQAWHPRLEQAPATAGCGSGCVRCVASKKSPHKCGQKYWKQCEQCR

TEYPSDLLNYSVMRKIIFLI

>lcl|NZ\_FO834906.1\_prot\_WP\_016529822.1\_2420 [locus\_tag=BN49\_RS13615] [protein=zinc-binding alcohol dehydrogenase family protein] [protein\_id=WP\_016529822.1] [location=complement(2483957..2484877)] [gbkey=CDS]

MKAAVVFDLAEGPVWADFIDPQPAPGQTLIDVRAAAISHVVKARSSGRHYSFDGNLPFVPGIDGVGTTPQ

GQRVYFAFPTAPFGSMAQRAPVALQNCLPLPDALDDIQAAAMANPGMSAWASLVTRAQLQAGETVLINGA

TGSAGQLAVQIARYLGAKKIIATGRNAQSLAALDADECIQLAADDKTLSGQFSAVSAAQIDVVIDYLWGH

SAELLLPALAKYTPAGSPVRYVQVGSLAGADIALNGAVLRSAPLLLMGSGIGSLSVSQLLAATGEMLQAA

VPGKLTIATTPRPLQEIAAAWPQDDS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529823.1\_2421 [locus\_tag=BN49\_RS13620] [protein=MarR family winged helix-turn-helix transcriptional regulator] [protein\_id=WP\_016529823.1] [location=2484952..2485410] [gbkey=CDS]

MQDAHNDYDITDFHGALLDIISVMNQPLRDEQILQAAGVQLEQMLFPLLVAVGRHGPVGVVELADHLGRD

YTTVSRQVKKLEAQGLACKQPNRHDRRISEVTLSASGQQMIDSIAVARRQLMNQVLAQWPEDEVQALFRL

TRKYADSLQQPG

>lcl|NZ\_FO834906.1\_prot\_WP\_004179448.1\_2422 [locus\_tag=BN49\_RS13625] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004179448.1] [location=complement(2485453..2486361)] [gbkey=CDS]

MDINQLRCFVVLGDELHFGRAARKLEMMPASLSRFIKLLEDDLGIRLLNRSTRNVSLTPEGAAFLNEAKT

VIADFDALRQRFRKNSLLQKRTLRIGAIDSAAKGLLPELLNLFVRRFPEADIHLTEDKSHKLIPRLISGW

LDVVFVRPPEHIDATLTARFIANETCVLAVPAHHRLVSYDEVSIDDFRHEPVILPERRTRRHSHDLTMNI

FKEGGSMPVIAQYAEEKQTILSFVAAGLGIALVPASYKDMNADGVKYLALTPKKHVEGLPLSAMWHQGNN

TLYVRSLLEILSDNIDELTREL

>lcl|NZ\_FO834906.1\_prot\_WP\_004179450.1\_2423 [locus\_tag=BN49\_RS13630] [protein=MFS transporter] [protein\_id=WP\_004179450.1] [location=2486490..2487800] [gbkey=CDS]

MKNDLEKKVMRKVTLRIIPFIMLLYFIAFLDRVNIGFAALTMNQDLGFSPTVFGLGAGIFFLGYFLFEVP

SNLILHKVGARIWIARVMITWGFVSGCMAFVQGTTSFYILRFLLGVAEAGFFPGIILYLSYWFPAARRAQ

VTAIFMAAAPLSTALGSPVSAALLEMHGFLGYAGWQWMFVLEALPALVLGVVVLFFLTDRPAKAKWLTDQ

ERAWLENAMQDEERARAAKQSHSSAWRGLADIRVLALALVYFGTSAGLYTLGIWSPQIIRSFGASSLEIG

FLNAFPAVIGVIAMILWARHSDRTKERSWHVIGACLLAGAGLIYAGNVSTLFTVMVALTLVTVGISASKP

PLWSMPTLFLSGPAAAAGIAAINSIGNLGGFVGPMMIGVIREQTGSYSWGLYFVAGLLALSALVVMILSA

RANKSPTAELPHPHTH

>lcl|NZ\_FO834906.1\_prot\_WP\_002901724.1\_2424 [locus\_tag=BN49\_RS13635] [protein=tartrate dehydrogenase] [protein\_id=WP\_002901724.1] [location=2487815..2488903] [gbkey=CDS]

MRHYKIAAIPADGIGPEVISAGIEVLHALTRHDPQLKFDIETFDWGSDYYKKHGVMMPEEGLNMLKAFDA

IYFGAVGAPDVPDHITLWGLRLPICQGFDQYANVRPTKILPGVTSPLRNRGPGDLDWVIVRENSEGEYSG

NGGRTHRGLPEEVGTEVAIFTRVGVTRIMRYAFRLAQSRPRKLLTVVTKSNAQRHGMVMWDEIAAEVAQE

FPDVQWDKMLVDAMTHRMTLHPQTLDTIVATNLHADILSDLAGALAGSLGVAPTANIDPERRFPSMFEPI

HGSAFDITGKGIANPIATFWTAVQMLEHLGERHAAALIMESIEYVCEKGILTPDVGGSANTAEVTRAVVH

YIDAKADIAETA

>lcl|NZ\_FO834906.1\_prot\_WP\_004892790.1\_2425 [locus\_tag=BN49\_RS13640] [protein=glycerate kinase] [protein\_id=WP\_004892790.1] [location=2488906..2490165] [gbkey=CDS]

MNNEQAAEILQDIFQHAVNSARAGPVTLANLPEKPRGRCVVIGAGKASAAMAAAVDAAWPDVAVSGVVVT

RYGYAVPAGRIRIIEAAHPVSDAMSEVAAMLIVETLRGLTADDLVLALISGGGSALMALPAPGLTLADKQ

TITRALLHSGASIKEMNLVRRHLSAVKGGKLATMAQPARIVSLIISDVPGDNPTDVASGPTVADNSAPRD

ALRVLQRYGIAIPKPVSERLNQPAGPVENAATGEVRLIATPAMALAAAALAARQHGFTPLILGDAIEGES

REVAVVMAGMAKSAKQYGHPISGPAVLLSGGETTVTVNNTQPGKGGRNTEFLLSLACALQGEHGIWAMAG

DSDGIDGTEDAAGAIVFPDTLARGKLSGLNAVQYLDGHDSYCYFHALNDLLITGPTLTNVNDIRAILIA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529824.1\_2426 [gene=trpA] [locus\_tag=BN49\_RS13645] [protein=tryptophan synthase subunit alpha] [protein\_id=WP\_016529824.1] [location=complement(2490384..2491193)] [gbkey=CDS]

MERYETLFAQLKNRQEGAFVPFVTLGDPGPEQSLKIIDALIEGGADALELGIPFSDPLADGPTIQGAALR

AFAAGVTPAQCFEMLAAIRQKHPTIPIGLLMYANLVFSPGIDAFYAQCARVGVDSVLVADVPVEESAPFR

QAAMRHNIAPIFICPPNADDDLLRQIASYGRGYTYLLSRAGVTGAENRAALPLHHLVEKLAEYHAAPPLQ

GFGISAPEQVSAAIDAGAAGAISGSAIVKIIERHLDEPQTMLDELKAFVQSLKAATKTG

>lcl|NZ\_FO834906.1\_prot\_WP\_004148107.1\_2427 [gene=trpB] [locus\_tag=BN49\_RS13650] [protein=tryptophan synthase subunit beta] [protein\_id=WP\_004148107.1] [location=complement(2491193..2492386)] [gbkey=CDS]

MSTLLNPYFGEFGGMYVPQILMPALRQLEEAFVSAQKDPAFQAEFTDLLKNYAGRPTALTKCRNLTDGTR

TTLYLKREDLLHGGAHKTNQVLGQALLAKRMGKTEIIAETGAGQHGVASALASALLGLKCRIYMGAKDVE

RQSPNVFRMRLMGAEVIPVHSGSATLKDACNEALRDWSGSYEKAHYMLGTAAGPHPFPTIVREFQRMIGE

ETKAQILEKEGRLPDAVIACVGGGSNAIGMFADFIEETNVGLIGVEPAGHGIESGEHGAPLKHGRVGIYF

GMKSPMMQTADGQIEESYSISAGLDFPSVGPQHAFLNSTGRADYVSITDDEALDAFKALSRHEGIIPALE

SSHALAHALKMMRENPEKEQLLVVNLSGRGDKDIFTVHDILKARGEI

>lcl|NZ\_FO834906.1\_prot\_WP\_016531385.1\_2428 [gene=trpCF] [locus\_tag=BN49\_RS13655] [protein=bifunctional indole-3-glycerol-phosphate synthase TrpC/phosphoribosylanthranilate isomerase TrpF] [protein\_id=WP\_016531385.1] [location=complement(2492396..2493754)] [gbkey=CDS]

MQTVLAKIVADKAIWVEARKQQQPLASFQNEIVPTQRNFYDALAGTRTAFILECKKASPSKGLIREDFDP

AAIASIYKHYASAISVLCDEKYFQGSFDFLPIVSQVAPQPILCKDFTIDPYQIYLARYYQADACLLMLSV

LDDEQYRQLSAVAHSLNMGVLTEVSNEEELERAIALKAKVVGINNRDLRDMSIDLNRTRQLAARLGPDVT

VISESGIHTYAEVRELSHFANGFLIGSALMEQADLEAAVKRVLLGENKVCGLTRPQDAQVAWESGAIYGG

LIFVPTSPRAVNDAQAKAVIAAAPLQYVGVFRNAPLEEVAARAQALGLAAVQLHGDEDQAYIDALRDALA

DNVRIWKALSVGETFPARTLRHVDKYLLDNGQGGSGQRFDWSLLQDQDLRNVMLAGGLGADNCVEAAKSG

CAGLDFNSGVESQPGIKDASKLASVFQTLRAY

>lcl|NZ\_FO834906.1\_prot\_WP\_004148109.1\_2429 [gene=trpD] [locus\_tag=BN49\_RS13660] [protein=bifunctional anthranilate synthase glutamate amidotransferase component TrpG/anthranilate phosphoribosyltransferase TrpD] [protein\_id=WP\_004148109.1] [location=complement(2493758..2495353)] [gbkey=CDS]

MADILLLDNIDSFTYNLADQLRANGHNVVIYRNSVPAQALIERLGTMDNPVLMLSPGPGTPSEAGCMPEL

LTRMRGKLPIIGICLGHQAIVEAYGGYVGQAGEILHGKASSIEHDGQAMFAGLANPLPVARYHSLVGSNI

PAGLTINANFNGMVMAVRHDADRVCGFQFHPESILTTQGARLLEQTLAWALQKLEHTNTLQPILEKLYQA

ETLSQQESHQLFSAVVRGEVKPEQLAAALVSMKVRGEQPQEIAGAATALLENAAPFPRPDYLFADIVGTG

GDGSNSINISTASAFVAAACGLKVAKHGNRSVSSKSGSSDLLAAFGINLDMNADKSRAALDELGVCFLFA

PKYHTGFRHAMPVRQQLKTRTLFNVLGPLINPAHPPLALIGVYSPELVLPIAETLRVLGYQRAAVVHSGG

MDEVSLHAPTVVAELHNGEIKSYQLTADDFGLTPYHQAQLAGGTPEENRDILTRLLQGKGEAAHEAAVAA

NVAMLMRLHGHEDLKANAQQVLDVLHSGAAYDRVTALAARG

>lcl|NZ\_FO834906.1\_prot\_WP\_004176488.1\_2430 [locus\_tag=BN49\_RS13665] [protein=anthranilate synthase component 1] [protein\_id=WP\_004176488.1] [location=complement(2495353..2496915)] [gbkey=CDS]

MQTSKPALELLTSDAIYRENPTALFHQLCGARPATLLLESADIDSKDDLKSLLLVDSALRITALGDTVTI

QALSANGAALLELLDGALPSGINNQRQPNGRILTFPAVSALLDEDARLCSLSVFDAFRLLQELVSVPDNE

REAMFFGGLFAYDLVAGFEDLPQLQSDTACPDYCFYLAETLLVIDHQTKHTRIQASLFTPLESEKQRLEQ

RLSQLRQQLNEPPAPLPVTTVAEMRCDVDQSDEEYGAVVRKMQRAIRAGEIFQVVPSRRFSLPCPSPLAA

YDVLKKSNPSPYMFFMQDNDFTLFGASPESSLKYDAVSRQIEIYPIAGTRPRGRRADGSLDRDLDSRIEL

EMRTDHKELSEHLMLVDLARNDLARICTPGSRYVADLTKVDRYSFVMHLVSRVVGELRQDLDVLHAYRAC

MNMGTLSGAPKVRAMQLIAAAEGKRRGSYGGAVGYFTAHGDLDTCIVIRSAYVQEGIATVQAGAGIVLDS

VPQSEADETRNKARAVLRAIAQAHHAKEIF

>lcl|NZ\_FO834906.1\_prot\_WP\_016532159.1\_2431 [gene=yciV] [locus\_tag=BN49\_RS13670] [protein=RNase AM] [protein\_id=WP\_016532159.1] [location=2497204..2498067] [gbkey=CDS]

MSDSQYAVIYDLHSHTTASDGRLTPQELVHRAHEMRVGTLAITDHDSVAAIPAAREEIARAGLPLTLVNG

VEISTLWENHEIHIVGLNIDIAHPTMTTLLEEQKARRQQRGQMIAERLEKARIPGAWEGTLRLADGGAVT

RGHFARFLVEAGHAKNMAEVFKKYLARGKTGYVPPQWCTIKQAIDVIHHSGGKAVIAHPGRYDLSAKWLK

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SWEAAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002901738.1\_2432 [locus\_tag=BN49\_RS13675] [protein=L-threonylcarbamoyladenylate synthase] [protein\_id=WP\_002901738.1] [location=2498084..2498704] [gbkey=CDS]

MSQFFYIHPDNPQARLINQAVEIVRKGGVIVYPTDSGYALGCKIEDKGAMERICRIRQLPDGHNFTLMCR

DLSELSTYAFVDNVAFRLMKNNTPGNYTFILKGTKEVPRRLLQEKRKTIGMRVPSNPIAQALLETLGEPM

LSTSLMLPGSDFTESDPEEIKDRLEKVVDLIIHGGFLGQQPTTVIDLTEDTPVVLREGVGDVRPFL

>lcl|NZ\_FO834906.1\_prot\_WP\_002901739.1\_2433 [locus\_tag=BN49\_RS13680] [protein=DMT family transporter] [protein\_id=WP\_002901739.1] [location=complement(2498726..2499634)] [gbkey=CDS]

MRVIDYGRLLLLAALWGASFLFMRITTPAFGALNSAFLRVLFAAIALGLLLGVQGKWSGYQGKFTSTLQL

GVINSGLPFLMYCLAAQWLPAGYSATLNATAPMMGVLIGALCFAEPLTLRKGGGAILGAIGVAVIARPTS

GLSAALLLPGIGACLTATACYGLAGFLTRRWIQQRGGLEAERVALGSQVGATLFLFPFFLWSCWHGPAVD

WRQSLPWIAIVMLGVVCTAAGYIIYFRLIADIGPLRSLSVTFLIPPFAALWGYLCLGETVEKGLILGALL

VCVALWMIIVPSGRKRGVPDGA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532154.1\_2434 [gene=gcvA] [locus\_tag=BN49\_RS13685] [protein=transcriptional regulator GcvA] [protein\_id=WP\_016532154.1] [location=2499746..2500642] [gbkey=CDS]

MKLPPLNALRCFEAAARLLSLKLAASELCVTPSAVSQQIARLEETLNVPLFIRTPRRLQLTAVGEIYLRA

IQPAFHQIAAATQRLQVPPGPEKVAISCTSGFAIQWLLPRLADFEQRYPQIEIQIGTTNRRVDLLSEGID

FAVRHGVGGWPELQAYRLQDDDLMPVCSPQLIAPRRTLTDASDLLQYPLLHDEHREDWALWCKAVGLAPH

FARRGPVFTDSNGVTEAAFAGMGMALLRRSFIAPALTQGRLVNPLAQPIACPLAYHLVYHETALLAPANR

CFRDWLLGQRPAVAEERA

>lcl|NZ\_FO834906.1\_prot\_WP\_002901746.1\_2435 [gene=rluB] [locus\_tag=BN49\_RS13690] [protein=23S rRNA pseudouridine(2605) synthase RluB] [protein\_id=WP\_002901746.1] [location=2500924..2501826] [gbkey=CDS]

MSEKLQKVLARAGHGSRREIEAKIEAGRVSVDGKIATLGDRVEIVPGLKIRIDGHLISVKESAEQICRVL

AYYKPEGELCTRNDPEGRPTVFDRLPKLRGARWIAVGRLDVNTCGLLLFTTDGELANRLMHPSREVEREY

AVRVFGQVDDDKLRQLSRGVQLEDGPAAFKTIKFTGGEGINQWYNVTLTEGRNREVRRLWEAVGVQVSRL

IRVRYGDILLPKGLPRGGYTELDLAQTNYLRELVELTPETSSKVAVEKDRRRLKANQIRRAVKRHSQTSA

NPRQGNNSNRRSSTRNKTNG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532153.1\_2436 [gene=cobO] [locus\_tag=BN49\_RS13695] [protein=cob(I)yrinic acid a,c-diamide adenosyltransferase] [protein\_id=WP\_016532153.1] [location=complement(2501887..2502477)] [gbkey=CDS]

MSDERYRERQQRLKDKVDARVAAAQDERGIVMVFTGNGKGKTTAAFGTATRAVGHGKKVGVIQFIKGTWP

NGERNLLEPHGVEFQVMATGFTWNTQDRDSDTAACLTVWEHARRMLADDQLDLVLLDELTYMVAYDYLPL

ESVLSALRERPAHQSVIITGRGCHRDIIELADTVSELRPVKHAFDAGIKAQMGIDY

>lcl|NZ\_FO834906.1\_prot\_WP\_004196459.1\_2437 [locus\_tag=BN49\_RS13700] [protein=YciK family oxidoreductase] [protein\_id=WP\_004196459.1] [location=complement(2502474..2503235)] [gbkey=CDS]

MHYQPQRHLLKDRIILVTGASDGIGREAALTYARYSASVILLGRNDDKLRTVAQEIEREGGIPPRWFTLD

LLTCTPQACQQLAQQISMHYPRLDGVLHNAGLLGDICPMEEQKPEVWQQVMQVNVNGTFMLTQALLPLLL

RSESGSLVFTSSSVGRQGRANWGAYAVSKFATEGMMQVLADEYQSRHLRVNCINPGGTRTGMRASAFPTE

DPLKLKTPADIMPVYLWLMGDDSRRKTGMTFDAQPGRKPGIAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004148112.1\_2438 [locus\_tag=BN49\_RS13705] [protein=hypothetical protein] [protein\_id=WP\_004148112.1] [location=2503230..2503445] [gbkey=CDS]

MHGNSLGDRFPIALHLWYLTFALLCLKAPAIAIGEAESIHKINILQRFQPREKKRNPLRREHKAQRLLAS

G

>lcl|NZ\_FO834906.1\_prot\_WP\_016532152.1\_2439 [gene=sohB] [locus\_tag=BN49\_RS13710] [protein=protease SohB] [protein\_id=WP\_016532152.1] [location=2503490..2504536] [gbkey=CDS]

MELLAQYGLFLAKIATVVVAIAVIAAIIVNLAQRKKQRGELRVTNLSEHYKEMKESLAVALLDGPQQKQW

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ESPGGVVHGYGLAASQLQRLRVKQIPLTVAVDKVAASGGYMMACVANKIVSAPFAILGSIGVVAQIPNLH

RFLKNKDIDIELHTAGQYKRTLTMLGENTEEGRRKFREDLNETHHLFKDFVHRMRPGLDIEQVATGEHWY

GVQALEKGLVDAVETSDELLLGLMESHEVIGVRYQQRKKMLDRFTGSAAESADRLLLRWWQRGQKPLM

>lcl|NZ\_FO834906.1\_prot\_WP\_002901761.1\_2440 [locus\_tag=BN49\_RS13715] [protein=YciN family protein] [protein\_id=WP\_002901761.1] [location=complement(2504584..2504835)] [gbkey=CDS]

MQGTTQPIDRQTLLEKANKLIREHEDTLAGIEATDVVQRNNVLVFSGEFYLDEQGLPTPKSTAVFNMFKY

LAHELSDKYHLVD

>lcl|NZ\_FO834906.1\_prot\_WP\_002901763.1\_2441 [gene=topA] [locus\_tag=BN49\_RS13725] [protein=type I DNA topoisomerase] [protein\_id=WP\_002901763.1] [location=2505242..2507839] [gbkey=CDS]

MGKALVIVESPAKAKTINKYLGNDYVVKSSVGHIRDLPTSGSASKKSADSTATKGAKKPKKDERSALVNR

MGVDPWHDWNAHYEVLPGKEKVVSELKQLAEKADHIYLATDLDREGEAIAWHLREVIGGDEQRYSRVVFN

EITKNAIRQAFEKPGELNIDRVNAQQARRFMDRVVGYMVSPLLWKKIARGLSAGRVQSVAVRLVVERERE

IKAFVPEEYWEVDASTTTPGGDALPLQVTHKDDKPFRPVSRDETMAAVSLLEKASYSVLEREDKPTSSKP

GAPFITSTLQQAASTRLGFGVKKTMMMAQRLYEAGHITYMRTDSTNLSQDALNMVRGYISDKFGKKYLPD

SANQYASKENSQEAHEAIRPSDVNVLAETLKDMEADAQKLYQLIWRQFVACQMTPAQYDSTTLTVAAGDF

KLKARGRTLRFDGWTKVMPALRKGDEDRTLPLVKQGDRLSLVELTPAQHFTKPPARFSEASLVKELEKRG

IGRPSTYASIISTIQDRGYVRVENRRFYAEKMGEIVTDRLEENFRDLMNYDFTAQMEDRLDQVANHQAEW

KEVLNHFFGDFTTQLATAEKDPEEGGMQPNPMVLTSIDCPTCGRKMGIRTASTGVFLGCSGYALPPKERC

KTTINLVPENEVLNVLEGDDAETNALRAKRRCQKCGTAMDSYLIDPKRKLHVCGNNPTCDGYEIEEGEFR

IKGYDGPVVECEKCGSEMHLKMGRFGKYMACTNDECKNTRKILRNGEVAPPKEDPVPLPELPCEKSDAYF

VLRDGAAGVFLAANTFPKSRETRAPLVEELYRFRDRLPEKLRYLADAPQQDPEGNKTLVRFSRKTKQQYV

ASEKEGKATGWSAFFIDGKWTEAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004224280.1\_2442 [gene=cysB] [locus\_tag=BN49\_RS13730] [protein=HTH-type transcriptional regulator CysB] [protein\_id=WP\_004224280.1] [location=2508185..2509159] [gbkey=CDS]

MKLQQLRYIVEVVNHNLNVSSTAEGLYTSQPGISKQVRMLEDELGIQIFARSGKHLTQVTPAGQEIIRIA

REVLSKVDAIKSVAGEHTWPDKGSLYVATTHTQARYALPGVIKGFIERYPRVSLHMHQGSPTQIAEAVSK

GNADFAIATEALHLYDDLVMLPCYHWNRSIVVTPEHPLANKGSVSIEELAQYPLVTYTFGFTGRSELDTA

FNRAGLTPRIVFTATDADVIKTYVRLGLGVGVIASMAVDPVSDPDLVKLDANGIFSHSTTKIGFRRSTFL

RSYMYDFIQRFAPHLTRDVVDTAVALRSNEDIEAMFKDIKLPEK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901776.1\_2443 [locus\_tag=BN49\_RS13735] [protein=YmiA family putative membrane protein] [protein\_id=WP\_002901776.1] [location=2509405..2509572] [gbkey=CDS]

MISNIDYMKLAMSYENDKTEIDPVLRSRVWGVVLVGLAMFWSIIALTICNIWIVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176472.1\_2444 [gene=acnA] [locus\_tag=BN49\_RS13745] [protein=aconitate hydratase AcnA] [protein\_id=WP\_004176472.1] [location=2509961..2512633] [gbkey=CDS]

MSSTLREASKDTLQVNDKTWHYYSLPLAEKQLGEISRLPKSLKVLMENLLRWQDGDSVTEEDIRALAGWL

QQAHADREIAYRPARVLMQDFTGVPAVVDLAAMREAVKRLGGDTAKVNPLSPVDLVIDHSVTVDRFGDDE

AFEDNVRLEMERNHERYAFLRWGQQAFSRFSVVPPGTGICHQVNLEYLGRAVWSEEVNGQWMAWPDTLVG

TDSHTTMINGLGVLGWGVGGIEAEAAMLGQPVSMLIPDVVGFKLSGKLREGITATDLVLTVTQMLRQHGV

VGKFVEFYGDGLDTLPLADRATIANMAPEYGATCGFFPIDDVTLSYMRLSGRSEEQVALVEAYAKAQGMW

RQPGDEPVFTSTLALDMSSVEASLAGPKRPQDRVALGDVPKAFAASGELEVNHLQRQRQPVDYTLNGHHY

SLPDGAVAIAAITSCTNTSNPSVLMAAGLLAKKAVERGLQPQPWVKASLAPGSKVVSDYLAHAGLTPYLD

QLGFNLVGYGCTTCIGNSGPLPEPIEEAIKKGDLTVGAVLSGNRNFEGRIHPLVKTNWLASPPLVVAYAL

AGNMNIDLTREPLGQGKNGEPVYLKDIWPSGEEIARAVEQVSTEMFRKEYAEVFSGTEEWKAIKVEASDT

YDWQEDSTYIRLSPFFDEMGAEPLPVEDIRGARILAMLGDSVTTDHISPAGSIKADSPAGRYLQEHGVAR

RDFNSYGSRRGNHEVMMRGTFANIRIRNEMVPGVEGGMTRHLPDPEPMAIYDAAMLYKAEGTPLAVIAGK

EYGSGSSRDWAAKGPRLLGIRVVIAESFERIHRSNLIGMGILPLEFPQGVTRKTLRLTGEERIDISNLQS

LQPGATVPVTLTRADGSQEAIPCRCRIDTATELTYYRNDGILHYVIRNML

>lcl|NZ\_FO834906.1\_prot\_WP\_002901778.1\_2445 [gene=ribA] [locus\_tag=BN49\_RS13750] [protein=GTP cyclohydrolase II] [protein\_id=WP\_002901778.1] [location=complement(2512680..2513282)] [gbkey=CDS]

MQLKRVAEAKLPTPWGDFLMVGFEELATGQDHVALVYGDISGQSPVLARVHSECLTGDALFSLRCDCGFQ

LEAALSHIAEEGRGILLYHRQEGRNIGLLNKIRAYALQDQGYDTVEANHQLGFAADERDFTLCADMFKLL

NVEQVRLLTNNPKKVEILTEAGINIVERVPLIVGRNPKNAHYLDTKAAKMGHLLNSKPTE

>lcl|NZ\_FO834906.1\_prot\_WP\_002901779.1\_2446 [gene=pgpB] [locus\_tag=BN49\_RS13755] [protein=phosphatidylglycerophosphatase B] [protein\_id=WP\_002901779.1] [location=2513446..2514213] [gbkey=CDS]

MLLIARRTALAAALLLVMPLTVWLSGWLWQPGLPVAMLKSLWWVTETVTQPWGIITHVVLCGWFLWCLRF

RLRAALILFLILAAAILAGQGAKSWVKARVQEPRPFVIWLENTRQVPVTQFYALKRKERAKLVHEQLAQA

QDIPSFLRKHWQKETGFAFPSGHTMFAASWALLAAGLLWPRRRWGTIAVLLVWATAVMGSRLALGMHWPL

DLIVATLISWLLVTVACWLTQRLCGPLSPPGEEAQDIKKRMPEAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002901780.1\_2447 [locus\_tag=BN49\_RS13760] [protein=LapA family protein] [protein\_id=WP\_002901780.1] [location=2514349..2514657] [gbkey=CDS]

MKYLLIFLLVLAIFVISVTLGAQNDQQVTFNYLLAQGEFRISTLLAVLFAAGFAIGWLICGLFWLRVRVS

LARAERKIKRLEHQIAPVSPAAVDAGVPAVKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002901781.1\_2448 [gene=lapB] [locus\_tag=BN49\_RS13765] [protein=lipopolysaccharide assembly protein LapB] [protein\_id=WP\_002901781.1] [location=2514664..2515833] [gbkey=CDS]

MLELLFLLLPVAAAYGWYMGRRSAQQSKQDDASRLSRDYVAGVNFLLSNQQDKAVDLFLDMLKEDTGTVE

AHLTLGNLFRSRGEVDRAIRIHQSLMESASLTYDQRLLAVQQLGRDYMAAGLYDRAEDMFKQLVDETDFR

LGALQQLLQIYQATSDWQSAIEVAERLVKLGKEKHRGEIANFWCELALQQMAANDLDKAMALLRKGAAAD

RTSARVSIMMGRVWMEKGDYAKAVESLERVIDQDKELVGETLEMLQTCYQQLGKTDEWEVFLRRCVEENA

GATAELMLAQILEQREGVEAAQNYVTRQLERHPTMRVFHKLMDYHLNEAEEGRAKESLGVLRNMVGEQVR

SKPRYRCQKCGFTAHTLYWHCPSCRSWATIKPIRGLDGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004151907.1\_2449 [gene=pyrF] [locus\_tag=BN49\_RS13770] [protein=orotidine-5'-phosphate decarboxylase] [protein\_id=WP\_004151907.1] [location=2516025..2516762] [gbkey=CDS]

MTSTAIPSSRAVTSSPVVVALDYDNRDKALAFVDRIDPRDCRLKVGKEMFTLLGPQFVRDLHQRGFEVFL

DLKFHDIPNTTARAVAAAAELGVWMVNVHASGGARMMTAAREALLPFGKDAPLLIAVTVLTSMESSDLQD

LGITLSPADYAAKLAALTQRCGLDGVVCSAQEAVRFKHELGQAFKLVTPGIRPQGSDAGDQRRIMTPEQA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002901782.1\_2450 [gene=yciH] [locus\_tag=BN49\_RS13775] [protein=stress response translation initiation inhibitor YciH] [protein\_id=WP\_002901782.1] [location=2516762..2517088] [gbkey=CDS]

MSDSNSRLVYSTETGRIDEAKPAPVRPKGDGIVRIQRQTSGRKGKGVCLISGIDADDAALTALAAELKKK

CGCGGAVKDGVIEIQGDKRDLLKSLLEAKGMKVKLAGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002901783.1\_2451 [gene=osmB] [locus\_tag=BN49\_RS13780] [protein=osmotically-inducible lipoprotein OsmB] [protein\_id=WP\_002901783.1] [location=complement(2517220..2517438)] [gbkey=CDS]

MTSTSKKMAAVVLAVTVAMSLSACSNMSKRDRNTAIGAGAGAIGGAVLTDGSALGTLGGAAVGGIIGHQV

GK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901785.1\_2452 [locus\_tag=BN49\_RS13790] [protein=DNA-binding transcriptional regulator YciT] [protein\_id=WP\_002901785.1] [location=complement(2517713..2518462)] [gbkey=CDS]

MNARQQSILQVVIDKGRMSVADLAKMTGVSEVTIRQDLNLLEKQSYLRRTHGYAVPLDSEDVETRMMTHF

AIKRELASRAAALVNTGETVFIENGSSNALLARTLAERGDITIITVSSYIAHLLKETPGEVILLGGIYQK

RSESMVGPLTRQFIQQVHFSKAFIGIDGWQAETGFTGRDMMRADVVNAVLEKHCEAIILSDSSKFSAVHP

YPLGPAGRFNRVITDDRLPDACREQLLRSGLTVDIVPYI

>lcl|NZ\_FO834906.1\_prot\_WP\_002901786.1\_2453 [locus\_tag=BN49\_RS13795] [protein=hypothetical protein] [protein\_id=WP\_002901786.1] [location=complement(2518534..2518713)] [gbkey=CDS]

MSDVNAHLLAQRIDTVLDILVAGDYHSAIHNLEILKAELLALAADDAEQQNQPKAPWEI

>lcl|NZ\_FO834906.1\_prot\_WP\_002901787.1\_2454 [locus\_tag=BN49\_RS13800] [protein=exoribonuclease II] [protein\_id=WP\_002901787.1] [location=complement(2518872..2520806)] [gbkey=CDS]

MFQDNPLLAQLKQQLHSQTPRAEGVVKGTEKGFGFLEVDAQKSYFIPPPQMKKVMHGDRIVAVIHSEKER

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RGFYAELTQFITFSDDHFVPWWVTLARHNLEKEAPDGVATEMLDEGLTRRDLTALDFVTIDSASTEDMDD

ALYAESTADGKLLLTVAIADPTAWIAEGSKLDNAAKVRAFTNYLPGFNIPMLPRELSDDLCSLRANEVRP

VLACRMTLAADGTIEDNIEFFAATIESKAKLAYDDVSDWLEGRGSWQPDSEAIAQQITLLKDVCQRRSEW

RQTHALVFKDRPDYRFVLGEKGEVLDIVAEPRRIANRIVEESMIAANICAARVLRDKLGFGVYNVHTGFD

PANTEQLAALLKTHDVHVDPTEVLTLEGFCKLRRELDAQPTGFLDSRIRRFQSFAEISTEPGPHFGLGLE

AYATWTSPIRKYGDMINHRLLKAIIKGETIARPQDEATVQMAERRRLNRMAERDVADWLYARFLNDKAGT

DTRFAAEIIDVSRGGMRVRLVDNGAVAFIPAPFLHAVRDELVCSQENGTVQIKGEVVYKVTDVIDVTIAE

VRMETRSIIARPAV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043101.1\_2455 [locus\_tag=BN49\_RS13805] [protein=carboxymuconolactone decarboxylase family protein] [protein\_id=WP\_046043101.1] [location=complement(2520888..2522045)] [gbkey=CDS]

MEPRRVNGKNHWYHETQSTICPVDVLPLVPEAAHVEDRFLLDLTLPAAWLRAHADWLHPARQLAELLFPD

QVAVSRLQTFTAYDRLSTALTVAQVYGVQRLCNHYAARLAPLPGPDSSRESNRRLAQITQYARQLAGSPS

VINALSRSQLDEVGLTSRDIILFNQIIGFVGFQARAIAVLQAAQGFPVRWIPGMPQQEEAPAELFAPPPG

AWQADIADPDLQYADDERQRRIAGWQSLPGLGELAPLLACDPQLFAPLETLIRQLSTDDTFGPQVALLTA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004140277.1\_2456 [gene=fabI] [locus\_tag=BN49\_RS13815] [protein=enoyl-ACP reductase FabI] [protein\_id=WP\_004140277.1] [location=complement(2522236..2523024)] [gbkey=CDS]

MGFLSGKRILITGVASKLSIAYGIAQAMHREGAELAFTYQNEKLKGRVEEFAAALGSDIVLPCDVAEDES

ITALFTELEKVWPKFDGFVHSIGFAPADQLDGDYVDVVTRDGFKIAHDISAYSFVAMAKACRGMLNPGSA

LLTLSYLGAERAIPNYNVMGLAKASLEANVRYMANAMGPEGVRVNAISAGPIRTLAASGIKDFRKMLAHC

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>lcl|NZ\_FO834906.1\_prot\_2457 [locus\_tag=BN49\_RS13820] [protein=HutD family protein] [pseudo=true] [location=complement(2523223..2523765)] [gbkey=CDS]

MMVPFQLSTLPVTPWKNGGGETREIICVPAPDAPFLWRASIATLQADGPFSPFPGVDRVITLLAGQPLRL

CGENIDQPLALWQPWAFPGEWALSSVGIVAPGLDFNIMTQRGRASATVQVVSDL\*CPASEGVAYVLQGEW

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151902.1\_2458 [locus\_tag=BN49\_RS13825] [protein=cytosine permease] [protein\_id=WP\_004151902.1] [location=2524013..2525392] [gbkey=CDS]

MSERRSIDYIPESERHGHPFSQFTLWFGGNLQITAIVTGALAVVLGGDVVWSLVGLLVGQMLGAAVMSLH

ALQGPRLGLPQMILSRAQFGVFGAVVPLVLVCVMYIGFSASGTVLAGQAMAKLLNISHVAGMLIFSAIII

VIAVLGYKVIHKLGKLASIVGILAFVYMFITLLLSADLSALAHNNHFSLPTFLLAVSLSSSWQIAFCPYV

SDYSRYLPRDVSATKTWCSVFFGTVLGTQTSMTLGVLTAAIAGSAFPGHEVSYLVGLGKSQAMAMVIYFA

ICFGKITFTTLNAYGSFMSLTTIVSAFRRQTVLSQKCRIAFVVLMVTASCIIALLSEPAFLKHFTHFLLF

LLAFFVPWSAICLTDYYLISKGAIDIPALSDPQQRYGFWNLYAITLYIVGVLIQLPFIENPLFHGSLTWI

FAGNDVSWIIGWFGTGVLYYALRRFDRRSLPAQSLFPST

>lcl|NZ\_FO834906.1\_prot\_WP\_004140269.1\_2459 [gene=sapF] [locus\_tag=BN49\_RS13830] [protein=peptide ABC transporter ATP-binding protein SapF] [protein\_id=WP\_004140269.1] [location=complement(2525437..2526246)] [gbkey=CDS]

MVETLLEVRQLSKTFRYRTGWFHRQTVEAVKPLSFTLRERQTLAIIGENGSGKSTLAKMLAGMVEPTSGE

LLIDDHPLTFGDYSYRSQKIRMIFQDPSTSLNPRQRISQILDFPLRLNTDLDAEARQKQIIDTLRMVGLL

PDHVSYYPHMLAPGQKQRLGLARALILRPKVIVCDEALASLDMSMRSQLINLMLELQEKQGISYIYVTQH

LGMMKHISDQVLVMHNGEVVERGSTADVLASPLHDLTRRLIAGHFGEALTADAWRKDGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532044.1\_2460 [gene=sapD] [locus\_tag=BN49\_RS13835] [protein=peptide ABC transporter ATP-binding protein SapD] [protein\_id=WP\_016532044.1] [location=complement(2526248..2527240)] [gbkey=CDS]

MPLLDIRHLTIEFKTSEGWVKAVDRVSLTLTEGEIRGLVGESGSGKSLIAKAICGVTKDNWRVTADRMRF

DDIDLLRLPNRERRKLIGHNVSMIFQEPQSCLDPSERIGQQLIQSIPGWTYKGRWWQRLGWRKRRAIELL

HRVGIKDHKNAMRSFPYQLTEGECQKVMIAIALANQPRLLIADEPTNAMEPTTQAQIIRLLTRLNQNNNT

TILLISHDLQMLSKWADKINVMYCGQTVESGPSEELITLPHHPYTQALIRAIPDFGSAMPHKSRLNTLPG

AIPLLEQLPIGCRLGPRCPYAQRECIETPRLTGARNHLYACHFPLNMEKE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151901.1\_2461 [gene=sapC] [locus\_tag=BN49\_RS13840] [protein=peptide ABC transporter permease SapC] [protein\_id=WP\_004151901.1] [location=complement(2527240..2528130)] [gbkey=CDS]

MPYDSVYLEKRPPGALRTVWRKFYGDTTAMIGLYGCAGLLLLCVFGGWFAPYGIDQQFLGYQLLPPSWSR

YGEVSFFLGTDDLGRDVLSRLLSGAAPTVGGAFVVTLGATLFGLVLGVIAGSTHGLRSAVMNHILDTLLS

IPSLLLAIIVVAFAGPHLSHAMFAVWLALLPRMVRSVYSMVHDELEKEYIIAARLDGASTLNILLFAILP

NIASGLVTEITRALSMAILDIAALGFLDLGAQLPSPEWGAMLGDALELIYVAPWTVMLPGAAIMLSVLLV

NLLGDGIRRAIIAGVE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532045.1\_2462 [gene=sapB] [locus\_tag=BN49\_RS13845] [protein=putrescine ABC transporter permease SapB] [protein\_id=WP\_016532045.1] [location=complement(2528117..2529079)] [gbkey=CDS]

MIIFTLRRLLLLITLFFLTFVGFSLSYFTPHAPLQGASLWNAWLFWFEGVLHWDFGVSSINGQLISEQLR

EVFPATMELCILAFGFALLIGIPVGMIAGVMRNKWPDTLISAVALVGFSIPVFWLALLLTLFFSLTLGWL

PVSGRFDLLYEVKNVTGFALIDAWLSDSPWRHEMIVSAARHMVLPVLTLAVAPTTEVIRLMRISTSEVYD

TNYVKAAATRGVSRRKILLRHVLHNALPPVIPRLGLQFSTMLTLAMITEMVFSWPGLGRWLINAIRQQDY

AAISAGVMVIGALVIIVNVISDILGAMANPLKHKEWYALR

>lcl|NZ\_FO834906.1\_prot\_WP\_002901817.1\_2463 [gene=sapA] [locus\_tag=BN49\_RS13850] [protein=peptide ABC transporter substrate-binding protein SapA] [protein\_id=WP\_002901817.1] [location=complement(2529076..2530719)] [gbkey=CDS]

MRLKLSSLLAAVSLLCGPAFAAPALPDRADIRDSGFVYCVSGQVNTFNPQKVSSGLIVDTLAAQIYDRLL

DVDPYTYRLVPELAESWEVLDNGATYRFHLRRHVPFQRTAWFTPTRDFNADDVIFTFGRIFNRDHPWHNV

NGSSFPYFDSLQFADSVESVRKLDNQTVEFRLKRPDASFLWHLATHYASITSAEYAARLTQDDRQEQLDR

QPVGTGPFQLSDYRSGQYVRLQRHPGYWRGKPLMPQVVVDLGSGGTGRLSKLLTGECDVLAWPAASQLTI

LRDDPRLRLTLRPGMNIAWLAFNTAKPPLDNPEVRHALALAINNQRLMQSIYYGTAETAASMLPRASWAY

DNDAKITEYNPQEARARLKALGLENLTLKLWVPTSSQAWNPSPLKTAELIQADMAQIGVKVIIVPVEGRF

QEARLMDMSHDLTLSGWATDSNDPDSFFRPLLSCAAIASQTNFAHWCNREFDDVLQKALLSQQLSSRMDA

YKEAQRILARELPVLPLASSLRLQAYRYDMKGLVLSPFGNASFAGVSRENTEEVKKP

>lcl|NZ\_FO834906.1\_prot\_WP\_009484624.1\_2464 [locus\_tag=BN49\_RS13855] [protein=SDR family oxidoreductase] [protein\_id=WP\_009484624.1] [location=complement(2531053..2531961)] [gbkey=CDS]

MMRIFLTGASGFIGSRILPALQASGHQVIGLARSESTAQALKAAGAEVHRGTLDAPESLLAGVGNADAVI

HTAFDHDFSRFAANCEKDRQAILALGQALRGSTRPLVITSGTLMGDDGSGAPARESFFNSGHPSPRTASE

LAGQQLLEAGVDVRVVRLPQVHDTVRQGLLTCYIERAVANGAVALRGEGSNRWSAAHVDDVARLYVSALL

QGAAGERYHAVAEEGIALRDIAAVIAHGLNLPLTHLDESQVDAWFGWFAPFTALDLRASSAWTRERLQWQ

PVGPGLLEDLQNMDYHKVTLSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004140254.1\_2465 [locus\_tag=BN49\_RS13860] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004140254.1] [location=2532069..2532911] [gbkey=CDS]

MNTSDNHALGDFLRARRQRLDPATFGFPAGRRRTPGLRREEVAQLASISPTWYTWLEQGRGGAPSREVLE

RIARGLRLTTPEREHLFILAFGHPPQTRLTVTDDMTPRLQRVLDAFTIPAIIRTASWDVIAWNAPAARVL

TDYSQLPLAERNVLRRLFTRPEARCTLEDWQRVGQLIVNAFRADVTRMGATKETDQLIAELSQQSVEFAR

FWQSHDVAGHGEGYKRINHPQMGPLDLEFTSFAVEGRPDLSLLVFNPATTESQRKIHGLLQGAGSAPEES

>lcl|NZ\_FO834906.1\_prot\_WP\_046043105.1\_2466 [locus\_tag=BN49\_RS13865] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_046043105.1] [location=complement(2532878..2535199)] [gbkey=CDS]

MEHHAGDFSVTVRDVRQLTQPESDLLTLLWVLEGSVNLAVAEGASQPLAADGLAIVNLNRRWSLRSAGAN

AVMILTLSASWLARLDNAFFAVDYQITPRTRDADDGLRRLMRQLLVSGLVNHPGHYRLEANRWLSEIALL

LATRFSQPIASTPRRDTEKWSRRIASVVARIDANYQRRLSLQEVAAAEFVSEAWLSRLFRKEVGVSFVQY

LTALRLRHAADQLLTTRKTVQQIAREQGFASTRMMSDLFKRQHGVTPRQYREQHPLELARPRPPQADRWQ

PVAADRLYARLNEPEPRDRESPPLPINPPQTREINLRDRPARPAALRHTRMVVTVRELDDLLREDVRREL

EQLHHALPVYAIDINDPFLSSRLFGTGWDDPQMAGYACWYNLQQIFSWLAAMGWQVILHTGVTTRSDLLQ

RFLQLAANHFPPATLNSWRFVWHWSPQASEAARQAAWRQQRGVLHRLLPQPQLGIWHRFAPSDPGNDPLF

HSPLLAEADFLACQADANEQLDLAQADSSRLASSEHYPLHKLRQIHSALRQRQLNLPLWLLSWNTLTGDT

RDTNGRFFRGALLMDNLLGVADQVWLAGFWLNSGLQGEARANGKLDTSSLALHYLHGLPRPVYWVLWLWR

RLRGEILVHDKNLLLLHHQGHYQLLLRNTVVYNPWLSSEAAFIQRFSQPYSVRLQGLDGSWRIKQHLFDQ

HHGALFPLVDAFRSRSGPDAEDYQWLMHQARPALSVDEARLDGYWLRIDSLQSNALVLYEFTPQLSSGAD

PAP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043107.1\_2467 [locus\_tag=BN49\_RS13870] [protein=M20 family metallopeptidase] [protein\_id=WP\_046043107.1] [location=2535371..2536540] [gbkey=CDS]

MTHPLLEALQVNEAQFIALRRRFHQQPEIGFEEHQTSSEVARLLGEWGYEVHRGLAGTGVVGTLRVGEGK

KRLGLRADMDALPMQERSGKPWASQVEGRFHGCGHDGHTTTLLYAAEYLARTRQFTGTLQLIFQPAEELL

YGGRVMVEDGLFDQFPCDAIFGLHNMPGQTLGKIGLRDGAMMASSDTLHIEVKGVGGHGAVPEHTVDATL

VACHITLALQSIVSRNITPFEPAVVTVGSIQAGHAPNIINDHVLMKLTVRTLNEQVRETVLQRIHDIAVA

QAESFNATATLTHVNGSPVLRNDPATNAVVREVATALFGAEQVGEVKPFMGSEDFAFMLEQHPHGSYFTI

GAGDEPDRCMVHNPGYDFNDALLLTGAALWCGLTERYLR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043109.1\_2468 [locus\_tag=BN49\_RS13875] [protein=MFS transporter] [protein\_id=WP\_046043109.1] [location=2536566..2537957] [gbkey=CDS]

MSTVTKSDTPFVGNDRLLVGIVLSVLTFWLFAQSMINVVPAMKSSLDISLETLTLAVSLSALFSGCFVVA

SGGLADKFGRMRMTTLGLGLSIVGSAMLVVAQGPGLFLAGRVLQGLSAACIMPATLALIKTWYEGRARQR

AVSFWVIGSWGGSGLCSFVGGAIATGLGWRWIFVFSIAVALLALFLLRGTPESRSASASQHKLDVGGLLS

LIVALVLVNLFISKGHGWGWSSPLSLTMLAGALAAGTIFIRNGMRKGEAALIDFALFRNRAYGAAVLSNF

LLNGAIGTMMIASIWLQQGHHLTPLESGMMTLGYLVTVLAMIRVGEKLLQRYGARLPMMAGPVLTAIAIA

LISCTFLEKALYIGVVFASNVLFGLGLGCYATPSTDTAVANAPENKIGVASGIYKMGSSLGGAMGIAVTA

SLFALFLPLGMAHAAQYALWFNAVLCLGAMAVSALLLPRASHS

>lcl|NZ\_FO834906.1\_prot\_WP\_004148137.1\_2469 [gene=pspF] [locus\_tag=BN49\_RS13880] [protein=phage shock protein operon transcriptional activator] [protein\_id=WP\_004148137.1] [location=complement(2537948..2538937)] [gbkey=CDS]

MAKFIMAQYKDNLLGEANSFLEVLEQVSRLAPLDKPVLVIGERGTGKELIANRLHYLSSRWQGPFISLNC

AALNDNLLDSELFGHEAGAFTGASKRHPGRFERADGGTLFLDELATAPMLVQEKLLRVIEYGELERVGGS

QPLQVNVRLVCATNADLPQMVEEGHFRADLLDRLAFDVVQLPPLRDRQSDIMLLANQFAIQMCRELGLPL

FPGFSERATATLLGYRWPGNIRELKNVVERSVYRHGDSEHELDAIIINPFRQSPGSPPEAAPGDELPALP

LDLRDFQLQQEKRLLQRSLEQAKYHQKQAAELLGLTYHQLRALLKKHQL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531923.1\_2470 [gene=pspA] [locus\_tag=BN49\_RS13885] [protein=phage shock protein PspA] [protein\_id=WP\_016531923.1] [location=2539090..2539752] [gbkey=CDS]

MGIFSRFADIVNANINSLLEKAEDPQKLVRLMIQEMEDTLVEVRSTSARALAEKKQLSRRIEQAVAQQAE

WQEKAELALRKEKEDLARAALIEKQKLTDLIAQLDHEVQLVDETLARMKKEIGELENKLSETRARQQALA

LRHQAASSSRDVRRQLDSGKLDEAMARFESFERRIDQMEAESHRFGKQQTLDQQFAELKADDEISEQLAA

LKAKMNQSNQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002901911.1\_2471 [gene=pspB] [locus\_tag=BN49\_RS13890] [protein=envelope stress response membrane protein PspB] [protein\_id=WP\_002901911.1] [location=2539808..2540032] [gbkey=CDS]

MSMLFLAIPLTLFVLFVLPVWLWLHYNNRGANGSLTQNEQQRLLQLTDDAKRMRERIQALEAILDAEHPN

WRDK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901913.1\_2472 [gene=pspC] [locus\_tag=BN49\_RS13895] [protein=envelope stress response membrane protein PspC] [protein\_id=WP\_002901913.1] [location=2540032..2540391] [gbkey=CDS]

MAGLDLNKKLWRIPQRGMVKGVCAGIAQHLDVPVKLVRLITVLAMIFGLFFFVLVAYIILTFALDPIPDS

ELYGHKAPSNGDLLAAVDAELASGEQRLREMERYVTSDTFTLRSRFRQL

>lcl|NZ\_FO834906.1\_prot\_WP\_002901915.1\_2473 [gene=pspD] [locus\_tag=BN49\_RS13900] [protein=phage shock protein PspD] [protein\_id=WP\_002901915.1] [location=2540420..2540638] [gbkey=CDS]

MNSKWQRAGQQVKPGLKIVGKLALLTALRYGPAGVAGWAVKSVARRPLKMLLAVALEPLLSRLANRVTRG

MK

>lcl|NZ\_FO834906.1\_prot\_WP\_002901917.1\_2474 [locus\_tag=BN49\_RS13905] [protein=YcjX family protein] [protein\_id=WP\_002901917.1] [location=2540741..2542138] [gbkey=CDS]

MKRLKTELNALVNRGVDRHLRLAVTGLSRSGKTAFITALVNQLLNIHTGARLPLLSAAREERLLGVKRVP

QRDFGIPRFTYDEGLAQLYGQPPMWPTPTRGVSEIRLALRYRSNDSLLRHFKDTSTLYLEIVDYPGEWLL

DLPMLAQDYLSWSRQMTGLLQGQRAEWSARWRQLCAGLDPLAPADEARLADIAAAWTDYLHACKREGLHF

IQPGRFVLPGEMAGAPALQFFPWPDVDAVGEAKLAQADKHSNAGMLRERYKYYCERVVKGFYKEHFLRFD

RQIVLVDCLQPLNSGPQAFNDMRLALTQLMQSFHYGQRTLFRRLFSPVIDKLLFAATKADHVTIDQHSNM

VSLLQQLIQDAWQNAAFEGISMDCLGLASIQATQSGLIEVNGEKIPALRGNRLSDGQPLTIYPGEVPARL

PGQAFWQQQGFQFENFRPQVMDVDRPLPHIRLDAALEFLIGDKLR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043112.1\_2475 [locus\_tag=BN49\_RS13910] [protein=YcjF family protein] [protein\_id=WP\_046043112.1] [location=2542135..2543196] [gbkey=CDS]

MSEPLKPRIDFDGPLQAEKIPPLKGARAFDTLEADNFAPARLVTGEEEEGAAEAVVESVLRPKRSLWRRM

VSAGLAIFGVSVVAQGVQWTANAWQTQDWIALGGCVAGALIVGAGVGSVATEWRRLWRLRQRAHERDEAR

DMLHSHVVGKAKAFCEKLAQQAGLDQSHPALQRWYAAIHETQSDREVVSLYAQLVQPVLDAQARREISRS

AAESTLMIAVSPLALVDMAFIAWRNLRLINRIATLYGIELGYYSRLRLFRLVLLNIAFAGASELVREVGM

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PEK

>lcl|NZ\_FO834906.1\_prot\_WP\_227504847.1\_2476 [locus\_tag=BN49\_RS13915] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_227504847.1] [location=complement(2543286..2544155)] [gbkey=CDS]

MQTFEVTARHLSFTLAAHEMNLTQGAVSHRIRRLEMHIGFRLFIRMTRKLALTEEGKRLLATLSHSLRAI

NDEIEDIRDQDLRGTLHIGIAPTLAHLWLMPRLPRFQTQWPGLNLQFRVRAGVMDFNEERVDLAIYYGAT

RYPDLYQQRLMAESLLPVCSPRYRQQYRPLSGGDPAALVWIHACESTDVQDQFAEWRLWCQHSGQALPFD

GRYYAVNNHSLAIEMALNGLGMVMGRKTLIQPLLDAGRLVALSENEAPSPFGYDLICPQENRSRPRFRAF

SEWLAAECA

>lcl|NZ\_FO834906.1\_prot\_WP\_002901977.1\_2477 [locus\_tag=BN49\_RS13920] [protein=6-phospho-beta-glucosidase] [protein\_id=WP\_002901977.1] [location=2544299..2545612] [gbkey=CDS]

MSGLKIVVIGGGSSYTPELIEGLLNRYHEMPVASLWLVDIEEGKEKVEIIAGLARRMIAKAGLTIEVVAT

LDRESALRDADFVCSQFRAGCLDARISDERISLKYGLIGQETNGLGGFANACRTIPIALEIAADMERLCP

DAWLLNFTNPSGMVTEAILRHSRIKAVGLCNVPVIMQKGITTLLQCADEKEVVMQVAGLNHFIFVRQILH

KGKEWLPEVIAEINAGRDPLVPRNIPPFRWPSHLLQGLGMIPCAYLRYYYMKDDLLRQELAEAGGEGTRG

EVVKQLEKILFDQYRDPHLAVKPKALEGRGGQYYSEAACELMNAIYNDKRIIMHVNTRNNGAINGLPDDC

AVEVSSLITASGPLPLNVAPFPEDTLRLLQLMKSFERLTIEAALTGNRHTAWRALMLNPLIVSGEKLELA

LDEVIAENRQWLPAFHA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043114.1\_2478 [gene=tyrR] [locus\_tag=BN49\_RS13925] [protein=transcriptional regulator TyrR] [protein\_id=WP\_046043114.1] [location=2545785..2547326] [gbkey=CDS]

MRLEVFCEDRLGLTRELLDLLVLRGIDLRGIDIDPIGRIYLNFAELEFATFSSLMAEIRRIAGVTDVRTV

PWMPSEREHLALSALLVAMPEPVLSLDTKGRVELANPASCLLFGQSQAKLRNHPVAQLIADFNVQRWLES

SPQETHAEHVVVNGQNYLLEVTPVYLEGEHNERVLTGAVAMLRSTVRMGRQLQTMTSQDTSAFSQILAVG

PKMRHVVEQARKLAMLSAPLLIVGDTGTGKDLLAHACHLASPRAGKPYLALNCGSIPEDAVESELFGDAL

QGKKGFFEQANGGSVLLDEIGEMSPRMQTKLLRFLNDGTFRRVGEDHEVHVDVRVICATQKNLIELVQKG

LFREDLYYRLNVLTLYLPPLRDCSQDIMPLTELFVARFADEQGIPRPKLSADLSTVLTRYSWPGNVRQLK

NAVYRALTQLEGFELRPQDILLPDHDVASLPVGEEAMEGSLDDITRRFERSVLTQLYRSYPSTRKLAKRL

GVSHTAIANKLREYGLSQKKGDE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531914.1\_2479 [locus\_tag=BN49\_RS13930] [protein=AbrB family transcriptional regulator] [protein\_id=WP\_016531914.1] [location=2547428..2548480] [gbkey=CDS]

MASRRAIGHWLILLLLSVLFSSLLLRIHLPAALLLGPLIAGLILSLRGVKLSIPRPCYLVAQAIVGCMIA

RAINPSVFGVLFNNWALVLAILLTTLAISGLTGWLLVRYSALPGATGAWGSSPGGASAMVVMAQEYGADV

RLVALMQYLRVLFVVGAAALVVRYALGNEAQEMTQDIVWFPSLTLNFPFTLLLTAVACWLGMRLRIPSGA

MLLPMLLGALAQGGGWLMLELPEWLLAMAYAVLGWTVGLQFNKAIFLLALKTLPQIIASILGLILMCALM

ALALTHILQMDFMTAYLATSPGGLDTVAIIAAGTRADMSFIMALQTLRLFTILLTGPAMARAISRYAPRQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004152131.1\_2480 [gene=tpx] [locus\_tag=BN49\_RS13935] [protein=thiol peroxidase] [protein\_id=WP\_004152131.1] [location=complement(2548551..2549057)] [gbkey=CDS]

MSQTVHFQGNPVSVQGTIPQAGAKAQPFTLVAKDLSDVALSQYAGKRKVLNIFPSIDTGVCAASVRKFNQ

LAAELDNTVVLCISADLPFAQSRFCGAEGLSNVVTLSTLRGASFLADYGVAIATGPLAGLAARAVVVIDE

NDQVVYSQLVNEITEEPDYDAALAALKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531913.1\_2481 [gene=ycjG] [locus\_tag=BN49\_RS13940] [protein=L-Ala-D/L-Glu epimerase] [protein\_id=WP\_016531913.1] [location=2549160..2550125] [gbkey=CDS]

MRNVRVYEEAWPLHTPFVIARGSRSEAKVVVVELEEDGVKGVGECTPYPRYGESIASVMAQVMAIGEQLE

AGLTREQLQRLLPAGAARNAIDCALWDLQARREGKTLAQLLGVALPNRVITAQTVVIGTPDQMAASAAAL

WQAGAQLLKVKLDDRLISERLIAIRQAAPEATLIVDANESWHSEGLAARCQLLADLGVAMLEQPLPADDD

TALENFVHPLPICADESCHTRESLPRLRGRYEMVNIKLDKTGGLTEALALAGEAERQGFERMLGCMLCTS

RGIAAALPLAPLARFADLDGPTWLAVDVEPALRFSTGVLHL

>lcl|NZ\_FO834906.1\_prot\_WP\_004152134.1\_2482 [gene=mpaA] [locus\_tag=BN49\_RS13945] [protein=murein tripeptide amidase MpaA] [protein\_id=WP\_004152134.1] [location=complement(2550122..2550829)] [gbkey=CDS]

MSISRPRPQRGDFPPGTRQYGSSELGAPLLWFPAPQADSRSGLIIAGTHGDENSSIVTLSCALRTLKPEL

RRHHVVLTVNPDGCQLGLRANARGVDLNRNFPAANWKQGETVYRWNSAAAERDVVLLTGEQPGSERETEA

LCQLIHQIHPAWVVSFHDPLACIEDPGHSPLGRWLADAFSLPLVGSVGYDTPGSFGSWCADIGLPCITAE

FPPVSADEATERYLPAMTDLLRWQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004148146.1\_2483 [locus\_tag=BN49\_RS31025] [protein=hypothetical protein] [protein\_id=WP\_004148146.1] [location=2550902..2551018] [gbkey=CDS]

MKSDGTSIFYHMSFAISGDETNNYRSVGGIFFILKGIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004176446.1\_2484 [locus\_tag=BN49\_RS13955] [protein=peptide ABC transporter substrate-binding protein] [protein\_id=WP\_004176446.1] [location=2551015..2552631] [gbkey=CDS]

MKYPVALTCGALWLASVSSLAWAADVPPGTVLAEKQLLVRHIKDEPASLDPAKAVGLPEIQVIRDLFEGL

VNQDAKGNLVPGVATRWQSNDNRVWTFTLRDNARWSDGTPVTAEDFVYSWQRLVDPKTTSPFAWFAALAG

IANAQNIIDGKAAPETLGVTAVDAHTLRVQLDKPLPWFSNLTASFAFYPVQKANVDSGANWTRPGSLVGN

GAYVLKDRVVNEKLVVVPNTHYWDNAKTVIQQVTFVPINQESAATKRYLAGDIDITESFPKNMYQKLLKD

IPGQVYTPPQLGTYYYAFNTQKGPTADERVRLALSMTIDRRVMAEKVLGTGEKPAWRFTPDVTAGFTPQP

SQFESMSQAELNAQAKALLAAAGYGPNRPLKLTLLYNTSENHQKIAIAVASMWKKNLGVEVKLQNQEWKT

YIDSRNTGNFDVIRASWVGDYNEPSTFLSLLTSTHSGNISRFNDPAYDKILAQAAVENSAKARNDDYNAA

EKIIMVKAPIAPIYQYTNGRLIKPWLKGYPITNPEDVAYSRTMYIVKH

>lcl|NZ\_FO834906.1\_prot\_WP\_046043117.1\_2485 [locus\_tag=BN49\_RS13960] [protein=hypothetical protein] [protein\_id=WP\_046043117.1] [location=2553044..2554057] [gbkey=CDS]

MMANILRSIPMLLVIGFNLLLAILFSLIYARKHPETDLFIIITFTGMLSISTYIISFYSVSTFATKEKKK

IKGVFPRRRGKLKRIITDSMVLILFFFVSGSIVFSGSDLNYGLALLAISTGYFTFLLVNYYFLCMSRVKE

KIVKIINKILFIVFSIILFFSKMIANGFVKEFFDVDIAKVPYISWSFSILFAIPFFLITSHVGCMILEGT

TDLFRTRKIKVPPMIHYSIFCLSCVFFSISYISYLGSAGWLFNAVTKKVYSYDTRSSFRCNNKYWTIPEL

GKDARYLAETSDSYRVIYIRGNNINVEVVKCKKNEEYILFPIENANDILKKQVPKGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004224315.1\_2486 [locus\_tag=BN49\_RS13965] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004224315.1] [location=complement(2554148..2555032)] [gbkey=CDS]

MAKRENYNDLYLFMQVVREGSFTAAAQRLGLAQSGVSRAVRELEERLGVQLLVRTTRRLSLTQAGEQLYH

NVESGFDALDMGLATLAHYRQTPSGTVRINASQHAIDKVLLPKLAVFKHRYPDIRLELISESRFVDIIAQ

RFDAGVRLGPEVGSGMIAVRISPDMEMAVVGTPEHFRRYGFPQTPADLVAHPCIAYQFGDGSLYAWELNV

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VSPALRAVIDTLRM

>lcl|NZ\_FO834906.1\_prot\_WP\_004224319.1\_2487 [locus\_tag=BN49\_RS13970] [protein=alpha/beta hydrolase] [protein\_id=WP\_004224319.1] [location=2555205..2556341] [gbkey=CDS]

MTVFTKKLTAAIPAMLLCASLTGVTTMSSAETTNPNAPVSMIEKWDKTFAESSKVDHRKVTFQNRYGITL

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TEDFSAAVDFLGLQKEVDRNRIGLLGICGWGGMALNDAAMDTRVKAVATSVMYDMSRAMGHGVGDGKDRY

TTADRRAVLRYLNVQRWKDAANGTFVPGGHDIYVDDKGNVSAADRILPETLPANPNPVLKEFFDYYRMPR

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>lcl|NZ\_FO834906.1\_prot\_WP\_004179500.1\_2488 [locus\_tag=BN49\_RS13975] [protein=MFS transporter] [protein\_id=WP\_004179500.1] [location=2556414..2557616] [gbkey=CDS]

MSALGHTRAHWSGVLAMTLCVFVLIASEFMPVSLLTPIAGDLHITEGLAGQGIALSGALAVLTSLTISRL

TGSLDRKWLLLGLTALMAASGVIIALASSFPVYMLGRALIGIVIGGFWSMSAATAIRLVPQRQVPRALAI

FNGGNALATVVAAPLGSYLGATVGWRGAFLCLVPLAVLAFVWQCISLPSMKSPRAPQRQGSVLRLFRLST

LSLGLLACGLFFMGQFTLFTYVRPFLETVTQVSPSGLSLILLTMGIAGFIGTLLITTVLNARFYPTLVAI

PLLMAAIAGTLLLAGHHTGSVAVLLSLWGLLATAAPTGWWTWIARTLPEDAETGGGLMVAVIQLSIALGS

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MEYSVLSNARKMPMLGFGVFKVTDKAECKQAVLNAIRTGYRLIDTAAVYDNEDAVGEAVREAIAEGLCTR

EALFITSKLWVQDMANTGMAKAGIAASLKKSGLEYFDLYLLHQAMGDYFSAWRALEEAYEAGTLKAIGVS

NFYPHVLANFCETVRIKPMVNQVELHPYFAQPAALEAMKHYHVQPEAWAPLGGGRHNPYQDALLRGIADA

HQKTIAQVVLRWNVQRGVTVIPKSTRQERIEENFAIWDFVLTDNEMAQISALDLGYVGEAVKHFNPEFVR

GCLGVKIHD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529241.1\_2490 [locus\_tag=BN49\_RS13990] [protein=ATP-binding protein] [protein\_id=WP\_016529241.1] [location=2558732..2559040] [gbkey=CDS]

MDASVAVAFKAAVSREIFAANDRVTLRFIDAGEIFPAERLALARNDEHFDVDTLAEGGRGLRLILRAVDY

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>lcl|NZ\_FO834906.1\_prot\_WP\_004176439.1\_2491 [locus\_tag=BN49\_RS29055] [protein=hypothetical protein] [protein\_id=WP\_004176439.1] [location=complement(2559111..2559299)] [gbkey=CDS]

MIEHIHFRCPCCHGSQYRTSQFDVTEKNPFGAKCIFCKSAMMTLDTIRPHHLGVHSAAQAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529242.1\_2492 [locus\_tag=BN49\_RS13995] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016529242.1] [location=complement(2559601..2560515)] [gbkey=CDS]

MDKLDTLTLFVRIVERGSFSAAAADLGVSRPVATAAIKALEVSLGARLLHRTTRHVRPTAEGSLYYQRCV

SILAALEEANRSAGGSISGTIRVDVAGNLARTLLLPALPQFLARYPDITLQIGESERDVDLVREGVDCVI

RGGHLPDSEMICRPLAGLQEITCASPTYLARYGTPHTIEGLTGHVMIGFVSSRTQRTLPLSFTQNGRQSE

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QVFIDWVTALMKPPLAQQASGRLK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529243.1\_2493 [locus\_tag=BN49\_RS14000] [protein=SDR family oxidoreductase] [protein\_id=WP\_016529243.1] [location=2560624..2561385] [gbkey=CDS]

MNNSAKIALVTGGSRGLGRATVEALAQRGVNVVLTYKTRLAEANEVVTRVEALGARAIALPFSAGEIDTF

DAFVSAFQGALTELGADKFDYLVNNAGNASGMGFLNATEAEFDALYRIHVKSVFFLSQKLLPLLADGGRI

VNVSSGLTRIVMANRAPYAIMKSAVETLTRYMAFELGSRGITVNCVAPGAIATDFSGGVVRDNPQVAQAV

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529244.1\_2494 [locus\_tag=BN49\_RS14005] [protein=HD domain-containing protein] [protein\_id=WP\_016529244.1] [location=2561602..2563134] [gbkey=CDS]

MDFENELTSKILDPIHGTIRLTTLEIAFINHPLFQRLRNIKQNSFLYKVFPSAVHSRFEHSLGVLHLSSE

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AYHSIIDVLSKPEQKVEHEHLSLLFSLMIYHDLRKQGKVDDEINIENVLKIIEKRYGDQQIIEEINGKAT

DILPLMTSIISSCPIDADRMDYLLRDGYFSGVKCGIYDYNRLFMSIVPVEEQGKLYLAYKESGIDSIAEF

IGARSSLFSQVYYHKTNRAFATMLSTLCEIMQSKDPQNVIIADVTDRIVDHSDESFIDALKDFYLACSDD

YFLNDKVGEWIDISDTEAVNKKILDDIINRHPWSKVYEAKHSVYKANIADKENKAWKSQLTGLLTSVLQP

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TPEIIYKINEIVVKQIALLN

>lcl|NZ\_FO834906.1\_prot\_WP\_004190556.1\_2495 [locus\_tag=BN49\_RS14010] [protein=DJ-1/PfpI family protein] [protein\_id=WP\_004190556.1] [location=complement(2563333..2563899)] [gbkey=CDS]

MSKKILMLVGDYAEDYETMVPFQALQMIGHQVDAVCPDKAAGDYVMTAIHDFDGAQTYSEKPGHRFTLNA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530462.1\_2496 [gene=tssB] [locus\_tag=BN49\_RS14020] [protein=type VI secretion system contractile sheath small subunit] [protein\_id=WP\_016530462.1] [location=2564540..2565031] [gbkey=CDS]

MADTFQNEVPRARINLKLSLHTGGAQKKVELPLKLLTIGDFSHGKENRPLSEREKINVNKNNFNSVLSEF

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530463.1\_2497 [gene=tssC] [locus\_tag=BN49\_RS14025] [protein=type VI secretion system contractile sheath large subunit] [protein\_id=WP\_016530463.1] [location=2565074..2566612] [gbkey=CDS]

MSVTTENAPVQGQTTLQENSAGEGVYASLFEKINLTPASRLGDINDFLDDAALSEAPAAERLTAAMQVFM

ERIRQSGQRVEKLDKTLIDHHIAELDFQISRQLDAVMHHQEFQQVESLWRGLKQLVDNTDYRQNVKTEIL

DVAKDDLRQDFEDAPELIQSGLYWHTYTAEYDTPGGEPIGSVISAYEFDASPQDVALLRNISRVSAAAHM

PFIGAVGPAFFLKETMEEVAAIKDIGNYFDRAEYIRWKAFRETDDARYIGLVMPRVLGRLPYGPDTVPVR

SFNYVEQVKGPDHEKYLWTSAAFSFASNMVKSFVNNGWCVQIRGPQAGGAVKDLPIHLYDLGTGNQVKIP

SEVMIPETREFEFASLGFIPLSYYKNRDYACFFSANSAQKPALYDTADATANSRINARLPYIFLLSRIAH

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>lcl|NZ\_FO834906.1\_prot\_WP\_171819472.1\_2498 [gene=tssK] [locus\_tag=BN49\_RS14030] [protein=type VI secretion system baseplate subunit TssK] [protein\_id=WP\_171819472.1] [location=2566622..2567965] [gbkey=CDS]

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RLTRLMAMRRESNERMADFAVADVSLFWLLNALNSAEPVLGYFLRYRQSPPERLYPELARLAGSLLTFSL

THQANAVPIYQHDQLNAVFPPLFDLLNDLLEASLPSRVVAIALEHDVRLHFWQARLHDARLREGADYYLS

VRSSVPVAQLQEQFLHQCKVGSPDHVKAIVNSSRTGVPLTPLRHVPAAIPLRLENQYFSLDVSHPLATEM

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>lcl|NZ\_FO834906.1\_prot\_WP\_004176431.1\_2499 [gene=tssL] [locus\_tag=BN49\_RS14035] [protein=type VI secretion system protein TssL, short form] [protein\_id=WP\_004176431.1] [location=2567962..2568651] [gbkey=CDS]

MNEPKRGNAASIDIDALLQNTWLQVISLRHGPQFRDEEGYTLWQRCIADVERVQHELKASGLDDASCQHI

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043125.1\_2500 [locus\_tag=BN49\_RS14040] [protein=OmpA family protein] [protein\_id=WP\_046043125.1] [location=2568648..2570354] [gbkey=CDS]

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DALTSALLALRWQLSQLRQQTGYAVPLALQGQVGSAMSRDLLWQAAIPGEAVKVWQPSCAPCSVPARVSA

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DIARYERIAMDDYRPKASAVRVLREDAALLDSWARNGVPLRLSLGLYHGEQIRLPLLEAIRGYVPPPPPP

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>lcl|NZ\_FO834906.1\_prot\_2501 [gene=hcp] [locus\_tag=BN49\_RS14045] [protein=type VI secretion system effector Hcp] [pseudo=true] [location=2570359..2570850] [gbkey=CDS]

MAIPVYLWLKDDGGADIKGSVDVQDREGSIEVVAQEHNLYIPTDNNTGKLTGTRIHTPFLFTKEIDASSP

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043127.1\_2502 [gene=tssH] [locus\_tag=BN49\_RS14050] [protein=type VI secretion system ATPase TssH] [protein\_id=WP\_046043127.1] [location=2571115..2573769] [gbkey=CDS]

MENPASLLRRLNPCCARAMEGAASLCQTRAHAEILPEHWLLKLLEQGEGDLTVLARRYEWDMDALWQDLL

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LERLRPLLDAQSDERPPAQQEAALAQPHGGDVEFVGRPAGSELNADGLNPALQNALDKFTLDVTAKARDG

LIDPVFGRDTEIRQMVDILSRRRKNNPILVGEPGVGKTALVEGLALRIAEGNVPDALKPVSVRTLDLGLL

QAGAGVKGEFEQRLKNIIEAVQQSPSPVLLFIDEAHTIIGAGNQGGGADAANLLKPALARGELRTIAATT

WSEYKQYFERDAALERRFQMVKVDEPDDDTACLMLRGLKSRYADHHGVHITDDAVRAAVTLSRRYLTGRQ

LPDKAVDLLDTASARLRMSLDTVPEPLTRMKAQLTALAMEKQALLEDIALGNSARGDRLAAIEQEEIRLI

LALDTLETQYGQELQLTEALLACRRDISRQAEINDLQTALIAVQQGNPLLGLDVDVRTVATVIADWTGVP

LSSLMKDEQTELLSLEESLGKRVVGQEAALSAIARRLRAAKTGLTPENGPQGVFLLVGPSGTGKTEKALA

LADALFGGEKALITINLSEYQEPHTVSQLKGSPPGYVGYGQGGILTEAVRKRPYSVVLLDEVEKAHRDVM

NLFYQVFDRGVMRDGEGREIDFRNTVILMTANLGSDLLMQLLDEQPEASESDLHELLRPVLRGHFQPALL

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>lcl|NZ\_FO834906.1\_prot\_2503 [gene=vgrG] [locus\_tag=BN49\_RS14055] [protein=type VI secretion system tip protein VgrG] [pseudo=true] [location=2573771..2576257] [gbkey=CDS]

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LRGQDFLFSLTKTYPRREQVMQYGEDDLRFITRLLGEVGIWFRFTADTRLHIDVAEFCDSQQGYEKGLTL

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AGNAHDRHPAPESGAFYARLRHERYLNGQTRMQATTSCPTLCPGQVLKVTGGEEVAGEFADGVLITAMHS

HARRDADFAVEFAGIPDSPDVGYRPEPGARPVMAGTLPARVTSTRENDTYGHIDKHGRYRVNMLFDRARW

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DTHISSGRKMVITAQDELTLICGGGYIKITGGNVEIGGSGKLLIKNSGIKKAGAGSMQGVMRSFEPSTFD

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>lcl|NZ\_FO834906.1\_prot\_WP\_227504841.1\_2504 [locus\_tag=BN49\_RS14060] [protein=hypothetical protein] [protein\_id=WP\_227504841.1] [location=2576259..2577083] [gbkey=CDS]

MRWSQSDRKVLTIIAIVGLLLYVIYKGLQFLAGVSMGASFGVGLGGMSGSQKVEESRKVETDAPPQVLYR

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>lcl|NZ\_FO834906.1\_prot\_WP\_227504842.1\_2505 [locus\_tag=BN49\_RS31445] [protein=hypothetical protein] [protein\_id=WP\_227504842.1] [location=2577116..2577307] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_042940556.1\_2506 [locus\_tag=BN49\_RS14065] [protein=DUF3274 domain-containing protein] [protein\_id=WP\_042940556.1] [location=2577297..2579231] [gbkey=CDS]

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PPRKYYAHAAKRLADMVDSIRNKYPKDTVTIISHSQGTMIAMAAVAIAKNAPDALFLLNSPYALDHNDLN

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>lcl|NZ\_FO834906.1\_prot\_WP\_032102817.1\_2509 [locus\_tag=BN49\_RS14075] [protein=type VI secretion protein VasK] [protein\_id=WP\_032102817.1] [location=2581020..2584415] [gbkey=CDS]

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LARLPGLETLAFNDGTPFADEVTLNWLNERVLDEMAGWQDEPVMAATSADEVLSLEPEVLTRADDEGIES

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>lcl|NZ\_FO834906.1\_prot\_WP\_004190503.1\_2512 [gene=tssG] [locus\_tag=BN49\_RS14090] [protein=type VI secretion system baseplate subunit TssG] [protein\_id=WP\_004190503.1] [location=2587801..2588886] [gbkey=CDS]

MGREAQPPHSRLTPRLEADLPRINFYRFCQLLEKRRPGQPLMGGTSHPADDPVRFYPHPGMGFPASELKA

VEYDEADDSRPPVIRTTFMGLYGVDSPLPTAYLDDIAQHREGHEALQGLLDIFSHRIMTQFYRIWRKYSW

PATFEPGGTDRLSQSLLGLAGLGIPGTTQHIASPASRFLALTGVLRQPGKTQQGIQALVTLLAPETTVRV

SPYSLRPVAISQPLGFYGDDDFFLDGNTPLGDEAMDASSQLLVALTTDNPAEAQGWKPDGPLFRDFLILL

RVYLGWRFRANITLTAPTRLLAVPPLGDEPFWLGMNGVLGVGEGESEGDIPQTFTTELGTYTGLQPATFL

QGNRRVTYKFD

>lcl|NZ\_FO834906.1\_prot\_WP\_004176417.1\_2513 [gene=tssJ] [locus\_tag=BN49\_RS14095] [protein=type VI secretion system lipoprotein TssJ] [protein\_id=WP\_004176417.1] [location=2588864..2589406] [gbkey=CDS]

MLRISLTKTACLLPLLALCLSGCGLTQRVSEGTKSAFNAVFYKKINTLHLDFTAREALNTDARENHSLSE

PVVVRIYQLKDRQTFDRLVYQQLLEEGDILLAADLLASRDVVIGPGGDASLNMPLEAEATFVAVVGLFRH

PDTQRNTWKQVLAREELDPDKPRIFTAEHNQLRLRPEAAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176416.1\_2514 [locus\_tag=BN49\_RS14100] [protein=hypothetical protein] [protein\_id=WP\_004176416.1] [location=2589533..2590027] [gbkey=CDS]

MTARERFFKKLQQQQNPRRTAALDGSAAADIARFRQQMAELAQQISQWFDGTGIEVVISTRHLHDLSTLG

YSLNSGICRYDIPAIRLQNGERSVNIVPQQLLDGVEKGIVTLSLEAPDGAGSREVFYLSLAPEEGWMIRK

AHQSPEARLMLTEDRFFMAVDSLA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043130.1\_2515 [gene=bdcA] [locus\_tag=BN49\_RS14105] [protein=SDR family oxidoreductase] [protein\_id=WP\_046043130.1] [location=complement(2590094..2590768)] [gbkey=CDS]

MTAFHNKSVLVLGGSRGIGAAIVRRFVADGASVVFSYSGSPEAAERLAAETGSTAVQADSGPLDVLVVNA

GIALFGDALEQDSDAIDRLFRINIHAPYHASVEAARRMPEGGRIIVIGSVNGDRMPVPGMAAYAVSKSAL

QGLARGLARDFGPRGITVNVVQPGPIDTDANPENGPMKELMHSFMAIKRHGRPEEVAGMVAWLAGPEASF

VTGAMHTIDGAFGA

>lcl|NZ\_FO834906.1\_prot\_WP\_004179574.1\_2516 [locus\_tag=BN49\_RS14110] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_004179574.1] [location=2590842..2591435] [gbkey=CDS]

MTTTKQGRTPGRPRQFDAEQAIETAQRLFHARGYDAVSVADLTQAFGINPPSFYAAFGSKLGLYTRVLQR

YSQTGAIPIDALLRDDQPVAASLIAVLQEAARRYVADPAAAGCLVLEGVHCQDADARVAAGEWHAAARAK

IQQYIARHRPQDALRVTDYMDTLMLGLSAKAREGDSLPRLLETVRLAGLALERILPA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530650.1\_2517 [locus\_tag=BN49\_RS14115] [protein=SDR family oxidoreductase] [protein\_id=WP\_016530650.1] [location=complement(2591440..2592195)] [gbkey=CDS]

MTKIALITGANRGLGRQTALDIARQDGDVIVTYRGSLEQAEAVVADIRALGRKAIALPLDMAQTASFPAF

ADSLGSALATVWGRATFDHLINNAGHGEFAPLAETREAQFDGLFNVHVKGVFFLVQTLLPLLADGGRIVN

FSSGLTRVSYPGFSAYAAAKAAVEMLSVYMARELGGRGITVNTIAPGAIATDFGGGLVRDDAEVNAQFAA

MTALGRVGVPEDIGPMIASLLRDDNRWVTAQRIEVSGGQTI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151595.1\_2518 [locus\_tag=BN49\_RS14120] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004151595.1] [location=2592354..2593232] [gbkey=CDS]

MRDALFDLCRRFADAHVDSSGVAVTPVPGITLVRALHPGDLQAAIARPLVAMLLQGRKSVTTGLASFDYG

PGEAMVIAADVPTTSQITEASQRFPYYALVLELDLAILRELQEAGPSGPDEAPRVGIEPMNADVTDAAYR

LARLFDQPGALAVLGEGLRRELHYWLLQSVHGPAIRALGAVDSHSARIRRAVAMLRRDFMQPVSVDALAD

AAGMSVSVFHRHFRAMTTLSPLQFQKQLRLIHARRLMLAEGMSIAQAAGEVGYISVSQFTREYARLYGAP

PGRDRRREKMSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016528839.1\_2519 [locus\_tag=BN49\_RS14125] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_016528839.1] [location=complement(2593283..2593489)] [gbkey=CDS]

MNKLMPLIVLSCLLPLAANARTITATGDTLDHAESKIRQQAAREGVTTYRITEARMGNKVHITAKIAD

>lcl|NZ\_FO834906.1\_prot\_WP\_016528838.1\_2520 [locus\_tag=BN49\_RS14130] [protein=aromatic alcohol reductase] [protein\_id=WP\_016528838.1] [location=complement(2593515..2594444)] [gbkey=CDS]

MKTDNFNHAEKVLVLGAGQLGTAVLDALVPAVIERQGTVSVIVSPAAWDEAGQLRSSNHQALADAGATFL

AVDIAGSAMETLADQFRGFTTVINCMGFVAGPGTQLKITRAVLAAGVPRYFPWQFGVNYDVVGKGSGQPV

WDEQYDVRTLLRAQRATEWVIVSTGMFTSFLFEPDFDVVNLSNRTLHALGSWDTQVTVTSPADIGRLTTA

IYLHQPQIVNEVVFVAGETTSYRQLADTVERVTQQTFSKAVHTLPALLEQLRTNPDDAMLRYRAAFARGD

GVWWPMGDTWNARHQLPTQDIAGWLQTAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004190483.1\_2521 [locus\_tag=BN49\_RS14135] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004190483.1] [location=2594585..2595490] [gbkey=CDS]

MDKLDAMQVYVAVVDAHSFARAAEVLGQPRSTVSRVVKELEAWLGAQLLQRTTRKLSVTAEGRRYYEECK

RLLAEMAAMEASFPGRSAQPAGRFKVGMPQSLARHCILPRIGEFLQQYPDLELILCSSDNVEDIIQEGFD

CVIRTGRIEDSTTLVARPLARYRWMVLASPAWLAAHGRPQSIDELHQHRAVGYLNHRTGRTIDWLFSLDE

GDCAIRMRETLVVDDTDAYIQAGIQGLGLIRVASYLAQPYLQSGALVACLEQAASDLPLSLVYPQNRYLP

PAVRAFYDWSRRVLQPPHSEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043132.1\_2522 [locus\_tag=BN49\_RS14140] [protein=LysR family transcriptional regulator] [protein\_id=WP\_046043132.1] [location=complement(2595510..2596433)] [gbkey=CDS]

MKKIIENDFSRIDLNLLTVLMVLYREGSVTRTAEVLHLGQPAISGALKRLREMFDDPLFVRSARGMLPTP

RAQALMTDLQPLMENLHSAMFGAGEFVPARAQQLFRIGLSDWSEHWLMPQLLPGMMQEAPGVSLQSIAAD

PFQVRQLLEEERIDVAVSVNKQSRGEVVSEPVMTMGVTTLWSPQQIPCRGPLSVSDFVAWEHVMVAYRET

GHGEIDRQLASQGLARRVRFATQNFSTFPLLLTTLPLFATVPQGLAQRWQAQYALRADAPPVAYPEFTLC

ILRHKRRAQDPALNWLVTMLKQAMRGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_014907706.1\_2523 [locus\_tag=BN49\_RS14145] [protein=MBL fold metallo-hydrolase] [protein\_id=WP\_014907706.1] [location=2596521..2597390] [gbkey=CDS]

MMQTYQTGDSLIFKVPEREISLQPAALYPEAFPVAEAEAVIQPIALSIHSWVVQTPYDLIVIDTATGNGR

ERGGNPLYHQLNTPYLENLRAAGVNPEDVTLVLLTHLHTDHVGWNTVWQDDRWVPLFPNARYLCSAKELS

RVKNSERYRALWLDSLLPVIEAGQLETVDVATRPRVGGRIDFIPTPGHSPDHAALVLAAGDDYACFSGDL

LHSPIQFAHPQWNSAFCGDPRQAEVSRREMMAWGASHHAQWFTGHFAGPSCGWLEKDKQGDYRWREAGKQ

AADKGNSDE

>lcl|NZ\_FO834906.1\_prot\_WP\_032417074.1\_2524 [locus\_tag=BN49\_RS14150] [protein=NmrA/HSCARG family protein] [protein\_id=WP\_032417074.1] [location=2597383..2598294] [gbkey=CDS]

MNNAQTVLVFGATGQQGGSVARALLHRGWRVRALVRDPFSAGAAALAARGAELVVGTFEDRAAMRSAMAG

VDGVFSVQPSSPGGTVTDEQEVRYGITIADLAVECGVKHLVYSSGSATGETPTGVAHYDTKAEIERHIRR

LPLAATIVRPATFMELLVMPGFGLDEGRFQFFMLPEGRMQVLAVEDIGHLVAAVFAAPARFAGKTFEIAS

DSVTGRQLEGLFSAAAGRPIPYSRFSDEVLAASPFLHKLTGLVDDGRLAGHADLDALRQLHPQLHTFAGW

LAGPGRPAFERALTSGARWAFDR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043136.1\_2525 [locus\_tag=BN49\_RS14155] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_046043136.1] [location=complement(2598351..2598899)] [gbkey=CDS]

MRADARKNYDLLIEVARDVFVEQGAEASLRDIARRAGVGMGTLYRHFPNRDSLLEALLRSRFAALTARAE

SLLLAADPAAALLEWLAESVAFTHQHRGIITPLMSAIDDPESALHSACVALRAAGTSLLTRAQQAGLARP

DLSGEELFDLIAALAWLREQPSHAPRAERILAVLADAILTAG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043138.1\_2526 [locus\_tag=BN49\_RS14160] [protein=NADP-dependent oxidoreductase] [protein\_id=WP\_046043138.1] [location=2598988..2600022] [gbkey=CDS]

MSTQMMKAVQQHAFGGPEVLSYEDAPMPVLQAGEVLVQVHAVGVNPPDSYLRDGYQQLPPEWRPEVRFPL

ILGTDLSGVVVARADDVREVAVGDEVYAMARFPEGAAGGSRAYAEYVSVPVSDLARKPLTLSHQQAAAVP

MSLLTAWQFMIDPGHEVANPLQPGPHRPVPLAGKRVLVNGAAGGVGHFAVQLAKWQGAEVIAVAAGRHEA

FLRQLGADSVIDYITTAVEETVRDLDLVIDAPGGPASGRFLRTLRPGGALYPIFPLGFAGAEEARQRGVT

VSTTQVRSSGAQLARLADLQDAGVIRVAIDSVFPLAQAQMAHERAAQGHLEGKIVLSVMDSSAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532114.1\_2527 [locus\_tag=BN49\_RS14165] [protein=aminotransferase class I/II-fold pyridoxal phosphate-dependent enzyme] [protein\_id=WP\_016532114.1] [location=complement(2600067..2601242)] [gbkey=CDS]

MPDFTASPLVDALEENLFSLLEKLAAEVNTEALPLIDLSSGSPDQPTPPEVIDSLQSAIHRRENHGYPSF

WGKPQVREAIARFYRRQYDVELDPHSEIAVFQGSHIGIGGIPRALLSPGQYLISTDPCYPIYRSAALQSQ

AAFYGLPLRAENHFLPDFNDLPREVADKAGLVVLNYPHNPTGALATPALFASALQFARRHQVPILHDFAY

AAIGSAASDAPLSLFSQPDAKAWGVETYTFSKTFNMAGWRFGFAVGNASIIRAFKKLHTHSYSTVFGAIQ

DAAIAALNLPAERIAQLTAVYHQRREWVLRRLAALRWPARDAQGTFFLWLGVPPGYRSQEFARLLLQEAH

ILVAPGTGFGAGGEGFIRISLTAGDEALSNALDRLARLALF

>lcl|NZ\_FO834906.1\_prot\_WP\_002902393.1\_2528 [locus\_tag=BN49\_RS14170] [protein=MetQ/NlpA family ABC transporter substrate-binding protein] [protein\_id=WP\_002902393.1] [location=2601463..2602269] [gbkey=CDS]

MNKSVARGIALALLSATSFYAAADAHLIRVGFNPGPYKEQFEKGVAPYLLSKGYKIEYKDFSDGIQVNDA

VARGDIEANIMQHPVYLKAINERLGIDNVGIVQVPTPPMGLYGGKLTTLGTPAAGTVVSVPNQPSNEYRA

VLVLESLGWVKIKPDSDPATFSQRNIVDNPYKIVLKEMDNAQQVRALPDVDYGLIQGNFAVSSGMSLTSA

LKLEAATSHFINVVTVAGKNQKAQFAKDIIDGYHSAEFKKYILSHPQYDGYLLPDYLK

>lcl|NZ\_FO834906.1\_prot\_WP\_032102808.1\_2529 [locus\_tag=BN49\_RS14175] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_032102808.1] [location=2602278..2603291] [gbkey=CDS]

MIEFRHVSKSFSRKGHPVLALQDINLSIERGDIFGIIGYSGAGKSTLLRLINRLETPGEGEVLLNGEPLQ

ACSGQRLQAIKKDIGMIFQNFNLLNSKTVFHNIAIPLILQGRDKAFIHARVAELLAFVDLSDKIHSYPNE

LSGGQKQRVGIARALATNPSVLLCDEATSALDPHTTVQILLLLQEINRRYGITIVLITHEMSVIQKICHK

VAVMQAGRIVEQGAVFDLFAQPQHPVTASFVQSVVHDRLPQRVASFLQRDNGARALRLEFVGATAQQPII

NHLIREYAVEVNILFASMSEVQGRILGFMIVQLLGEPDETDRAITHLVDAGVKITHV

>lcl|NZ\_FO834906.1\_prot\_WP\_004183826.1\_2530 [locus\_tag=BN49\_RS14180] [protein=ABC transporter permease] [protein\_id=WP\_004183826.1] [location=2603284..2603952] [gbkey=CDS]

MFDLIDTAITGDQFLLALRDTLIMVAVSLGFGALIGVPLGIVLVVCRPGGIVANPVVHQALNPLINVLRS

LPFIILLIVILPFTRLLVGTTIGTAGAIVPLIVFVAPYIARLVESSLLEVDEGILEAADAMGATPLQTVW

HFMLPEAAASLILALTTATIGLLGATAMAGTVGGGGIGDLAITYGYQRFDAFATLTTALVLIVIVQLIQT

LGTRLARRLRRE

>lcl|NZ\_FO834906.1\_prot\_WP\_032102807.1\_2531 [locus\_tag=BN49\_RS14185] [protein=hypothetical protein] [protein\_id=WP\_032102807.1] [location=2604243..2604989] [gbkey=CDS]

MKHVHKLAWVGLFVNIIICFVARNLLLDEGQLNFHSRADGVWSWLVLALFIAVVVQAISIMLSGRYPYLA

IVLAFVGGIVMVPASVIFLVGSLFSLQTRINAGFTPWRSTTAVGEADNQQLLTFNASGFYPQGALALIAG

IIILMIGMGIGGVFIAAGIVALCNGYRLQNRVVIGVSGESMIFTPGLYADTYVIPLRDVAVVERSNNDAK

VRLLIRSSGRSFTLRKKLLAGDKVNDAFAAILAKLTTV

>lcl|NZ\_FO834906.1\_prot\_WP\_004176404.1\_2532 [locus\_tag=BN49\_RS14190] [protein=hypothetical protein] [protein\_id=WP\_004176404.1] [location=complement(2605102..2605296)] [gbkey=CDS]

MYYTLGDTTLHFYRYQCKFYVAHWEGGNVMSEKFKSFIEQITEKTGLDAKRVETAARDYFTNVD

>lcl|NZ\_FO834906.1\_prot\_WP\_014907696.1\_2533 [locus\_tag=BN49\_RS14195] [protein=oxidoreductase] [protein\_id=WP\_014907696.1] [location=complement(2605533..2606651)] [gbkey=CDS]

MIPSSLYILLTLNNVENLMSNNTINIALIGYGFVGKTFHAPLIRSVPGLNLAFVASRDEEKVKRDLPDVT

VIASPEAAVQHPDVDLVVIASPNATHAPLARLALNAGKHVVVDKPFTLDMQEARELIALAEEKQRLLSVF

HNRRWDSDYLGIRQVIEQGTLGAVKHFESHFDRFRPEVRVRWREQNVPGSGLWFDLGPHLIDQALQLFGL

PQSVQGNIATLRDGAEINDWAHVVLNYPAHKVILHCSMLVAGGSSRFTVHGDKGSVIKARADQQESQLLA

GVVPGSAGWGQDDDPLVIYDASLQAHAQATPQGDQRQYYMLIRDALKGQIANPVPPVEALAVMAVLEAAV

RSAESGMVQTLDLSDDERNTLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532117.1\_2534 [locus\_tag=BN49\_RS14200] [protein=DeoR/GlpR family DNA-binding transcription regulator] [protein\_id=WP\_016532117.1] [location=complement(2606614..2607357)] [gbkey=CDS]

MHKLARQKHILDRLSETGQLSIAELVAELQVSADTIRRDLSDLEQQGVLQKSHGGAIALNVPAMTRQGRN

ALLTQTKQRLGQQVAARIPSGSTLFLDAGSTLLAVAAQLKGPLTVITASLDIAQLFSDRADIQLILLGGQ

WDSKQRLFAGSATLSLVTRYRADIAILGACALHAGLGLSASQEADADVKRAMLAASAEHWLVADHTKLNR

CEPWRVAGLSDIHHLFLDRPWAELGDDPVLSVHIADA

>lcl|NZ\_FO834906.1\_prot\_WP\_004148192.1\_2535 [gene=zntB] [locus\_tag=BN49\_RS14205] [protein=zinc transporter ZntB] [protein\_id=WP\_004148192.1] [location=2607637..2608620] [gbkey=CDS]

MDAIKGSELQIPDAIFAWVLDGQGGVKPLADDDIIDKDKPCWLHLNYTHSDSADWLAATPLLPNNVRDAL

AGESTRPRVTRIGDGALITLRCINGSTDERPDQLVAMRLYMDERLIVSTRQRKVLALDDVLGDLKEGNGP

TDGGSWLVEVCDALTDHASEFIEQLHDRIIDLEDDLLDQQVPPRGFLALLRKQLIVMRRYMAPQRDVYAR

LASERLPWMSDDQRRRMQDIAERLGRGLDEIDSCIARTAIMSDEIAQIMQESLARRTYTMSLMAMVFLPS

TFLTGLFGVNLGGIPGNSWHLGFSLFCLMLVVVIGGVAWWLHRSKWL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043142.1\_2536 [gene=dbpA] [locus\_tag=BN49\_RS14210] [protein=ATP-dependent RNA helicase DbpA] [protein\_id=WP\_046043142.1] [location=2609146..2610519] [gbkey=CDS]

MTAFSTLTVLPAAQLANLNELGYLSMTPVQAAALPAILGGKDVRVQAKTGSGKTAAFGLGLLQHIDPARF

ETQSLVLCPTRELADQVAGELRRLARCLPNIKILMLCGGQPFGAQRDSLQHAPHIIVATPGRLLDHLQKG

TVSLDALQTLVMDEADRMLDMGFSDAIDEVIRFAPADRQTLLFSATWPAAIAAISGRVQRNPQTIEIDTV

DALPAIEQQFFEVSRHGKIALLQRLLSRHQPASCVVFCNTKRDCQAVCDALNAAGQSALSLHGDLEQRDR

DQTLVRFANGSVRVLVATDVAARGLDIKSLALVVNFELAWDPEVHVHRIGRTARAGEQGLAISFCAPEEA

QRATILADMLQLSLNWLPAPTGNTIAPLTAEMATLCIDGGKKAKMRPGDVLGALTGDMGFDGADIGKITV

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>lcl|NZ\_FO834906.1\_prot\_WP\_002902422.1\_2537 [gene=ttcA] [locus\_tag=BN49\_RS14215] [protein=tRNA 2-thiocytidine(32) synthetase TtcA] [protein\_id=WP\_002902422.1] [location=complement(2610565..2611500)] [gbkey=CDS]

MLQNQEISKKEKYNIDKLQKRLRRNVGEAIADFNMIEEGDRIMVCLSGGKDSYTMLEILRNLQKSAPISF

SLVAVNLDQKQPGFPEHILPAYLEQLGVEYKIVEENTYGIVKEKIPEGKTTCSLCSRLRRGILYRTATEL

GATKIALGHHRDDILQTLFLNMFYGGKMKGMPPKLMSDDGKHIVIRPLAYCREKDIERFSQAKGFPIIPC

NLCGSQPNLQRQVIADMLRDWDKRYPGRIETMFSAMQNVVPSHLSDVNLFDFKGITHGSEVVDGGDLAFD

REDIPLQPAGWQPEEEDARLDELRLNVVEVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140161.1\_2538 [gene=uspF] [locus\_tag=BN49\_RS14220] [protein=universal stress protein UspF] [protein\_id=WP\_004140161.1] [location=complement(2611734..2612168)] [gbkey=CDS]

MSRMILVPIDISDKEFTERIISHVESEARIDDAEVHFLTVIPSLPYYASLGMAYTAELPGMDELREGSET

QLKEIAKQFSIPEDRMHFHVAEGSPKDKILALAKSLPADLVIIASHRPDITTYLLGSNAAAVVRHAECSV

LVVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002902432.1\_2539 [locus\_tag=BN49\_RS14225] [protein=KTSC domain-containing protein] [protein\_id=WP\_002902432.1] [location=complement(2612250..2612462)] [gbkey=CDS]

MHHHPVKSSRIISVAYDDASATLEIYFYHQPPLQYTGVPPRIFHDFLQVVSKGRYYDGVIKGKFPERKLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530075.1\_2540 [gene=ompK37] [locus\_tag=BN49\_RS14230] [protein=porin OmpK37] [protein\_id=WP\_016530075.1] [location=complement(2612606..2613760)] [gbkey=CDS]

MKRKVLALVIPALLAAGAAHAAEIYNKDGNKLDLYGKVDGLHYFSSDSKKDGDQTYLRFGFKGETQINDM

LTGYGQWEYNVQANNTETSSDQAWTRLAFAGIKVGDYGSFDYGRNYGVLYDVEGWTDMLPEFGGDSYTYA

DNFMAGRANGVATYRNSDFFGLVEGLNFALQYQGKNEGQNAQDINVGTNNRSSDSDVRFDNGDGFGLSTS

YDFGMGISAAAAYTSSDRTADQQHFTSDNNFATGDKAEAWTAGLKYDANDIYLATMYSETRNMTPYGSTS

STNGGGIANKTQNFEVTAQYQFDFGLRPAISYLQSKGKDLYNNGRYADKDLVKYMDVGATYYFNRNMSTY

VDYKINLLDGNDKFYEDNGISTDNIVALGLVYQF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530074.1\_2541 [gene=nifJ] [locus\_tag=BN49\_RS14235] [protein=pyruvate:ferredoxin (flavodoxin) oxidoreductase] [protein\_id=WP\_016530074.1] [location=complement(2614117..2617644)] [gbkey=CDS]

MITIDGNGAVASVAFRTSEVIAIYPITPSSTMAEQADAWAGNGLKNVWGDVPRVVEMQSEAGAIGAVHGA

LQTGALSTSFTSSQGLLLMIPTLYKLAGQLMPFVLHVAARTVATHALSIFGDHSDVMAVRQTGCAMLCAS

SVQEAQDFALISHIATLQSRVPFIHFFDGFRTSHEINKIAPLADDTIRALLPQDKIAEHRQRALNPEHPV

IRGTSANPDTYFQSREATNPWYDAVYDHVEKAMDDFAAATGRQYKPFEFYGHPQAERVIVIMGSAIGTCE

EVVDELLSRGEKVGVLKVRLYRPFSAAHLLAALPESARAVAVLDRTKEPGALAEPLYLDVMTALAEAFNR

GERETLPRTIGGRYGLSSKEFGPECVLAIFSELQAAQPKPRFTVGIYDDVTNLSLPLGENTLPAEAKLEA

LFYGLGSDGSVSATKNNIKIIGNSTPWFSQGYFVYDSKKAGGLTVSHLRVSEKPIRSSYLISQADFVGCH

QLQFIDKYQMAERLKPGGIFLLNTPYSADEVWSRLPQEVQATLNQKKARFYVVNAAKIARECSLGARINT

VMQMAFFHLTQILPGDSALAELQAAIAKSYSSKGQELVERNWQALALARESLAEVPLQPVNASSPNRPPV

VSDAAPDFVKTVTAAMLAGLGDALPVSALPPDGTWPMGTTRWEKRNIAEEIPIWKEALCTQCNHCVAACP

HSAIRAKVVAPEEMENAPASLHSLDVKSRDMRGQKYVLQVAPEDCTGCNLCVEVCPAKDRQNPEIKAINM

MSRLEHVEEEKVNYEYFLNLPEIDRSKLERIDIRTSQLISPLFEYSGACSGCGETPYIKLLTQLYGDRML

IANATGCSSIYGGNLPSTPYTTDANGRGPAWANSLFEDNAEFGLGFRLTVDQHRQRVMRLLSEFADKLPA

ELNAALHAEATPEVRREQVAALRQALAGVAGAEELLTDADALVEKSVWLIGGDGWAYDIGFGGLDHVLSL

TENVNILVLDTQCYSNTGGQASKATPQGAVTKFGEHGKRKARKDLGVSMMMYGHVYVAQISLGAQLNQTV

KAIQEAEAYPGPSLIIAYSPCEEHGYDLALSHDQMRQLTATGFWPLYRFDPRRADEGKIPLALDSRPPSD

ALAETLLNEQRFRRLNAQQPEVAEQLWKDAAADLQKRYDFLAQLAGKAEKSPSEG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043145.1\_2542 [locus\_tag=BN49\_RS14240] [protein=DUF333 domain-containing protein] [protein\_id=WP\_046043145.1] [location=2618007..2618270] [gbkey=CDS]

MRAAMLVGCAALLLSACSSEPVQQATAAHVTPGMRAAMSNAGQANCAMIGGSLSVARQLDGSAIGMCALP

NGKRCSEQALAGGSCGY

>lcl|NZ\_FO834906.1\_prot\_WP\_002902513.1\_2543 [gene=hslJ] [locus\_tag=BN49\_RS14245] [protein=heat shock protein HslJ] [protein\_id=WP\_002902513.1] [location=complement(2618316..2618756)] [gbkey=CDS]

MNKFAALLAAGMLLSGCVYNSKVSTGAEQLQHHRFVLTSVNGQAVNASDRPLELSFGEKMAITGKMYVSG

NMCNGFSGEGKVSDGELKVKSLAMTRMLCHDAQLNTLDATIDKMLREGAQVDLTENQLTLATADQTLVYK

LADLMH

>lcl|NZ\_FO834906.1\_prot\_WP\_002902515.1\_2544 [locus\_tag=BN49\_RS14250] [protein=2-hydroxyacid dehydrogenase] [protein\_id=WP\_002902515.1] [location=complement(2618879..2619868)] [gbkey=CDS]

MKIAVYSTKQYDKKYLQHVNDAYGFELEFFDFLLTAKTAKTANGCEAVCIFVNDDGSRPVLEELKAHGVK

YIALRCAGFNNVDLEAAKELGLRVVRVPAYSPEAVAEHAIGMMMSLNRRIHRAYQRTRDANFSLEGLTGF

TMYGKTAGVIGTGKIGVAMLRILKGFGMRLLAFDPYPSAAALELGVEYVDLATLYKESDVISLHCPLTDE

NYHLLNREAFDQMKDGVMVINTSRGALIDSQAAIDALKHQKIGALGLDVYENERDLFFEDKSNDVIQDDV

FRRLSACHNVLFTGHQAFLTAEALISISETTLGNLQQVANGETCPNAIV

>lcl|NZ\_FO834906.1\_prot\_WP\_002902516.1\_2545 [locus\_tag=BN49\_RS14255] [protein=DedA family protein] [protein\_id=WP\_002902516.1] [location=complement(2620016..2620516)] [gbkey=CDS]

MSLIISLIESAQDHYPWVLLIVFLLTFTKSCALVSLAIPGTSGLLLLGTFASASLGHFLLMWSSASLGAI

GGFWLSWRLGIRYRHRLTHLRWLTAERLARSRLFFQRYGPWAIFFSRFLSPLRATLPFVSGASSLPLWSF

QLANVSSGLLWPLLLLAPGAFSLSLW

>lcl|NZ\_FO834906.1\_prot\_WP\_046043147.1\_2546 [locus\_tag=BN49\_RS14260] [protein=YdbH family protein] [protein\_id=WP\_046043147.1] [location=2620723..2623362] [gbkey=CDS]

MKGKYKAAIALVLVLVLLPLTLLLTLTHWVPTLAGIWLPVGTRISLQESPRLTRSALLIPDLRYLVGDCE

IARVTDARLSRPSRWRLHIGQLEINSACLSKLPASDPAPGSPRTLAEWQSMLPYSWLTIDNLRLSPWEKW

QGRLVMSLTPAQQDIGFAGKELSLQARLRGQALTVSQFSARLTDDQPPVKLVGTFHLPLVPDCLPVDGQM

QGTFEFPQTAEWIDAELEWQHNRGQLLVTPRGEVEPILDLPWEITPERITISDGRWRTRYEAYPLRGRVA

LSVGNWQQGTEQMIVSGRLNVLTEGHAGKGNAVLNIGPGKLSMDNSDLPLRLTGEAKLGEMILYAALPAQ

LSGPLISPQLAFHPGALLRSRGRVIDALNIDEIRWPLAGVKVTQQGVDGRLQAILRAHEQQMGDFTLHLD

GQASDFLPDSGRWQWRYWGEGHFTPMQARWDVKGSGEWRDNAITLSSLSTGFDKLEYGTMRVSTPRLTLE

QPIRWLRDAEHPRLTGALSLDAAKTTFSGGSYLPASTLKFALDGRDPTWFQFTGALHAEAIGPVRLSGRW

DGERLRGQAWWPKQSLTVFQPLVPPDWKMNLREGSLYAQVAFSAAAGQGFEAGGHGVLKGGSAWMPDNQI

NGVDFVLPFRFSDGHWQLGIRRPVSLRIGEIVNQVTARNLTADLQGTWPWSEANPLQLSDVSVDLLGGKL

TLLQLRMPQRDPALIRLQHISSSELTSAVKVKQFAMSGAVSGALPLWLENNQWIIHDGWLRNDGPMTLRL

DKDTADALVADNVSAGAAINWLRYMEISRSWTQINLDNLGVLTLKASINGTSRVEGKSSTVHLNYAHEEN

IFDLWRSLRFGDNLQAWLEQNATLPVRRCTDGKTCKEPK

>lcl|NZ\_FO834906.1\_prot\_WP\_002902519.1\_2547 [locus\_tag=BN49\_RS14265] [protein=YnbE family lipoprotein] [protein\_id=WP\_002902519.1] [location=2623359..2623544] [gbkey=CDS]

MKKLLLAMAASMLLAGCTPRIEIAASKEPITINMNVKIEHEIHIKVDKDVENLLKSRSDLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002902522.1\_2548 [locus\_tag=BN49\_RS14270] [protein=YdbL family protein] [protein\_id=WP\_002902522.1] [location=2623552..2623875] [gbkey=CDS]

MRKRLLTAALTLALLSAPALALTLSEARQQGRVGETLNGYLAPLRQDKETLALVKQINAARSESYQQLAD

DNNLPVDEVAKMAGQKLVARAQPGEYVQGLNGQWLRK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140140.1\_2549 [gene=feaR] [locus\_tag=BN49\_RS14275] [protein=transcriptional regulator FeaR] [protein\_id=WP\_004140140.1] [location=complement(2623876..2624778)] [gbkey=CDS]

MMTTAEGGLAYQRWLATINQVCGHFAARPLEESFHGEIDARYAGSLKVSTVTAAGVNLYRTRNEIKRDND

AWFYTVFQLAGEAIIEQDDRQVTLAAGDITLIDAARPCSIVWQQTSRQASLLLPRQRVAPTGDITTACRL

DKSLPMVQLSQRLLLESMGGTTLSASESEAALEAIACLLRPVLHQRDPAPSRREKQFQKIIALIDASIQS

EHLRPEWLASETGMSVRSLYRLFADQGLVVAQYIKNRRLDLCAQALQNVHDDEKLAGIGYRWGFSDHSHF

STAFKQRFGVTPGEYRKRCR

>lcl|NZ\_FO834906.1\_prot\_WP\_004140136.1\_2550 [locus\_tag=BN49\_RS14280] [protein=aldehyde dehydrogenase family protein] [protein\_id=WP\_004140136.1] [location=2625014..2626513] [gbkey=CDS]

MSTSQIALLASVQQFLDRQHGLYIDGAPCAAQSENRLTVWDPATGQAIATTADASPADVDRAVMSAWRAF

VDRRWAGRTPADRERILLRFADLVEQHGEELAQLETLEQGKSIAISRAFEVGCTLNWMRYTAGLTTKISG

RTLDVSIPFPQGARYQAWTKKEPVGVVAGIVPWNFPLMIGMWKVMPALAAGCSIVIKPSETTPLTLLRVA

ELATQAGIPDGVFNVVTGSGAGCGAALTAHPQVAKVSFTGSTATGKQIARVAADRLTRVTLELGGKNPAI

VLKDADPQWVIEGLMTGSFLNQGQVCAASSRIYIEAPLFDTLVSGFEQAVKSLQVGPGMQETAQINPVVS

RAHCDKVAAYLEEARQQKAELISGSAGPDAGGYYIPPTLVVNPDAGLRLSREEVFGPVVNLVRVADGEEA

LRLANDSDFGLTASVWTRDLTQALNYTDRLQAGTVWVNSHTLIDANLPFGGMKQSGTGRDFGPDWLDGWC

ETKSVCVRY

>lcl|NZ\_FO834906.1\_prot\_WP\_016531163.1\_2551 [locus\_tag=BN49\_RS14285] [protein=oxidoreductase] [protein\_id=WP\_016531163.1] [location=2626638..2627528] [gbkey=CDS]

MTAFPKVALIGPGAIGTTIAAALFERGRAPMVCGRTAHSALVLRTDEGEIVVPGPVHTDPMAIAAPFDLV

FVAVKTTQTEAIAPWLTALCSPDTVVCVLQNGVEQRQQFAPLTGGATVLPSVVWFPAQRDADASVWLRAA

PRLTLPDLPGAERVQQALAGTRCAVDLAADFTTVAWRKLLQNAVAGLMVLTGRRAGMFAREDITALGLAY

LRECLQVARAEGAALSENVPEEIIAGFHRAPADLSTSILIDRLNGRPLEWDIRNGVVQRRGRQHGIPTPL

SDIIVPLLAAASDGPG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043150.1\_2552 [locus\_tag=BN49\_RS14290] [protein=class II aldolase and adducin N-terminal domain-containing protein] [protein\_id=WP\_046043150.1] [location=complement(2627566..2628297)] [gbkey=CDS]

MRDSDEEQIRIDLAATFRIIAHLGMHEAVANHFSAALSADGKTFLLNPKWKHFSRIRASDLLVLNADDER

CAARPDVDATAWAIHGQIHQRLPDVRVVLHLHPVYTTSLACLATPQILPIDQNTARYFNRVAVDTLYGGM

ADTAAEGARLAGLLADKRRLLMGNHGVLVTAPTIGEAFDDIWTLERACQILITAWSTGQRLKVLSDAVAE

KTAQDWEKIADFSRQHFAEMKQLMIDLDPSLVD

>lcl|NZ\_FO834906.1\_prot\_WP\_016532056.1\_2553 [locus\_tag=BN49\_RS14295] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016532056.1] [location=complement(2628303..2629133)] [gbkey=CDS]

MTRFFAPRPLALLLCAVGALTSLNALAFQQSGKITAGSDMTFFPYEYMENNKPAGFDIELLNGLAKSMGR

EAVNIDTRFPNLIPGLQSGRFDITNSSMYITAERLKVIDMVPYLKSGEAILARKGSDYQPKTPEDFCGHK

IGSMGATSWLAQLQKLSADYCVKKGLKPIALSVYTTDPQTTQALLSRAVDAQITDAAVARGVVEKLGNRV

VISSDTLIYPVLNGFGVKKGNMEVKNALEEALKKYSATPEYAALLKKYHFQAPTEEDLQTLMPKAE

>lcl|NZ\_FO834906.1\_prot\_WP\_016947241.1\_2554 [locus\_tag=BN49\_RS14300] [protein=phytanoyl-CoA dioxygenase family protein] [protein\_id=WP\_016947241.1] [location=complement(2629157..2630029)] [gbkey=CDS]

MIAQWQIDQFHQQGFLVVEEVLSSADIAALQSDFDGWVEESRRHATAWGETLDGRPRFDIERDHAPDHPS

LRRVASPTEISEAYRHTALNSRMATIAAQLIGGSGTRFHHSKINSKLPHTATEVKWHQDFLFTPHSNDDI

ITALLMVSEVTPENGPLNVVPGSHQGPLWTHWQEGRFTGAVDDEVVATHCQQPQACFGPAGSVCFMHTRL

LHASSPNETALPRTLFISVYAAEDALPFGENPLPSRHAGQLVAGEESGLVRSTDNQLRLPQKPRGASFFV

QQAGTDRASM

>lcl|NZ\_FO834906.1\_prot\_WP\_052715515.1\_2555 [locus\_tag=BN49\_RS27995] [protein=amino acid ABC transporter permease/ATP-binding protein] [protein\_id=WP\_052715515.1] [location=complement(2630056..2631576)] [gbkey=CDS]

MTFNWNYMLSLLSNADFWWATWTVIKLSLLTWGCSIVLGFILALAKQSPRGWLSTPARLYIWLFRSMPLL

VLLIFVYNMPQALPSFAPVLNDPFWAGLLAMVLSEAAYIAEIHRGGLLSIPRGQSEAARALGLRYAGIQW

RVIIPQALRVALPALANEYIAIVKLSSLVSVISLTEILMVGQQLYSQNFLVMETMTAVAFYYIFIVTVFD

FLLKRLENYLDVTQRNTARPVDAEMQRLASARRPAMARSVTQSHEPALQASKLHKAYNNVEVLGAVSLQI

QPGEVVSVIGPSGSGKTTLIRLLNGLEQIDNGEIQINGQPFIHLDRQGQQKPRFMENAEHRLNIGMVFQS

FNLFPHLTVFGNLLLAPRYHHLASDAELRQHACELLHKVGMLEHAWKYPHQLSGGQQQRVAIARALMMRP

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GHHPRVEAFLKDVSLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004190428.1\_2556 [locus\_tag=BN49\_RS14310] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_004190428.1] [location=2632065..2632979] [gbkey=CDS]

MNRFTLKQLKYFVTVVETESIAEASRQLHIAQPSISIAIKNLESTFDQQLFIRHHAQGVSLTSSGRRIYD

KAKELLRLSWEFEQNSRADKELVSGMISIGCFESVAPLYMPKLVAGFKKCYPEITLHLYDGEQHELMHGL

HRGRFDLALVYDLELGHSINKERLNAPHKPYALLPAAHPLAQKAQVTLQELSREPMILLDAVPSKNYFIS

IFKEKGYHPEVAYSSPSIEMVRCMVGQGLGFSVLVTRPCCDMTYDGERVVQRDIADEMPASTLIMAHLAN

NEPTRPTQLFMDYCRSIELTPTHA

>lcl|NZ\_FO834906.1\_prot\_WP\_004892437.1\_2557 [locus\_tag=BN49\_RS14315] [protein=NAD(P)/FAD-dependent oxidoreductase] [protein\_id=WP\_004892437.1] [location=2633148..2634407] [gbkey=CDS]

MTEQITEIDTLVVGAGQAGVAMSEHLTRLDIPHLVLEKQGIAQAWRSGRWDSLVANGPAWHDRFPGMVFP

DCPADSFVGKEQVADYFAAYARSFNAPIRTGVEVFSAERLVGRPGFRIDTSQGVIEAQRIVAATGPFQRP

VIPAIAPQSQAIQQLHSAHYFNPQQLPEGGVLVIGAGSSGVQIADELQRAGRAVWLSVGAHDRPPRRYRQ

RDFCWWLGVLGMWDAAANAPGKEHVTIAVSGARGGHTVDFRQLAHQGVTLVGQTRGFDGDKALFHPDLAE

NIRRGDASYLALLDAADAWVARNGMDLPEEPSAREFLPDPACVTDPLLSLNLAEAGIGTIIWATGYTTDY

RWLKVNAFDDAQRPQHHRGVSTEPGVYFLGLPWLSRRGSTFIWGVWHDAKYIADQIAIQRQYQRYQPSC

>lcl|NZ\_FO834906.1\_prot\_WP\_004190423.1\_2558 [locus\_tag=BN49\_RS14320] [protein=RidA family protein] [protein\_id=WP\_004190423.1] [location=2634432..2634866] [gbkey=CDS]

MPTHTRIRMFNTKETYPNQALNNDLCQAVRAGNTVYVRGQVGTDFAGNLIGLGDPRAQAEQAMKNVEQLL

KEAGSDLSHIVKTTTYLIDPRYREPVYQEVGKWLKGVFPISTGVVVSALAQPQWLMEIDVTAVIPDDWQG

EAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532663.1\_2559 [locus\_tag=BN49\_RS14325] [protein=DUF1028 domain-containing protein] [protein\_id=WP\_016532663.1] [location=2634863..2635537] [gbkey=CDS]

MTLSISARCPESGQLGIAISSSSMAVGSRCPWLLPGVGAVASQNITLPSLGPQILSALEAGASVEQALNL

ALAEDRFREYRQVAAIDANGDTAVFSGEFTLGIGGALAGDNCVAAGNMLAGQGVIAAMVGAFEAATGELA

SRLLAGLRAGIVAGGEAGPVHSAAVKVVDDYPWPVVDLRIDWAEVDPLAALEQLWLAWEPQMEAYITRAL

DPREAPAYGVPGDE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043154.1\_2560 [gene=argE] [locus\_tag=BN49\_RS14330] [protein=acetylornithine deacetylase] [protein\_id=WP\_046043154.1] [location=2635530..2636699] [gbkey=CDS]

MNNTPGAILAALLAFDTTSRHSNLAMIDWIADFLAARGVASRRFYDPSGGKANLYARLGPSGGGGVMLSG

HTDVVPVDGQAWSVPPFSLTERDGRYYGRGSADMKGFLACVLAAVDDFLAVPLRMPLHLAFSYDEEVGCL

GVRSLVDFLQASPEKPALCLIGEPTEMQPVFGHKGKLAMRCCIEGQACHSAYAPQGVNAIRYAARLINHL

DRLGVRLARQQDSRFSPPFSTLQVGTIQGGAALNIVPQSCRFDFEIRYLPGMRPEAVTEALAAYAHRQLL

PEMRRVGSGSDIQFQLLSHYPPLLSDPQSDFARWLAQWCGSDRFSTVAFGTEGGLFDEMGVATLVCGPGS

MAQGHKADEYISIAQTERCMTMLRQLCAWMRAEPAEPLT

>lcl|NZ\_FO834906.1\_prot\_WP\_046043156.1\_2561 [locus\_tag=BN49\_RS14335] [protein=phytanoyl-CoA dioxygenase family protein] [protein\_id=WP\_046043156.1] [location=2636724..2637542] [gbkey=CDS]

MHNQHSPHIDQVTIDRWQADGAVLLKGVFTPWVERLAEGVTALMASPSEYGHARTVIPKDGSPPFFQDYC

NWARIPAFSEFVFQSAAAEIAAALMQSQTAKFFHEHTLVKPAGGSTVTPWHHDQPYYCVSGRQNVSFWIP

LDPVAEATSLRCIRGSHRWEAEYSPTRFNGTKLYEHTRFSALPDIDAHEDEYDIVSWALEPGDAVAFHFR

TVHGARGNPGARARRVFSARWVGDDAAFADRGGVTSPPFPELTLRDGDPLDSPLFPQVWPRA

>lcl|NZ\_FO834906.1\_prot\_WP\_171819473.1\_2562 [locus\_tag=BN49\_RS14340] [protein=zinc-dependent alcohol dehydrogenase family protein] [protein\_id=WP\_171819473.1] [location=2637565..2638548] [gbkey=CDS]

MIPPFAVWSQSMFNDAIVYDRYGPPAAVLTLKRLPLAPLAGGRVRVRMRFAPVNPSDLIPVTGAYRHRTR

LPAVAGYEGLGEVVAAPYGSRLCAGQRVLPLRGGGTWQRFIDLDETWLVPVLPAVDDLLAARGYINPLTA

MLMLKRWPVAGKHLVLTAASSSCASLLGQWALAMGARSVSGIIRSPQHRARLEQVGIYPILDTDRALMEK

VSQHSDLVFDAVGGELANTLLSVLPGSSTLISYGLLSGRPLTQTRGSATVRKFHLREALPTLSVAAWRAA

FDEIWQRLPTTSQPPAQRIALNDWREAIAAAGQPGRGGKILLDFTAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529609.1\_2563 [gene=tynA] [locus\_tag=BN49\_RS14345] [protein=primary-amine oxidase] [protein\_id=WP\_016529609.1] [location=complement(2638551..2640818)] [gbkey=CDS]

MANGLKFSPRKTALALAVAVVCAWQSPVFAHGSEAHMVPLDKTLQEFGADVQWDDYAQMFTLIKDGAYVK

VKPGAKTAIVNGKSLDLPVPVVMKEGKAWVSDTFINDVFQSGLDQTFQVEKRPHPLNSLSAAEISEAVTI

VKAAPEFQPNTRFTEISLHEPDKAAVWAFALQGTPVDAPLTADVVMLDGKHVIEAVVDLQNKKILSWTPI

KGAHGMVLLDDFVSVQNIINASSEFAEVLKKHGITDPGKVVTTPLTVGFFDGKDGLQQDARLLKVVSYLD

TGDGNYWAHPIENLVAVVDLEAKKIIKIEEGPVIPVPMEPRPYDGRDRNAPAVKPLEITEPEGKNYTITG

DTIHWQNWDFHLRLNSRVGPILSTVTYNDNGTKRQVMYEGSLGGMIVPYGDPDVGWYFKAYLDSGDYGMG

TLTSPIVRGKDAPSNAVLLDETIADYTGKPTTIPGAVAIFERYAGPEYKHLEMGKPNVSTERRELVVRWI

STVGNYDYIFDWVFHDNGTIGIDAGATGIEAVKGVLAKTMHDPSAKEDTRYGTLIDHNIVGTTHQHIYNF

RLDLDVDGENNTLVAMDPEVKPNTAGGPRTSTMQVNQYTIDSEQKAAQKFDPGTIRLLSNTSKENRMGNP

VSYQIIPYAGGTHPAATGAKFAPDEWIYHRLSFMDKQLWVTRYHPTERYPEGKYPNRSAHDTGLGQYAKD

DESLTNHDDVVWITTGTTHVARAEEWPIMPTEWAHALLKPWNFFDETPTLGEKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043160.1\_2564 [gene=paaZ] [locus\_tag=BN49\_RS14350] [protein=phenylacetic acid degradation bifunctional protein PaaZ] [protein\_id=WP\_046043160.1] [location=complement(2641459..2643504)] [gbkey=CDS]

MQQLASYLSGAWQTGRGRARTIHHAITGAALWEVTSEGLDMAQARRFAIERGGKALQAMTFIERSAMLKA

VAKHLLEQKDQFYAISAQTGATRADSWVDIEGGIGTLFTYAGLGSRELPDDILWPEDELIPLSKQGGFAA

RHVLTSKSGVAVHINAFNFPCWGMLEKLAPTWLAGMPAIIKPATATAQLTQAMVKAIVDSGLVPEGAISL

ICGGAGDLLDHLDSQDVVTFTGSAATGQQLRAHPNLVAKSIPFTMEADSLNCCVLGEDVIPEQPEFALFI

REVVREMTAKAGQKCTAIRRIIVPLAQINAVSDALISRLHKVTVGDPAQEGVKMGALVNSEQRQDVQESV

NKLIAAGCEVLLGGEADLSAAGAFFPPTLLYCSQPDETPAVHAIEAFGPVATLMPYRDRQHALTLARAGG

GSLAGTLVTASGELAREFILGAARAHGRIQILNEASSVESTGHGSPLPQLVHGGPGRAGGGEELGGLRSV

KHYMQRTAVQGSPTMLATIGQQWVRGAQVNEDRIHPFRKYFEEIQPGDSLLTPRRTLTEADIVNFACLSG

DHFYAHMDKIAAAESIFGERVVHGYFLISAAAGLFVDAGVGPVIANYGMENLRFIEPVKPGDTIQVRLTC

KRKTVKRQRSADEKATGVVEWAVEIFNQHQQAVALYSILTLVARQQGDFPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176377.1\_2565 [gene=paaA] [locus\_tag=BN49\_RS14355] [protein=1,2-phenylacetyl-CoA epoxidase subunit A] [protein\_id=WP\_004176377.1] [location=2643791..2644720] [gbkey=CDS]

MTEEQRFDQRIAQETAIEPQDWMPDAYRKTLIRQIGQHAHSEIVGMLPEGNWITRAPTLRRKAILLAKVQ

DEAGHGLYLYSAAETLGCAREDLYQKMLDGQMKYSSIFNYPTLSWADIGVIGWLVDGAAIVNQVALCRTS

YGPYARAMVKICKEESFHQRQGFEACMALAQGNDAQRQMLQDAINRFWWPALMMFGPNDDNSPNSARSMA

WKIKLHSNDELRQRFVDNTVPQVEILGMTVPDPDLQFDEASGHYRFGEIDWQEFNEVISGRGICNHERLA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002902768.1\_2566 [gene=paaB] [locus\_tag=BN49\_RS14360] [protein=1,2-phenylacetyl-CoA epoxidase subunit B] [protein\_id=WP\_002902768.1] [location=2644732..2645019] [gbkey=CDS]

MSKVYWPLYEVFVRSKQGLSHRHVGSLHAADDQMALENARDAYTRRSEGCSIWVVKASEIVASQPEDRGE

FFDPAESKVYRHPTFYTVPDGMEHM

>lcl|NZ\_FO834906.1\_prot\_WP\_004212293.1\_2567 [gene=paaC] [locus\_tag=BN49\_RS14365] [protein=phenylacetate-CoA oxygenase subunit PaaC] [protein\_id=WP\_004212293.1] [location=2645027..2645782] [gbkey=CDS]

MNNPNPVATYALRLGDNGLVLAQRLGAWCGHAPELEIDLALANIGLDLLGQARNFLSYAAELNGCGDEDT

LAFGRDERQFSNLLLVEQPNGNFADTIARQFFIDVWHVALFSRLVNSRDAQLAAIAAKGLKEVRYHQRFS

RGWLERLGNGTELSNRKMQQAVDNLWRFTGELFLADEVELSLVEQGIAVDPRELQAEWQSAVHTALLDSG

LQIPQEAAFRSGGKQGLHSEHLGPLLAEMQYLQRSHPGLQW

>lcl|NZ\_FO834906.1\_prot\_WP\_032439940.1\_2568 [gene=paaJ] [locus\_tag=BN49\_RS14370] [protein=phenylacetate-CoA oxygenase subunit PaaJ] [protein\_id=WP\_032439940.1] [location=2645794..2646291] [gbkey=CDS]

MQRLADIAPAEVRTIWGLLSAIPDPEVPVLTITDLGMVRSVARHGDGWVIGFTPTYSGCPATEHLLGEIR

TVMNDHGFQPVHIVLQLDPPWTTDWMSQDARERLRQYGISPPQGHACHADMPAEVSCPRCGSTHTSLISE

FGSTACKALYRCDSCREPFDYFKCI

>lcl|NZ\_FO834906.1\_prot\_WP\_046043163.1\_2569 [gene=paaK] [locus\_tag=BN49\_RS14375] [protein=phenylacetate-CoA oxygenase/reductase subunit PaaK] [protein\_id=WP\_046043163.1] [location=2646299..2647369] [gbkey=CDS]

MTTFYSLKVARVEPETRDAVTITFAIPQALQAEYCFRPGQHLTLKARLGGEELRRCYSICRSRTPGEISV

AVKAIDGGRFSRYAQHDIQQGMELEVMVPQGYFGYQPQAERQGEYLAIAAGSGITPMMAIISATLATEPQ

SRFTLIYGNRSSHSMMFRQALADLKDRYPQRLQVIHLFSQESMDSDLLQGRIDGDKLRQLADHLLDFSRF

DEAFICGPAAMMDEAEATLRELGVAEKSIHLERFNTPGGNVKRAAGVQAEGRTVTIRQDGRDRLIALSAE

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DARGMA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529912.1\_2570 [locus\_tag=BN49\_RS14380] [protein=2,3-dehydroadipyl-CoA hydratase] [protein\_id=WP\_016529912.1] [location=2647366..2648133] [gbkey=CDS]

MSDLLIHRHGRVLQLTLNRPQARNALNNALLTQIAEALEAAAVDDSVGVCVIRGNARFFAAGADLNEMAE

KDLPATLDDIRPRLWARIDAFTKPLIASVNGYALGAGCELALLCDLIVAGDNARFGLPEITLGIMPGAGG

TQRLIRSVGKALASRMVLSGESIDARQAQQAGLVSDIHPAALTDEYALKLATTIARHSPLALRAAKQSLR

LAQEVSLQAGLQQERQLFSLLSATEDRREGIDAFLQKRTPEFKGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004140117.1\_2571 [gene=paaG] [locus\_tag=BN49\_RS14385] [protein=2-(1,2-epoxy-1,2-dihydrophenyl)acetyl-CoA isomerase PaaG] [protein\_id=WP\_004140117.1] [location=2648136..2648924] [gbkey=CDS]

MEAFILSAVEQGVMTITLNRPDRLNSFNDLMHHQLAECLKQAERDDGVRCLLITGAGRGFCAGQDLNDRN

VDPSGPPPDLGMSVERFYNPLVRRLAALPKPVICAVNGVAAGAGATLALGCDIVLAARSAKFVMAFSKLG

LVPDCGGSWFLPRVAGRARAMGLALLGDSLSAEQAAQWGIIWQLVDDSELADTSLQLARHLAAQPTFGLG

LIKKALLASETNSLDAQLDLERDYQRLAGRSDDYREGVSAFLAKRPPQFSGK

>lcl|NZ\_FO834906.1\_prot\_WP\_074428861.1\_2572 [locus\_tag=BN49\_RS14390] [protein=3-hydroxyacyl-CoA dehydrogenase] [protein\_id=WP\_074428861.1] [location=2648925..2650349] [gbkey=CDS]

MMTTSLVNVAVIGSGTMGAGIAEVAAAAGHPVRIFDINPKAVDLAIEGIAGRLASRVARGKLASEQADAL

LARLHPAHDLAALADADLVIEAASERLEVKTALFAQLAAICAPSTLLTSNTSSISITAIAAGVKNPERVA

GLHFFNPAPVMKLVEVVSGLATSTEVVEQLCQCVSGWGKQPVRCRSTPGFIVNRVARPFYAEAWRALEEQ

VAAPEVIDAALRDGGGFPMGPLALTDLIGQDVNFAVTCSVFNAFWQDRRYLPSLLQQELALAGRLGKKSG

HGVYRWPAETLPNAALPPVMMGAESVTVRSDNVTELDDVLLLETEGETALALSVKHHRPVVVYDLCASDT

VVLAAAATNAPAATDKAVHYFQQQGKKVLRIADYPGLLVWRTVAMLINEALDAVQKGVASPQDIDTAMRL

GVNYPHGPLAWGERLGWRRVLQLLENLQHHYGEERYRPSSLLRQKALMEKHHEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004140110.1\_2573 [gene=paaI] [locus\_tag=BN49\_RS14395] [protein=hydroxyphenylacetyl-CoA thioesterase PaaI] [protein\_id=WP\_004140110.1] [location=2650339..2650761] [gbkey=CDS]

MSNDPWRNARVMYEKDTCARKMGIELIEIDDGFAQMSMTVSADMLNGHQTCHGGQLFTLADTAFAYACNS

QGLAAVASAASIDFLRPAFAGDRLVATARVKQQGKLTGVYDIEIVNQQQKIVALFRGKSHRIGGTITGDV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529910.1\_2574 [gene=pcaF] [locus\_tag=BN49\_RS14400] [protein=3-oxoadipyl-CoA thiolase] [protein\_id=WP\_016529910.1] [location=2650761..2651966] [gbkey=CDS]

MRDAFICDGIRTPIGRYGGALASVRADDLAAIPLRELLSRNPGLDPAAIDDVIFGCANQAGEDNRNVAHM

ATLLAGYPHTVPGTTINRLCGSGLDAIGFAARAIKAGDADLLIAGGVESMSRAPFVMGKASAPYQRQAEL

FDTTIGWRFVNPLMAQHFGTDSMPETAENVAELLNISRADQDAFAWRSQQRAAQAQRDGILAQEIVPVQI

VGRKGAVSDVREDEHPRPETTLEQLAKLKAPFRQGGVITAGNASGVNDGAAALIIASEQQAAIQGLTPRA

RIVAMATAGVEPRLMGLGPVPAVRKVLERAGLNINDMDLIELNEAFAAQALGGLRQLGVPDDAAHVNPNG

GAIALGHPLGMSGARLALSASLELQRRGGRYALCTMCIGVGQGIAMILERV

>lcl|NZ\_FO834906.1\_prot\_WP\_004179642.1\_2575 [gene=paaF] [locus\_tag=BN49\_RS14405] [protein=phenylacetate--CoA ligase] [protein\_id=WP\_004179642.1] [location=2651993..2653309] [gbkey=CDS]

MITTTKLDPIETASRDELQALQTQRLKWTLKHAYENVPMYRRKFDAAGVHPDDFRELDDLQKFPCTTKQD

LRDNYPFDTFAVPMEQVVRIHASSGTTGKPTVVGYTQNDIDNWANIVARSLRAAGGSAKDKIHVAYGYGL

FTGGLGAHYGAERLGATVIPMSGGQTEKQAQLIRDFQPDMIMVTPSYCLNLIEELERQMGGDARGCSLRV

GVFGAEPWTLAMRAEIERRLGITALDIYGLSEVMGPGVAMECLETVDGPTIWEDHFFPEIVNPDDGTPLE

DGEHGELLFTTLTKEALPVIRYRTRDLTRLLPGTARTMRRMDRISGRSDDMLIIRGVNVFPSQLEEEILK

FEHLAPHYQLEVNRRGHLDSLAVRVELKESGLALSHEQRCQICHQLRHRIKSMVGISTDITIVNCGSIPR

SEGKACRVFDLRKAVVSG

>lcl|NZ\_FO834906.1\_prot\_WP\_004194367.1\_2576 [gene=paaX] [locus\_tag=BN49\_RS14410] [protein=phenylacetic acid degradation operon negative regulatory protein PaaX] [protein\_id=WP\_004194367.1] [location=2653409..2654335] [gbkey=CDS]

MSKLDAFIQQAVTAMPISGTSLIASLYGDALLQRGGEVWLGSVAALLEGLGFGERFVRTALFRLNKEEWL

DVVRIGRRSFYRLSDKGLRLTRRAEHKIYRASAPEWDGTWLLLLSEGLEKNVLADVKKQLLWQGFGALAP

SLLASPSQKLADVQSLLHEAGVAENVICFEAHSPLALSRAALRSRVEECWHLTEQNEMYEAFIALFRPLL

PLLRDCDPSELTPDRCFQIQLLLIHFYRRVVLKDPLLPEELLPAHWAGQTARQLCINIYQRVSPGALAFV

SEKGESSVGELPVPGPLYYQRFGGLPGA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529906.1\_2577 [gene=paaY] [locus\_tag=BN49\_RS14415] [protein=phenylacetic acid degradation protein PaaY] [protein\_id=WP\_016529906.1] [location=2654345..2654941] [gbkey=CDS]

MPIYQIDGLTPVVPEESYVHPTAVLIGDVILGKGVYVGPNASLRGDFGRIVVKDGANIQDNCVMHGFPGQ

DTVVEEEGHIGHGAILHGCVIGRNALVGMSAVIIDGAVIGENSIVGASAFVKANAELPANHLIIGSPAKA

IRTLSEQELAWKKQGTREYQALVERCKQTLHQVEPLREVEAGRKRLAFDENLRPKAAT

>lcl|NZ\_FO834906.1\_prot\_WP\_129015082.1\_2578 [locus\_tag=BN49\_RS14420] [protein=GFA family protein] [protein\_id=WP\_129015082.1] [location=2654950..2655360] [gbkey=CDS]

MMAEKLSAHCHCGAVAFTVELSDGFNTVRRCNCSYCRMRGAVAVSSPRSGTEVVRGGDKLTEYRFNTGEA

VHFFCSVCGIYTFHQRRSNPQQYGVNVACIDGVSPFDFPCVEVNDGVNHPKDGGGGVVGYLRYEKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002902889.1\_2579 [gene=azoR] [locus\_tag=BN49\_RS14425] [protein=FMN-dependent NADH-azoreductase] [protein\_id=WP\_002902889.1] [location=complement(2655397..2656002)] [gbkey=CDS]

MSKVLVLKSSILAGYSQSGQLSDYFVEQWQEKHPGDEITVRDLAANPIPVLDGELVGALRPSDAPLTPRQ

QEALALSDELIAELKGNDVIVIAAPMYNFNIPTQLKNYFDLVARAGVTFRYTEKGPEGLVTGKRAVVVTS

RGGIHKDTPTDLVTPYLSTFLGFIGITDVNFVFAEGIAYGPEVAAKAQSDAKAAIDSVVAA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043168.1\_2580 [gene=hrpA] [locus\_tag=BN49\_RS14430] [protein=ATP-dependent RNA helicase HrpA] [protein\_id=WP\_046043168.1] [location=2656207..2660109] [gbkey=CDS]

MTEQQKITFPQLYQQLDGLMLRDKTRFARRLHGVKKVKNPESQQAILQEMALEISQAAGKVLLREAARPA

ITYPENLPVSQKKQEILEAVRDHQVVIVAGETGSGKTTQLPKICMELGRGLKGLIGHTQPRRLAARTVAN

RIAEELQSEPGGCIGYKVRFSDHVSENTMVKLMTDGILLAEIQQDRLLMQYDTIIIDEAHERSLNIDFLL

GYLKELLPRRPDLKIIITSATIDPERFSKHFNNAPIIEVSGRTYPVEVRYRPIVEEADDTERDQLQAIFD

AVDELGREGPGDILIFMSGEREIRDTADALNKLALRHTEVLPLYARLSNSEQNRVFQPHSGRRIVLATNV

AETSLTVPGIKYVIDPGTARISRYSYRTKVQRLPIEPVSQASANQRKGRCGRVSEGICIRLYSEDDFLSR

PEFTDPEILRTNLASVILQMTALGLGDIAAFPFVEAPDKRNIQDGVRLLEELGAITTDAQATAYKLTPLG

RQLSQLPVDPRLARMVLEAQKHGCVREAMIITSALSIQDPRERPMDKQQASDEKHRRFHDKESDFLAFVN

LWNYLGEQQKALSSNQFRRQCRVDFLNYLRVREWQDIYTQLRQVVKELGLPINSEPAEYREIHTALLTGL

LSHIGMKDADKQEYTGARNARFSIFPGSGLFKKPPKWTMVAELVETSRLWGRIAARIEPEWVEPVAQHLI

KRSYSEPHWERAQGAVMATEKVTVYGLPIVAARKVNYSQIDPALCRELFIRHALVEGDWQTRHAFFRDNL

KLRAEIEELEHKSRRRDILVDDETMFEFYDQRISHDVISARHFDKWWKQASRETPDLLNFEKSMLIKEGA

EQVSKLDYPNFWHQGNLKLRLSYQFEPGADADGVTVHIPLPLLNQVEEAGFEWQIPGLRRELIIALIKSL

PKPVRRNFVPAPNYAEAFLGRATPLELPLLDSLERELRKMTGVTIDREAWQWDQVPDHLKITFRVVDDKN

KKLQEGRSLQALKDALKGKVQETLSAVADDGIEQSGLHIWSFGTLAESYEQKRGNYKVKAWPALVDERDS

VAIKLFDNPQEQQQAMWRGLRRLLLLNIPSPIKYLHEKLPNKAKLGLYFNPYGKVLDLIDDCISCGVDKL

IDEAGGPVWTEEGFSQLHDKVRAELNDTVVEIAKQVEQILTAVFNINKRLKGRVDMTMALGLSDIKAQMA

GLVYRGFVTGNGFRLLGDTLRYLQAIEKRLEKMAIDPHRDRAQMLKVESVQQAWQQWLNKLPPNRREDDD

VREIRWMIEELRVSFFAQQLGTPYPISDKRVLQAMEQITP

>lcl|NZ\_FO834906.1\_prot\_2581 [locus\_tag=BN49\_RS14435] [protein=O-methyltransferase] [pseudo=true] [location=complement(2660170..2660846)] [gbkey=CDS]

MGKRHMQQQWSAVDNYLIKALIPGDPVLDRVLENNHRVPGSRHTMSPPIRVSFSPCWYG\*PRLSGYWRSA

PSAAIAPSGWRASFLPTANSSPWRPTRIMPRWRGRICSWRALTSGSRYGRDPRYSPWSRLANVPLSI\*SS

SMPISRITPIICAGRYVIPAQEP\*LLAITWYATAKWSTHRAPTSAFRVCVSSLR\*WAPSQG\*RQRRCKPW

ALKAGTALLWRG\*TL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531091.1\_2582 [locus\_tag=BN49\_RS14440] [protein=efflux transporter outer membrane subunit] [protein\_id=WP\_016531091.1] [location=complement(2660847..2662226)] [gbkey=CDS]

MIRPVALAIVLALVGCQSADVQRAQPTLTIPAAWRADVGPASPVEGVWWRNFHDSTLNQYVDQALRYNSD

VLIARERVNEYQARAYAPDSSLFPSLDASLTGTRARTQSAATGLPIHSTLYKGGLTASYDVDIWGANRSA

ANAAGASLEAQKAAAAAANLSVASSVAVGYVTLLSLDEQLRVTQQTLTSREDAWRLAKRQFETGYTSRLE

LMQADSELRSTRAQIPPLQHQIAQQENALSVLLGDNPGAVKRGEFAQLTPLRLPSQLPSTLLNRRPDIAQ

AERQLVAADATLASSQAQLLPSINLTATGSLQDRTLPDLLDNPLRLWSLGGSILAPLLNRQALNAQVDVS

MAQRNQALYSYEKTVRSAFKEVNDSLDAISRYGEQLTELQEQETVAQETLRIAQNRYRNGYSSYLDVLDA

QRTLFSTQLSVVQVKNNLLLAQIDLYRALGGGWSDSSGS

>lcl|NZ\_FO834906.1\_prot\_WP\_002902965.1\_2583 [locus\_tag=BN49\_RS14445] [protein=HlyD family secretion protein] [protein\_id=WP\_002902965.1] [location=complement(2662223..2663308)] [gbkey=CDS]

MSQQDAAKQQANTRNNIRVVSIFTAAAIGLVGVLVILYAWQLPPFTRHSQFTDNAYVRGQTTFISPQVNG

YITAVNVKDFAIVQPGEVLFQIDDRIYKQRVHQAQATLAMKEAALRNNLQQRKSAEATIAKNEAALQNAR

AQNLKIQADLKRIQQLTADGSLSIRERDSARASAAQGAADIEQAKAALEMSRQDRESTIVNRDSLEADVA

SAKAALELAQIDLQNTQIIAPTGGQLGQISVRLGAYVSAGTHLTSLVPPQHWVIANLKETQLAEVRVGQP

VTFTVDALNGETFHGKVQSISPATGVEFSAISPDNATGNFVKIAQRIPVRITVNDGQNNSERLRPGMSVQ

VTIDTRAEKQP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043170.1\_2584 [locus\_tag=BN49\_RS14450] [protein=MFS transporter] [protein\_id=WP\_046043170.1] [location=complement(2663337..2664989)] [gbkey=CDS]

MPRRQDNPYAPHDWAPHEKPALLGSPSTPLHSPAKRLAYGVVGLLVCLTGALGNAVVTANLQLLQGTFAA

WSTEIAWLPAVYVMTNVSINLLLVKFRQQFGLRAFTEGFLVLYVLVTFFHLFVNDLSSAMMVRAAHGMVA

AALSSLGIYYQVQAWPARHRLKGLTIGITGSSLAIPLARLFSTELLQTDEWRGLYFFELGLALVSLACVI

ALKLPPSDRKKVFEKKDFITFFLLAPGMALVCAVLSLGRLEWWFEAPWIGWALAAAVILIVAAITFEHNR

SNPLLNTKWLSSGSIVRLGLIMLLIRIVLAEQNTGVIGWLQYVGLQNEQMTNLAWSIFAGILCGIIASCL

TLNPQKLYWPTATALALIMIASLLDSQSNALTHPEQLMFSQFLLGFGSAFFLAPAMLAGIGGVFADPRNL

VSFSVLFGMSQNIGGLLGSAILGTFQTWREKFHSSQLADQITTLNPLIVERLQQYSQMYQSQIGDSTLLN

VQATTLLQNAATLQANILAWNDTYLLTAAISAGTLVWVFWRLIRLRLTARIALQRATGSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002902969.1\_2585 [locus\_tag=BN49\_RS14455] [protein=MarR family transcriptional regulator] [protein\_id=WP\_002902969.1] [location=complement(2664989..2665420)] [gbkey=CDS]

MDNRQLTFSHLLYLTAHHWRLAVNRRLKNLGLSQASWVAVASIARHQQPLSQSELAQELGVESPTIVPLI

HRLVALGLVERITTASDKRKRLLVVTDKGKALYEQVKTVADDLREEILTAITPQEQEQTQRVLEKLLREV

EKK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043173.1\_2586 [locus\_tag=BN49\_RS14460] [protein=LysR family transcriptional regulator] [protein\_id=WP\_046043173.1] [location=complement(2665528..2666475)] [gbkey=CDS]

MKTLPDLQQIEILILIVKHGSFRQAAKALNLSPPSLTVAINHLEEKLGVRLLNRSTRSLSLTAVGEEFLN

NITPVVNDYRRVVDSLNYHRLTPEGVVKVNLPRIVIDLFFQDYFIAFKNACPNVTLELYATDRKVNIIES

GFDAGIRYSQDVPKEMIAIPFGEKLSLIPVASPDYIREAGESDTPQSLVNFRCINRCFPGGEKYRWEFIG

PSGELSEVAVKGDLVVDADSAMIQAAESGLGIAFVYQSLVTQQLNAGSLVHLLPDYRYPADHFCVYYPSR

KHIPAPLRAFIAWVMAQNKNILGQQTARHGSRPED

>lcl|NZ\_FO834906.1\_prot\_WP\_009760653.1\_2587 [locus\_tag=BN49\_RS14465] [protein=aldo/keto reductase] [protein\_id=WP\_009760653.1] [location=2666576..2667574] [gbkey=CDS]

MKTRYLGKEKFQVSALGLGCMGMSFAYGGAETSQAINTIHAAMDMGVTFLDTAEVYGPFDNEVLVGKAIK

GFRDKVQIATKFGFRILPTGQGLERMAGVDSRPAHIRESVEGSLKRLNVETIDLLYQHRVDPAVPVEEVV

GTMADLVKEGKIRHIGLSEVSAQTLRRACKVHPIAAVQSEYSLWSREPEAGILHTCRELGVGFVPYSPLG

RGFLTGTITDPGVLAADDFRRHLPRFQAETMRKNQLLLERLQQVATRYDATLAQIALAWVMSKGEDIVPI

PGARKIAHLRDNAGAANITLAPEDILTIEHIFTADNVTGLRYTQGDFDLIEK

>lcl|NZ\_FO834906.1\_prot\_WP\_032421294.1\_2588 [locus\_tag=BN49\_RS14470] [protein=Glu/Leu/Phe/Val dehydrogenase] [protein\_id=WP\_032421294.1] [location=complement(2667729..2669003)] [gbkey=CDS]

MEKLSYASESSTSPWTTYLRQIDRVAPYLGDLAYWVETLRHPKRALIVDIPVQMDDGTIRHFEGYRVQHN

LSRGPGKGGVRYHPDVDLNEVMALSAWMTIKCAAVNIPYGGAKGGIRVDPFSLSEGELERLTRRYTSEIG

IIIGPQKDIPAPDVGTNGKVMAWMMDTYSMNHGTTITGVVTGKPIHLGGSLGREKATGRGVFVTGREVAR

RAGIEIEGAKVALQGFGNVGSEAARLFAGVGARIVVIQDHTATLYNEGGIDMTALTAWQAEKKQIAGFPG

AQEIDKDAFWTTPMDILIPAALEGQITRERAEKLTCKLVLEGANGPTYPEADDVLAERGVIVVPDVICNA

GGVTVSYFEWVQDMASFFWSEEEINAKMDRIMTDAIVHVWDKAAEKECTLRTAAYIVACERILMARKDRG

IYPG

>lcl|NZ\_FO834906.1\_prot\_WP\_004224524.1\_2589 [locus\_tag=BN49\_RS31035] [protein=hypothetical protein] [protein\_id=WP\_004224524.1] [location=complement(2669216..2669362)] [gbkey=CDS]

MVNAMLLCGLMLACEQQDCQYGQKQFIHFLKIIKIMKNIEKIFSYALK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176366.1\_2590 [locus\_tag=BN49\_RS14480] [protein=aspartate aminotransferase family protein] [protein\_id=WP\_004176366.1] [location=2669532..2670737] [gbkey=CDS]

MSGSMTREDFDAYLVPCFAPAPFIPVRAAGSRVWDQQGKEYIDMAGGIAVNALGHAHPALAQALQDQLAK

LWHIGNGYTNEPVLQLAKTLVQSTFADKVFFCNSGAEANEAALKLARKYAHDKFGGEKSEIIAFNHAFHG

RTLFTVSVGGQPKYSSDYAPLPQGITHLPYNDIEAVTAAISSRTCAVIVEPIIGEGGVIPADPAFLQALR

TLCDRHHATLIFDEVQTGAGRTGHLYAYQHYNVVPDILTSAKGLGGGFPIGAMLAKEAWAQVFQPGTHGT

TFGGNPLAATVANAVLAHLDAPLLAGVGERHALIVDQLNAISARYDAFSAVRGTGLLIGAELAGPLRGKA

KTLTNLAAEEGLIALIAGPDVLRFAPALNIPLADIAEAFVRLDRAVARLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004140076.1\_2591 [gene=astA] [locus\_tag=BN49\_RS14485] [protein=arginine N-succinyltransferase] [protein\_id=WP\_004140076.1] [location=2670756..2671778] [gbkey=CDS]

MLFRPVRENDLDDIVRLAARAGVGMTSLPHDVGRLAARIRRSIETFAGELPRSQQGFLFVLEDTALARVV

GVSAIEVAVGLDEPFYNFRIQKTVRASKALGVYKPQELLNLSYDHTGHSELCTLFLDPAYQRNRNGLLLS

KARFLFIAAFREWFSPHLFAELRGCSDEQGQSPFWDALGHHFFDIPFADADRLTGTGMKTFIAELMPAYP

IYISLLPEAARGVIGQVHPNTAPARAILEKEGFSWRGSVDIFDAGPVLEADTDQIRAVRDSQRLPVRQLM

GDLPAPTLVANGQFDNFRALLVAHEEQVSLDSAALDALQVSETDRVYTVTLNPEDNRSWR

>lcl|NZ\_FO834906.1\_prot\_WP\_023282534.1\_2592 [gene=astD] [locus\_tag=BN49\_RS14490] [protein=succinylglutamate-semialdehyde dehydrogenase] [protein\_id=WP\_023282534.1] [location=2671769..2673235] [gbkey=CDS]

MAVKAQFIAGQWLPGSGATMSKLAPADQSLLWQAASAGADDVQAACAAARAAFYPWSHRPLAERIDVVQR

FAALLETHKEALATLISRETSKPLWETRTEVQAMIGKAAISIEAYHQRTGFHESTLPDGKALLRHKPHGV

MAVFGPYNFPGHLPNGHIIPALIAGNTIVFKPSELTPATAEMTVQLWQQAGIPDGAINLLQGGKATGQAL

LENRDIDGVLFTGSAAAGFHFHRYFGGQPEKMLALEMGGNNALIVADVADIDAALHVIIQSAFISAGQRC

TCARRLIVPRGEQGDALLQRLVEASAQIRAGKWDDQPAPFMGGVISLDAAQNMLAAQQKLEGLGGKVLLR

MRQPDPRSTVLTPGIVDVTGIEVPDEEYFGPLLTIIRYDGFPEAIRLANQTRYGLAVGLISSDAAQFDQL

ADEARAGIVNWNKPLTGASSKAPFGGVGASGNHRAAAWYAADYCAWPMASLVSDTLTLPATVSPGLPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004148240.1\_2593 [gene=astB] [locus\_tag=BN49\_RS14495] [protein=N-succinylarginine dihydrolase] [protein\_id=WP\_004148240.1] [location=2673257..2674597] [gbkey=CDS]

MSGFEANFDGLVGPTHHYAGLSVGNEASQNNRDGLSNPKKAALQGLYKMKALADRGFVQGILPPQPRPNL

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EAPTTSAILGATFADPRYFAHHAALPQHGDLGDEGAANHNRFCREYDRQGVQFFVYGRRASGGIAPVKYP

ARQTLEASEAVARLHQLDPRYTVFAQQAPQAIDRGVFHNDVIAVSNRHVLFHHQQAFVDQATVLATLRAK

SDSLDIPFTSVEVPDERVSLDDAVASYLFNSQLLSKPDGKMLIVVPEECRQRENVWRYLSDLAADSASPI

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LLREVYQALDELTQILRLGAVYDFQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002903056.1\_2594 [gene=astE] [locus\_tag=BN49\_RS14500] [protein=succinylglutamate desuccinylase] [protein\_id=WP\_002903056.1] [location=2674608..2675603] [gbkey=CDS]

MEHLVNDLLHCRLQAWTFPAGIEARWLGEGILQLLPTAPWRQATILSAGVHGNETAPIELLLQLTHDLSQ

GRQPLTQALLIVFGNLPAIRAARRYLHNDLNRLFGGRHLAVTPGNESRRAFALEQAVQAFYRAADTAGPV

NRGHLDMHTAIRGSLYRQFALLPAHAGDFSPDFYQLLQASGMDAVVRHTEAGGTFTHFTCEKFAAQSATL

ELGKVMPFGANDLSLFAAADAAIRAWIADAPLPPRDKAPVDYFLVEESIIKREGEFTLNLAADVENFTAL

PAGYEIARQAEKRWVVQARAPYILFPNAGVATGQRAGLLLRAAALRLPQPA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043185.1\_2595 [locus\_tag=BN49\_RS14505] [protein=amino acid permease] [protein\_id=WP\_046043185.1] [location=2675613..2677043] [gbkey=CDS]

MTEHQHQASPAAGGEGASQLKPGLSARHIQMIALGGAIGTGLFMGAGRNIAVAGTSILVIYVLVGFFTYM

VMRAMGELLLTRHDYRSFADFVGEYLGPQASFYLGWTYWLSWVVTCIADVVVCGSYMQYWFPELSAWMPA

LSMLAILFLLNLLSVKMFGEAEFWFALIKVITIIALIGTGGWMIATGWTSPDGVTASLSHLTDPTAFMPH

GITGFFAGFQIAIFSFTGIELLGTMTAETRDPQRILPKAINALPLRIIIFYLLSMVVIIAVASWPGVSAE

TSPFVTLFAKAGLPAAAAVINFVALTSAMSSANSGVFSSTRMLYGLSVEKHAHWQFRILSRSTRIPVRSL

LFSCFCMLIGTLLLFLVPNVMTLFTIVSTLAAIMVVFSWGMILVAYLVYRRQRPDLHAGSIFKMPAGVVM

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>lcl|NZ\_FO834906.1\_prot\_WP\_004224544.1\_2596 [locus\_tag=BN49\_RS14510] [protein=MHS family MFS transporter] [protein\_id=WP\_004224544.1] [location=complement(2677250..2678575)] [gbkey=CDS]

MSNPQDNTASILQKNKKVLIASLTGSAIEWFDYFLYGTAAALVFNKIFFPMVDPVIGLILSWLSFSLTFF

IRPIGGVIFAHIGDRIGRKKTLVLTLSLMGSATVAIGLLPTYEMVGLWAPALLIILRIIQGMGIGGEWGG

ALLLAYEYAPEKRKGFFGSIPQAGVTIGMLMATFIVSLMTLFDEAQFLAWGWRIPFLLSSVLVFLGLWIR

KDIDETPAFKQVKKSGQVAKAPLRDTLKHHWREVLIAAGLKVVETAPFYIFSTFVVSYATTTLSYQKSQA

LESVTLGALVATVMIPLMGLLSDKVGRQKMYTLSVVLLGLFIVPWFLLLDTGTGWGIMLATIVAFGILWA

PVTAVLGTLCSEIFSANVRYTGITLGYQLGAALAGGTAPLIATGLLAKYDGDWRPVAIYLGITVAISLLA

IFCASRMKSALGTAPSRAESA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529462.1\_2597 [locus\_tag=BN49\_RS14515] [protein=YdcF family protein] [protein\_id=WP\_016529462.1] [location=2678956..2679756] [gbkey=CDS]

MAEQFPPLSAATLAAANQVGAWLAQDDLATLPALPQVDVVVLAGNAVIPTIDAACCLAAAQAVPLLISGG

VGHSTGYLYEAVRQDPRYRTLPVDGRPEAHVLADIAHDYWHIPHSRLVVEDQSTNCGENARFTRTTLESR

GLAHRRGIVIQDPTMQRRTMATFARVWQGATTPPQWLSFPGCSPVLEQTDGQLGFAGGGAGLWPVTCYLA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004140057.1\_2598 [locus\_tag=BN49\_RS31040] [protein=hypothetical protein] [protein\_id=WP\_004140057.1] [location=complement(2679818..2679955)] [gbkey=CDS]

MAAPVVHLYLTGDFFVKYRADKPLFGSTLTQFCELIHKNGPKMPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151568.1\_2599 [gene=aldA] [locus\_tag=BN49\_RS14525] [protein=aldehyde dehydrogenase] [protein\_id=WP\_004151568.1] [location=2679954..2681393] [gbkey=CDS]

MTAPVQHPMYIDGQFVSGRGDGWIDVLNPATEALLSRIPDGTAEEARLAIDAAERAQPGWEALPAIERAG

WLRKIAAGIRQRADEIAGLIVAEGGKIQQLAAVEVAFTADYLDYMAEWARRYEGEIVQSDRPGENILVFK

RALGVTTGILPWNFPFFLIARKLAPALITGNTIVIKPSEFTPNNAIAFAEIVHQVGLPKGVFNLVLGRGE

TVGQELAGNPKVAMVSMTGSVAAGEKIMAAAAKNITKVCLELGGKAPAIVMDDADLELAVKAVVDSRVIN

TGQVCNCVERVYVQQGIYDRFVNRLGEAMKAVQFGDPATRDDIAMGPLINAAARDQVAGKVAKAVAQGAR

VALGGQPLEGKGYFYPPTLLLDVRQEMDIIHEETFGPVLPVVAFSTLDEALAMANDSDYGLTSSIYTRDL

NVAMKAIKGLKFGETYINRENFEAMQGFHAGWRKSGIGGADGRHGLNEYLQTQVVYLQA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529461.1\_2600 [gene=gap] [locus\_tag=BN49\_RS14530] [protein=type I glyceraldehyde-3-phosphate dehydrogenase] [protein\_id=WP\_016529461.1] [location=complement(2681442..2682440)] [gbkey=CDS]

MSKLGINGFGRIGRLVLRRLLEVDSSLEVVAINDLTSPKVLAYLLKHDSNYGPFPWSVDFTEDALIVNGK

TITVYAEKEAQHIPWQAAGAEVIVECTGFYTSAEKSQAHLQAGARKVLISAPAGEMKTIVYNVNDDTLTP

DDTIISVASCTTNCLAPMAKVLQDAFGITVGTMTTIHAYTGTQSLVDGPRGKDLRASRAAAENVIPHTTG

AAKAIGLVIPALSGKLKGHAQRVPTKTGSVTELVSVLEKKVTAEEVNQAMRQAAEGNESFGYTEEEIVSS

DIIGSHFGSIYDATQLEIVEAGGVQLVKTVAWYDNEYGFVTQLIRVLEKFAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002903230.1\_2601 [locus\_tag=BN49\_RS14535] [protein=YqaE/Pmp3 family membrane protein] [protein\_id=WP\_002903230.1] [location=2682723..2682881] [gbkey=CDS]

MGFWRIVFTIILPPLGVLLGKGFGWAFILNIILTLLGYIPGLIHAFWVQTRD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043188.1\_2602 [locus\_tag=BN49\_RS14540] [protein=DUF1398 domain-containing protein] [protein\_id=WP\_046043188.1] [location=complement(2682916..2683308)] [gbkey=CDS]

MELLVRLGHFFEQARSDADYATFANELRRHQVSYYIYFVSTGNMNFVMANGEVVSVKSARGLLRVRAEAS

HCLTRAAVIRHFARAINFEQYCRDLASAGVFKWIVDLEEETRHYWSKDNTLLYKECLMPP

>lcl|NZ\_FO834906.1\_prot\_WP\_002903233.1\_2603 [gene=yedF] [locus\_tag=BN49\_RS14545] [protein=sulfurtransferase-like selenium metabolism protein YedF] [protein\_id=WP\_002903233.1] [location=complement(2683559..2683792)] [gbkey=CDS]

MKNIIPDYRLDMVGEPCPYPAVATLEAMPSLQKGEILEVVSDCPQSINNIPLDARNHGYTVLDIQQDGPT

IRYLIQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002903234.1\_2604 [gene=yedE] [locus\_tag=BN49\_RS14550] [protein=selenium metabolism membrane protein YedE/FdhT] [protein\_id=WP\_002903234.1] [location=complement(2683789..2684997)] [gbkey=CDS]

MTWQSFKQAWLIRFWSPVPAVIAAGILSTYYFGITGTFWAVTGEFTRWGGQLLQLLGVHSEQWGYYQLIH

LEGSPLTRIDGRMIIGMFGGCLAAALWANNVKLRLPRSRIRIAQAVAGGIIAGFGARLAMGCNLAAFFTG

IPQFSLHAWLFAIATAIGSWFGARFTLLPLFRIPVKMQKVSAASPLTQKPQQARRRFRLGMVVFFAMIGW

GLLTAADHPALGLAMLFGIGFGLLIERAQICFTSAFRDMWITGRTVMAKAIIFGMAASAIGIFSYVQLGM

APKIMWAGPNAAIGGLLFGFGIVLAGGCETGWMYRAVEGQVHYWWVGLGNVIGSTLLAWCWDDIAAPLAT

HWQKVNLLNAFGPFGGLLATYLLLLIALLLVIAWERHFFRRQAAVRTVKESA

>lcl|NZ\_FO834906.1\_prot\_WP\_004179665.1\_2605 [locus\_tag=BN49\_RS14555] [protein=DUF1304 domain-containing protein] [protein\_id=WP\_004179665.1] [location=complement(2685101..2685454)] [gbkey=CDS]

MLATLLVALVAIIHLAILVLEMFLWEGSAGRRAFNLSADFARQTRVLAANQGLYNGFLAAGLAWGLWLGA

PGVQVVIFFLACVLAAGIFGALTASRKILYIQALPALLALVAVLTQA

>lcl|NZ\_FO834906.1\_prot\_WP\_074181940.1\_2606 [locus\_tag=BN49\_RS14560] [protein=hypothetical protein] [protein\_id=WP\_074181940.1] [location=2685691..2686170] [gbkey=CDS]

MVAMPSTQAGELNLYSMNTGSYVYHMTGNHGQYNEHFNNNFFSVERKFSQDSKYSVLVGTMKNSFDDRCL

TLGVRRDWLKNDTGWVLKGVYAYTGEFFFDAFSHCGDSGTYRTAKKITGIGFSPYLYHGLQYNFTDYFGV

EGGIIVPAIFVMSVQWSFR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151566.1\_2607 [gene=ydfZ] [locus\_tag=BN49\_RS14565] [protein=putative selenium delivery protein YdfZ] [protein\_id=WP\_004151566.1] [location=complement(2686240..2686443)] [gbkey=CDS]

MKTYDRNRNAIATGSMVMIAGNGTTGVIKAIHGEGKTAEQLRRADCVEIDGCEGRFCPLDLIRLGFH

>lcl|NZ\_FO834906.1\_prot\_WP\_004179669.1\_2608 [locus\_tag=BN49\_RS14570] [protein=magnesium transporter CorA] [protein\_id=WP\_004179669.1] [location=2686755..2687783] [gbkey=CDS]

MSQDVTAKMLKPDFDSEVSGLVHGYLFHEQRPPQPIASGEVCARYQALADDKAFIWLHLNLNHATAEKWL

TSHFPVADFFFEEIRSGSHTTRIERQGENLFAVLNDVLFRPQDTSAETATLWLYCSPRLVVTARFKPLRF

IEWMLPRLQTLRVNTSTELLAFLLEEQEEVLEQVVRQASRHVDLIEERLLSNHVQRNRADLARLRRMLLR

FQRLLAPEPAAMFRLLNRPPAWMDRAVVQAFRQFTEEFSVVLNDLSGLIERISLLQEEIGARQLEQSNRT

LYTLTVITVLALPINIVAGFFGMNVGGIPLASNHHGFILLVVIVAVFTLGAGYLAFRRRDDL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530736.1\_2609 [locus\_tag=BN49\_RS14575] [protein=pyridoxal phosphate-dependent aminotransferase] [protein\_id=WP\_016530736.1] [location=complement(2687797..2688969)] [gbkey=CDS]

MFDFATPIDRHGTWCTQWDYVADRFGAADLLPFTISDMDFATAPCILDAVSQRLAHGVFGYSRWRNEAFL

GAIAHWYASRFNSDINPQSVVYGPSVIYMVAETIRQWSKEGDGVVVHTPAYDAFYNTITANRRRIAPVPL

ILKDNRWRCDMDRLEAALAEPKNTLLLLCSPHNPTGKVWRREELETMAALCQKHGVRVISDEIHMDMTWS

EHRHIPWSEVAQGPWALFTSGSKSFNIPAFTGAYGFIPEENERDSYLQALKGRDGLSSPSVPALVAHIAA

YRDGAPWLDALRDYLQANMRYVADTLNNAFPALCWQPPEATYLAWIDLRPLNVDDRALQQALIAEQKVAI

MPGYTYGPEGNGFLRLNVGCPREKLERGVEGLIAALRSLS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530737.1\_2610 [gene=malX] [locus\_tag=BN49\_RS14580] [protein=maltose/glucose-specific PTS transporter subunit IIBC] [protein\_id=WP\_016530737.1] [location=complement(2689021..2690613)] [gbkey=CDS]

MTAKTAPKITLWEFFQQLGKTFMLPVALLSFCGIMLGIGSSLSSHDVLTLLPWLNMPLLQAIFIWMSKVG

SFAFSFLPVMFCIAIPLGLARENKGVAAFAGFVGYAVMNLAVNFWLTAKGILPTTDAAILKANNIQNIIG

IPSIDTGILGAVIAGIIVWLLHERFHNIRLPDALAFFGGTRFVPIVTTVVLGLVGLAIPLVWPVFAMGIN

ALGKMINSAGDFGPMIFGTGERLLLPFGLHHILVALIRFTEAGGTLDVCGHSVSGALTIFQAQLSCPTTH

GFAESATRFLSQGKMPAFLGGLPGAALAMYHCARPENRHKIKGLLISGVIACVVGGTTEPLEFLFLFVAP

VLYVIHALLTGLGFTIMAVLGVTIGNTDGNIIDFVVFGILHGLATKWYLVPVVAAIWFAVYYAIFRFAIT

RFNLKTPGRDIDTAASVEKAVAGTIGKSGYNVPAILAALGGAENIVSLDNCITRLRLSVHDMSKVDAAAL

KAHRAIGVVQLNQHNLQVVIGPQVQSVKDEMATLMNTVQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004148253.1\_2611 [locus\_tag=BN49\_RS14585] [protein=Mal regulon transcriptional regulator MalI] [protein\_id=WP\_004148253.1] [location=2690786..2691814] [gbkey=CDS]

MAIAKKITINDVALAAGVSVSTVSLVLSGKGRISSATGERVNQAIEQLGFVRNRQAASLRGGQSGVIGLI

VSDLSKPFYAELTAGLTDALERQGKMVFLTQGGRSGEKMAQRFDTLAAQGVDGVIIAGAIDRGSELRERA

AEAGVPLVFASRASYLDDVDLIRPDNMQAAQLVTEHLIRRGHQRIAWLGGQSASLTRAERVGGYCATLLK

YGLPFHSEWVLECESSQKQAAEAMTGLLRQNPTITAVLCYNNVVATGAWFGLLRAGRQSGEDGVESYFEQ

RVALAAFADVPEAALDDLPLTWVTTPAREMGKSLADSMLRRLEEGTGETRNQIMPPRLVTRK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043190.1\_2612 [locus\_tag=BN49\_RS14590] [protein=YdgA family protein] [protein\_id=WP\_046043190.1] [location=complement(2691854..2693431)] [gbkey=CDS]

MKKSLVAAGVIVALGVVWTGGAWFTGKQLEGRIADMVQQANAQLRSSAPESGLELSYQDYQRGLFSSHLQ

LVVKPIAGQANGWLAAGQSVVLDEVVDHGPFPLASLKAFNLAPAMASVHTTLVKNDASQALFEIAKGDTP

FTVDTRIAYSGDSQSAIVLNALDYAKGDEKVTFSGGQFQLDADRDGKNISLKGQAGSGQIDALNEYNQKV

QLRFVNLTTDGATELASFNERIGQQKMTLDKLAISVEGKELALIDGMALDGGSTLTQDGKGVNSQVNYTV

NSLKLQGQNMGSGKLTLKVDNVDGQAWHQFSQQYSAQSQALLAKPELAQNPELYQQALTETLFNALPILL

KGNPSVTISPLSWRNAKGESTLNLSVLLKDPAQVTAPPQTLADSLDRVVQSLDGKVVIPVDMATEFMTKI

AGLEGYQPADAAKLADQQVKGLAAMGQMFRITTMEDNAISSSLQYANGQVTLNGQKMPLQDFAAMFGLEA

PSLPDSAPQEGQPQQEGQPQQDDAAPQQDDAAPQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002903312.1\_2613 [gene=manA] [locus\_tag=BN49\_RS14595] [protein=mannose-6-phosphate isomerase] [protein\_id=WP\_002903312.1] [location=complement(2693518..2694696)] [gbkey=CDS]

MQKLINAVQNYAWGSHTALTELYGIANPDNLPMAELWMGAHPKSSSQILAADGQPRSLREVIDADKAALL

GDKVAARFGELPFLFKVLCAAQPLSIQVHPNKQASEEGFARENAAGIPLSAAERNYKDPNHKPELVFALT

PFLAMNAFREFSEIVTLLQPVASAHPAIGAFLQQPDATHLSQLFASLLNMQGEEKAKALQVLRDVLAREQ

GEPWQTIRLIAEFYPDDSGLFSPLLLNVVKLNPGEAMFLFAETPHAYLQGVALEVMANSDNVLRAGLTPK

YIDIPELVANVKFEAKPAGELLTQPQRHGAELDFPIPVEDFAFSLHDLSAEASDLAQASAAIVFCVDGEA

VLRKGDQSLTLKPGESAFVAASESPVQVSGRGRVARVFNKLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043192.1\_2614 [locus\_tag=BN49\_RS14600] [protein=class I fumarate hydratase FumA] [protein\_id=WP\_046043192.1] [location=2694898..2696544] [gbkey=CDS]

MSNKPFVYQDPFPLKKDDTEYYLLSSDYVSVAEFAGQEVLKVDPQALTLLAQHAFHDASFMLRPAHQQQV

ADILNDPEASENDKYVALQFLRNSDIAAKGILPTCQDTGTAIIMGKKGQRVWTGGGDEAALAQGVYNTYI

QDNLRYSQNAPLDMYKEVNTGTNMPAQIDLYATDGDEYKFLCIAKGGGSANKTYLYQETKALITPAKLKN

YLVEKMRTLGTAACPPYHIAFVIGGTSAEATLKTVKLASTKYYDGLPTEGNEHGQAFRDVQMEQELLLEA

QNLGLGAQFGGKYFAHDIRVIRLPRHGASCPVGMGVSCSADRNIKAKINRDGIWIEKLESNPGKYIPEHL

RQAGEGEAVKVNLNQPMSEILAQLSQYPVSTRLSLSGTIIVARDIAHAKLKELIDNGEALPQYVKDHPIY

YAGPAKTPDGYASGSLGPTTAGRMDSYVDLLQSHGASKIMLAKGNRSQQVTDACHKHGGFYLGSIGGPAA

VLAQQSIKSLECVAYPELGMEAIWKIEVEDFPAFILVDDKGNDFFQQIQTSQCARCVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002903315.1\_2615 [gene=fumC] [locus\_tag=BN49\_RS14605] [protein=class II fumarate hydratase] [protein\_id=WP\_002903315.1] [location=2696884..2698284] [gbkey=CDS]

MTTHRSEKDSMGAIEVPADKLWGAQTQRSLEHFRISTEKMPGELIYALALTKRAAAKVNQDLGLLTAEKA

GAIVAAADEVLAGKHAQEFPLAIWQTGSGTQSNMNMNEVLANRASELLGGERGMARKIHPNDDVNKSQSS

NDVFPTAMHVAALIALREKVIPSLQALRATLNEKAVAFRDIVKIGRTHLQDATPLTLGQEISGWVAMLDH

SLKHIEASQPHLAELALGGTAVGTGLNTHPEYAVRVAAELASLSGQPFVTAPNKFEALATVDALVHAHGA

LKGLAASLMKIANDVRWLASGPRCGIGEIAIPENEPGSSIMPGKVNPTQCEALTMVCCQVMGNDVAVNIG

GASGNFELNVYRPMVIHNFLQSVRLLADGMASFNEHCAVGIEPNRERISQLLNESLMLVTALNTHIGYDK

AAEIAKKAHHEGLTLKASALALGYLTEAEFDSWVRPEEMVGSLAIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004148259.1\_2616 [gene=tus] [locus\_tag=BN49\_RS14610] [protein=DNA replication terminus site-binding protein] [protein\_id=WP\_004148259.1] [location=complement(2698274..2699206)] [gbkey=CDS]

MASYDLVERLNNTFRQIELELQALQQALSDCRLLAGRVFELPAIGKDAEHDPLATIPVVQHIGKTALARA

LRHYSHLFIQQQSENRSSKAAVRLPGAICLQVTAAEQQDLLARIQHINALKATFEKIVTVDSGLPPTARF

EWVHRHLPGLITLSAYRTLTPLVDPSTIRFGWANKHVIKNLTRDQVLMMLEKSLQAPRAVPPWTREQWQS

KLEREYQDIAALPQRARLKIKRPVKVQPIARVWYAGEQKQVQYACPSPLIALMSGSRGVSVPDIGELLNY

DADNVQYRYKPEAQSLRLLIPRLHLWLASE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151564.1\_2617 [gene=rstB] [locus\_tag=BN49\_RS14615] [protein=two-component system sensor histidine kinase RstB] [protein\_id=WP\_004151564.1] [location=complement(2699282..2700583)] [gbkey=CDS]

MKKLFVQFYLLLFVCFLVMTMLVGLVYKFTAERAGRQSLDDLMKSSLYLMRSELREIPPRDWSKTLKELD

LNLSFDLHIEPISKFKLSESSMQHLRAGDIVALDDQYTFIQRIPRSHYVLSVGPVPYLYFLHEMRLLDVA

LMAFIAISLAFPVFIWMRPHWQDMLRIETAAQRFGEGHLSERIHFDSMSSFERLGVAFNQMADNINALIA

SKKQLIDGIAHELRTPLVRLRYRLEMSENLTEAESQALNRDIGQLEALIEELLTYARLDRPQTELSLTTP

DFPAWISDHVEDIQMVNPQREVALATLTHGNYGALDMRLMERVLDNLVNNALRYSSQRVAVSLTLQGSRA

SLLVEDDGPGIAPEERERVFEPFVRLDPSRDRATGGCGLGLAIVHSIAQAMGGEVRCEASPLGGARFCFS

WPVYHQLPDFTSA

>lcl|NZ\_FO834906.1\_prot\_WP\_002903374.1\_2618 [locus\_tag=BN49\_RS14620] [protein=hypothetical protein] [protein\_id=WP\_002903374.1] [location=complement(2700839..2701201)] [gbkey=CDS]

MMKYVVLLALSLFTSLSGWAFSLDNADIRLLCPQRGQIEVILHRYEHTQQSWGQHHFETGGGHVRQGPLL

VIPFANLDQMIYHQTTGEFAYWYAETEKLVRCRLLSLTTTYPVDIPYYRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002903377.1\_2619 [gene=rstA] [locus\_tag=BN49\_RS14625] [protein=two-component system response regulator RstA] [protein\_id=WP\_002903377.1] [location=complement(2701444..2702163)] [gbkey=CDS]

MNKIVFVEDDPEVGTLIAAYLGKHDMDVVVEPRGDRAEEVIAREKPDLVLLDIMLPGKDGMTLCRDLRGQ

WQGPIVLLTSLDSDMNHILSLEMGASDYILKTTPPAVLLARLRLHLRQHIAPAGAGSASSTLTPHKTISF

GSLTIDPVNRQVLLGGENVALSTADFDLLWELATHAGQIMDRDALLKNLRGVTYDGMDRSVDVAISRLRK

KLLDNATEPYRIKTVRNKGYLFAPHAWDN

>lcl|NZ\_FO834906.1\_prot\_WP\_002903379.1\_2620 [locus\_tag=BN49\_RS14630] [protein=GlpM family protein] [protein\_id=WP\_002903379.1] [location=2702292..2702627] [gbkey=CDS]

MGLLIKGLLGALVVVLIGVLAKTKNYAIAGLVPLFPTFALIAHYIVASERGIEALRATIVFGMWSILPYF

IYLLSLWYFTGIMRLPLALAGAVGCWGLCAWLLILGWSRFH

>lcl|NZ\_FO834906.1\_prot\_WP\_016531082.1\_2621 [gene=folM] [locus\_tag=BN49\_RS14635] [protein=dihydromonapterin reductase] [protein\_id=WP\_016531082.1] [location=complement(2702624..2703346)] [gbkey=CDS]

MAEQQPRPILITGAGRRIGLALAHHFLQQRQPVIVSYRTPYPAIDGLHEAGALCLQADFSSDDGILTFAE

AVKSHTDGLRAIIHNASDWMAEKPGVPLSTVINRMMQIHVHAPYLLNHALEALLRGHGHAASDIIHITDY

VVERGSDKHIAYAASKAALDNMTRSFARKLAPEVKVNAIAPSLIMFNEGDDEAYRQQALDKSLMKIAPGE

KEISDLIDYLFTSRYVTGRSFAVDGGRPLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004183892.1\_2622 [locus\_tag=BN49\_RS14640] [protein=amino acid permease] [protein\_id=WP\_004183892.1] [location=complement(2703383..2704765)] [gbkey=CDS]

MEKKLGLSALTALVLSSMLGAGVFSLPQNMAAVASPSALLIGWAITGVGILFLAFAMLLLTRIRPDLDGG

IFTYAREGFGELIGFCSAWGYWLCAVIANVSYLVIVFSALSFFTDTPELRLFGDGNTWQSIVGASVLLWV

VHFLVLRGVQTAAGINLVATLAKLLPLGAFVALAALAFQLDTFRLDFSGLALGVPVWEQVKNTMLITLWV

FIGVEGAVVVSARARHKRDVGRATLLAVLSALAVYLLVTLLSLGVVPRSELAEMRNPSMAGLMVRLMGSW

GEIVIAAGLIVSVCGAYLSWTIMAAEVPFLAATHKAFPRLFARQNSNNAPSASLWLTNISVQVSLVLIWL

TGSDYGTLLTIASEMILVPYLLVGAFLLKIATRPLHKAVAIGACIYGIWLLYASGPVHLLLSVVLYAPGL

LVFLYARRTHQHDRSLKRREVALIGLLLVAAVPATWMLVG

>lcl|NZ\_FO834906.1\_prot\_WP\_002903384.1\_2623 [gene=ydgH] [locus\_tag=BN49\_RS14645] [protein=DUF1471 family protein YdgH] [protein\_id=WP\_002903384.1] [location=complement(2704943..2705893)] [gbkey=CDS]

MKLKNTLLASALLTTATLSAHAATELTPEQAAALKPYDRVVVTGRFNAIGDAVQAVSRKADKDGAASFYV

VDTSDYGNGGNWRVTADLYKEDAPKADAPKNRIINGVMELPKDQAVELMPYDTVTVQGFYRSQPEVNDAI

TKAAKAKGAYAFFIVRQVDANQGGNQRITAYIYKKDAEKRVLQSPDAIPADSEAGRAALAKGGEAAKNVE

IPGVATTAAVGSGTGVGRFFETQSSKGGRYTVTLPNGTKVEEVNKVTAAQMVPFDNIQFTGNYGNMTEIS

YQTAKRAAKKGAKYYHITRQWQERGGNITISADLYK

>lcl|NZ\_FO834906.1\_prot\_WP\_004140012.1\_2624 [locus\_tag=BN49\_RS14650] [protein=hypothetical protein] [protein\_id=WP\_004140012.1] [location=complement(2705890..2706072)] [gbkey=CDS]

MLVKRLFFQHIEKCYLSVVYDSGGKQKLTQTVTAIKCNNQTFSVNNNTSIWFAQGKGLFL

>lcl|NZ\_FO834906.1\_prot\_WP\_004148265.1\_2625 [gene=pntA] [locus\_tag=BN49\_RS14665] [protein=Re/Si-specific NAD(P)(+) transhydrogenase subunit alpha] [protein\_id=WP\_004148265.1] [location=2706415..2707944] [gbkey=CDS]

MRIGVPQERLAQETRAAATPKTVEQLLKLGFSVAVESGAGKLASFDDEAFAEAGAEIVTGDEVWQSDVIL

KVNAPNDDEIALLNPGTTLISFIWPAQNPQLMEKLAARNINVMAMDSVPRISRAQSLDALSSMANIAGYR

AIVEAAHEFGRFFTGQITAAGKVPPAKVMVIGAGVAGLAAIGAANSLGAIVRAFDTRPEVKEQVQSMGAE

FLELDFKEEAGSGDGYAKVMSEAFIKAEMALFAAQAKEVDIIVTTALIPGKPAPKLITREMVDSMKSGSV

VVDLASQNGGNCEYTVPGEVVTTANGVKIIGYTDLPGRLPTQSSQLYGTNLVNLLKLLCKEKDGNIVIDF

DDVVVRGVTVVREGEITWPAPPIQVSAQPQAAAKKVEAPKEAVKPASPWRKYALMALAIILFGWLANVAP

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NIFGGFTVTQRMLKMFRKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002903386.1\_2626 [gene=pntB] [locus\_tag=BN49\_RS14670] [protein=Re/Si-specific NAD(P)(+) transhydrogenase subunit beta] [protein\_id=WP\_002903386.1] [location=2707955..2709343] [gbkey=CDS]

MSGGLVTAAYIVAAILFIFSLAGLSKHETSQQGNYFGIAGMAIALIATILGPDAGNVGWIILAMVIGGAI

GIRLAKKVEMTEMPELVAILHSFVGLAAVLVGFNSYLQHETGMEQILVNIHLTEVFLGIFIGAVTFTGSV

VAFGKLRGKISSRPLMLPNRHKLNLAALVVSFILMVIFVRSDSTGTQVLCLLVMTAIALAFGWHLVASIG

GADMPVVVSMLNSYSGWAAAAAGFMLSNDLLIVTGALVGSSGAILSYIMCKAMNRSFISVIAGGFGTDGS

SSGGDEEVGEHREISAEETAEMLKNSHSVIITPGYGMAVAQAQYPVAEITEKLRARGIKVRFGIHPVAGR

LPGHMNVLLAEAKVPYDIVLEMDEINDDFSDTDTVLVIGANDTVNPAAQDDPKSPIAGMPVLEVWKAQNV

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>lcl|NZ\_FO834906.1\_prot\_WP\_002903388.1\_2627 [locus\_tag=BN49\_RS14675] [protein=hypothetical protein] [protein\_id=WP\_002903388.1] [location=2709492..2709680] [gbkey=CDS]

MDTELTPTQMAIEFLRRDPTVMTPAQYLKKLKLLELEFADLMALSSLELKEEIDLAWRLGIH

>lcl|NZ\_FO834906.1\_prot\_WP\_002903391.1\_2628 [gene=uspE] [locus\_tag=BN49\_RS14680] [protein=universal stress protein UspE] [protein\_id=WP\_002903391.1] [location=complement(2709790..2710740)] [gbkey=CDS]

MAKYQSMLVVIDPNQDDQPALRRAVYLHQRIGGRIKAFLPIYDFSYEMTTLLSPDERTAMRQGVIAQRTA

WIREQAKFYLESGVPIDVKVVWHNRPFEAIIQEVVSEKHDLLLKMAHQHDKLEAVIFTPTDWHLLRKCPC

PVWMVKDQPWPEGGKALVAVNLASEENYHNTLNEKLVRETLSLAEEVNHTEVHLIGAYPVTPINIAIELP

DFDPSVYNDAIRGQHLLAMKALRQKFGIDEKFTHVEKGLPEEVIPDLAEHLQAGIVVLGTVGRTGLSAAF

LGNTAEQVVDHLRCDLLVLKPEAYQTPVELDDDDDD

>lcl|NZ\_FO834906.1\_prot\_WP\_002903394.1\_2629 [gene=fnr] [locus\_tag=BN49\_RS14685] [protein=fumarate/nitrate reduction transcriptional regulator Fnr] [protein\_id=WP\_002903394.1] [location=complement(2710879..2711631)] [gbkey=CDS]

MIPEKRIIRRIQSGGCAIHCQDCSISQLCIPFTLNEHELDQLDNIIERKKPIQKGQTLFKAGDELKSLYA

IRSGTIKSYTITEQGDEQITGFHLAGDLVGFDAIGTGLHPSFAQALETSMVCEIPFETLDDLSGKMPNLR

QQMMRLMSGEIKGDQDMILLLSKKNAEERLAAFIYNLSRRFAQRGFSPREFRLTMTRGDIGNYLGLTVET

ISRLLGRFQKSGMLAVKGKYITIENSDLLAQLAGQARNVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002903396.1\_2630 [gene=ogt] [locus\_tag=BN49\_RS14690] [protein=methylated-DNA--[protein]-cysteine S-methyltransferase] [protein\_id=WP\_002903396.1] [location=complement(2711826..2712341)] [gbkey=CDS]

MLTLLQDKMDTPLGPLWVLCDEQFNLRAVEWDEHRDRMETLLEVHYRREGYQRVDCRNPGGLSSKLSDYF

AGDLAIIETLPTATAGTPFQRQVWQALREIPCGQVMHYGQLAEALGRPGAARAVGAANGANPVSIVVPCH

RVIGRNGTMTGYAGGVQRKEWLLRHEGYLLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002903398.1\_2631 [locus\_tag=BN49\_RS14695] [protein=hypothetical protein] [protein\_id=WP\_002903398.1] [location=2712634..2712792] [gbkey=CDS]

MQYILTGVIVLIFSGLVIHGMSLLLERGYRALFGIFAGAGEATRKFKVKISR

>lcl|NZ\_FO834906.1\_prot\_2632 [locus\_tag=BN49\_RS14700] [protein=AbgT family transporter] [pseudo=true] [partial=5'] [location=complement(2712825..>2713327)] [gbkey=CDS]

IEPHKDISI\*LCYLYKPCSTGAIWASLWPSG\*RTCWRVQA\*TVFRRLSALRCCRLFCVCLSPAARPSGRF

WRRSSCQCLCCWAFTRRLRRSCFVSLIHRCCRWRRCHRLCRCFSAFYSATGRMPASAPTTRWCSLTR\*FF

SPSGCCCWWAGIWWDCRSALASIRGCL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530209.1\_2633 [locus\_tag=BN49\_RS14705] [protein=pyocin activator PrtN family protein] [protein\_id=WP\_016530209.1] [location=complement(2713404..2713664)] [gbkey=CDS]

MNTMFLLMAEYGSATVPLSQVCEKYFGLKPATAEKRAAMGEIPIPTFRAAESQKAPRMIHIQDLANHIDA

QLKKGRDLLEQMKSGS

>lcl|NZ\_FO834906.1\_prot\_WP\_004213359.1\_2634 [locus\_tag=BN49\_RS14710] [protein=hypothetical protein] [protein\_id=WP\_004213359.1] [location=complement(2713784..2713969)] [gbkey=CDS]

MMHLLIISAAVIFGFLTFIAVMSFMTWENYFRLFGRNRIIRVIIVLLIFSAANYFIFGGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530208.1\_2635 [locus\_tag=BN49\_RS14715] [protein=hypothetical protein] [protein\_id=WP\_016530208.1] [location=complement(2713966..2714628)] [gbkey=CDS]

MTERGMIFNAEMVRAILDGRKTQTRRPVKFPVHDKNLGCELAGNELAGELSAGNYLNSAFGKPGDRIWVR

ETFQGPLFDYDLMDSYSKDPTPFEKPEFCVYKADGVPAPEFYDADDELHCCWRPSIHMPRWASRILLEIT

DVRVERLNAISEEDATAEGVPPAGSLLPDYPGTFLTPKGDFATAKVAFQRLWESIYGEESWKANGWVWVI

SFKRVEGGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004213355.1\_2636 [locus\_tag=BN49\_RS14720] [protein=hypothetical protein] [protein\_id=WP\_004213355.1] [location=complement(2714621..2714965)] [gbkey=CDS]

MSKSLNARCIRRWEVEFKPFCDSKRNPYWRKRDLRGYIREAALTTAYSMVESMAERNAKVDYDGEPNGWT

PEFSAWYRERHEQYLKEARDYLDEDATNDEIDEEIENELEAWND

>lcl|NZ\_FO834906.1\_prot\_WP\_004213351.1\_2637 [locus\_tag=BN49\_RS14725] [protein=ParB/RepB/Spo0J family partition protein] [protein\_id=WP\_004213351.1] [location=complement(2715093..2715878)] [gbkey=CDS]

MAKDSKVVYGASGKTNVLTFEPESLHLVTDKTHPLYDERVHLPIDEGMVLNIAELGVLEPIIVWKDPETG

LTCVVVGRQRVKHTLEANKLRLKEGKDPLLVPGVVKRGSANQMAKYMVSENEIRRPDTPLGRAKKMSDAL

DRGLDEDDIAVLFGCSVQTVRATLSLLDATQAVREAVEAGTVTVTQARQLASLKPEEQREKVSEIEAATA

GTTGHEKARRQRQILGEAKPRLKTRKEIIKALESAEGEYASALRWVLGEAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004213349.1\_2638 [locus\_tag=BN49\_RS14730] [protein=hypothetical protein] [protein\_id=WP\_004213349.1] [location=complement(2715878..2716177)] [gbkey=CDS]

MAKTANQLIKQAYEIAKTMPPEQAAIIKELATVLDVSNVALRQTRTERDALLAEVKSWAKECDRLTERHT

KKRTNLHVLEAMRDLKAICPTSFRNVEAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530207.1\_2639 [locus\_tag=BN49\_RS14740] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016530207.1] [location=complement(2716945..2717604)] [gbkey=CDS]

MKTEMKDRIRSRRVQLDITQQTLAKRLGVSRVSVTKWESGTTKPDGENLHQLAVALQTTPEWILYGRGEE

TPDDTKVIPFLKPPTAVPIISAVQAGMWTDTYACSRLSDVISWTQTTANVSNEAFGLVVRGESMTNPHGL

PSIPEGSIVIVEPHYGQLDDLYGKIVVAILDGSAEATVKKLVWDSPFAYLMPLNPAFKPIPIDGNCRIVG

KVVQITQNI

>lcl|NZ\_FO834906.1\_prot\_WP\_016530206.1\_2640 [locus\_tag=BN49\_RS14745] [protein=Cro/CI family transcriptional regulator] [protein\_id=WP\_016530206.1] [location=2717697..2717894] [gbkey=CDS]

MRKSEVIEHFGGVSKTASVLGISHPAVCRWGEVIPQKQAFVIERITKGKLKYDASLYQKATDSAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004213338.1\_2641 [locus\_tag=BN49\_RS14750] [protein=hypothetical protein] [protein\_id=WP\_004213338.1] [location=2717920..2718381] [gbkey=CDS]

MVEPNLKEAVKAMCKAYPGGREAMAGALGMTVTQFNNNLYEKNGCRFFEVSELEAMEDISNTSLLADYFA

RRRGALLVDVPHLEELDRVDLFSRAMRTSAARGQVDQIIEQALEDGVIERHEAEEIMVHHRRHLAAREEE

IAAIITLFSRKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004184738.1\_2642 [locus\_tag=BN49\_RS29100] [protein=DUF4222 domain-containing protein] [protein\_id=WP\_004184738.1] [location=2718619..2718798] [gbkey=CDS]

MRELNRWFRDHYGVPVRVIRWEPQTQRVIYLRKGYEHECFSPLEQFRRKFREIKDDHEH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530205.1\_2643 [locus\_tag=BN49\_RS14760] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016530205.1] [location=2718788..2719726] [gbkey=CDS]

MSTKLTGYVWDACASSGMKLSSVAIMARLADFSNDEGVCWPSIATISRQIGAGESTVRTAIAALEKEGWL

TRTQRRNGNRNASNVYQLNVSKLQKAAFSHLSVSDPSKSDASKTDPSKFEASKSTKKTSFDPSESGGDPS

VRSTTDPSDINPSCPDASQPDEQGSADEFLSRHPDAVVYSAAKRQWGSQDDLTCAEFIWGKIISMYELAA

ESDGEVVRPKEPNWTAWANEVRLMVMQDGRTHKQICSLFKRANKDSFWCKNVLSPSKLREKWDELSLKLS

VPLNSSRQEASISRASFEGVDYSLPENSGFRS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530204.1\_2644 [locus\_tag=BN49\_RS14765] [protein=Dam family site-specific DNA-(adenine-N6)-methyltransferase] [protein\_id=WP\_016530204.1] [location=2719723..2720532] [gbkey=CDS]

MSKPFLKWAGGKYTQLADLFVHIPAGKRLIEPFVGGGSIFLNSEKHADYLLADVNPDLINLYQMLAVVPD

EVELKARWMFEHMRSPDGYELIRSEFNAQTLDATERAAAFLYLNRHCFNGLMRYNQANKFNVGWGGYKAP

YYPMDEMKAFAAMAHNCVFMTADYRRTISLAGKGDVVYCDPPYEPMPGTTGFTAYAAGGFSWENQVDLAK

QCVSAFHRGARVVISNSSAPKVLDLYREHGFNLQFIKARRSISCKSSTREVAKDVVAIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004184734.1\_2645 [locus\_tag=BN49\_RS14770] [protein=RusA family crossover junction endodeoxyribonuclease] [protein\_id=WP\_004184734.1] [location=2720542..2720919] [gbkey=CDS]

MKLTLPFPPSVNSYWRAPSKGPLKGRHLVSETGRKFQQAARAAIIEQLRAVPRPSSDLAEVHIVLYPPDQ

RRRDIDNYNKALFDALTLTGVWEDDSQVKRMLVEWGNIVKKGKVEITIRRFRAVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004213334.1\_2646 [locus\_tag=BN49\_RS14775] [protein=DUF968 domain-containing protein] [protein\_id=WP\_004213334.1] [location=2720932..2721912] [gbkey=CDS]

MRVLLTPEIAPRMGVVLLRPGADLMPMFRRGRVLIEPAPEKYSDYATGAIPPATQPLSEDPVLKPVFENK

DVILRAGGISSLEAELERRFECQYPHGSWHSENFTLFRHEPGSIRLCWACDNLLRDQYTETLAGIARGNL

VSWLITVIRSQLGFNEDHQLTIPELCWWLVINNLAHVIPESLARKALRLPEIKHQPVMKESDIVPEPAAS

EVVQKKILGLRVDPETPESFMLRPKRRRWVNESWTRWVKSQSCVCCNKQADDPHHLIGHGQGGMGTKAHD

LFVLPLCRAHHDELHADTVAFEEKHGSQLELLFRFLDRSLAIGVLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004213332.1\_2647 [locus\_tag=BN49\_RS14780] [protein=DUF1133 family protein] [protein\_id=WP\_004213332.1] [location=2721926..2722504] [gbkey=CDS]

MINPSEVGKAGEMVRLKTLEAIWIQGKLRMWGRWSYIGGGSGGNMFNQLLASGKITKTAINDALRRMKKS

GITKPELEAFFKEILSGKNKSGLAFCTDEEGLIIDSVLSAQLVRSGNKALYQLIRDRYVCRMSKKAMAKE

LNEKHPEWCLRTCESRIDVWLNLAESMLYAPMCDALGTNGDRFYLNSCAKSA

>lcl|NZ\_FO834906.1\_prot\_WP\_129015083.1\_2648 [locus\_tag=BN49\_RS30450] [protein=hypothetical protein] [protein\_id=WP\_129015083.1] [location=2722616..2723188] [gbkey=CDS]

MWLGIPFLYVKERLADTVTIDKIPSITVDSSFSWETIIAAFISGLVPALISLYVIKNNNESIRYQQKQED

KRHFSAHVRVVISEYAYQLSKVKEIHAECLRFSSMFSSVKTSELADKMSDALLELERYKASLLISIPEDD

AGRKFKEEINEISESLSEQIKYGLKTTKMEKVWNDDYDAFISNSNRYLNK

>lcl|NZ\_FO834906.1\_prot\_WP\_004213330.1\_2649 [locus\_tag=BN49\_RS14785] [protein=phage holin family protein] [protein\_id=WP\_004213330.1] [location=2723281..2723676] [gbkey=CDS]

MSDPLTGTGLIFGGGLIGSVVYGVITHTDFGVVFGAFGGAVFYVATTANLTRGRQIAYFMTSFIVGVLAA

GLLGSKFTTWTGYTDRPLDALGAVVASAVTIKVLTFINSQDLSSLFGLLSRLRGGGSNGNK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530201.1\_2650 [locus\_tag=BN49\_RS14790] [protein=phage holin family protein] [protein\_id=WP\_016530201.1] [location=2723663..2723944] [gbkey=CDS]

MVINDPAALANAVICAVIVCALMFYQRRGARHRPGISILAYLLVLIYASIPFQFIFGLYVQSHWLVVMAN

VMICAAVLCARGNVARLVDTLRH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530200.1\_2651 [locus\_tag=BN49\_RS14795] [protein=glycoside hydrolase family 19 protein] [protein\_id=WP\_016530200.1] [location=2723944..2724573] [gbkey=CDS]

MNKSQFQKAAGISAGLAARWFPHIDAAMKEFGITAPLDQAMFIAQMGHESGGYKTLVESLNYAADRLVPT

FGKHRITAQQAAALGRTATQPANQRAIANLVYGGEWGKKNLGNQVAGDGWKYRGRGLKQVTGLSNYRSCG

QALKLDLVTQPELLERDDYAARSATWFYVSHGCLLHSGDVERVTLLINGGRNGLDKRRALFNQAKSVLV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530199.1\_2652 [locus\_tag=BN49\_RS14800] [protein=hypothetical protein] [protein\_id=WP\_016530199.1] [location=2724581..2724856] [gbkey=CDS]

MGIEMIIGLATALLAIVAGAFGLGHSRGSSKAEAKAEQQRTEENAAANVAAAERKEEATREASNVQQTVS

HMPDDDVDRELREKFTRPGSR

>lcl|NZ\_FO834906.1\_prot\_WP\_022615515.1\_2653 [locus\_tag=BN49\_RS31450] [protein=hypothetical protein] [protein\_id=WP\_022615515.1] [location=2724807..2724989] [gbkey=CDS]

MLIGSCAKSLPAPVVVDTACSWVRIIYLTDHDIDVLDKQTKRDILAHNRTVKRNCNQLKM

>lcl|NZ\_FO834906.1\_prot\_WP\_227504848.1\_2654 [locus\_tag=BN49\_RS14810] [protein=DUF4747 family protein] [protein\_id=WP\_227504848.1] [location=2725157..2726014] [gbkey=CDS]

MKLFQHLGDKLRKVLSSEGDLRNIAVPLRNDFFFAPYEINAREDMVYGRFLKFDKVDVVRKTISRVQTYA

AGFGESSKIYEYRFVFDPVLHILAIEDSPSLPSASVLYKVLNEVFKDARRKLYPSFRMSVDELTSSASLD

NVIKESKGYYSFKTEITFSNSNDFIEGLEELLEGVEAEMKDKGIDKLEHKESSDKDSIMTDVSTIALVYA

GLSCKFGNTEISYKDKSNKKKVFKMADYPVRKRVSESMKKRASILDYYYDVKNTINAANNESRTGSGLLK

KIRKG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530196.1\_2655 [locus\_tag=BN49\_RS14815] [protein=hypothetical protein] [protein\_id=WP\_016530196.1] [location=2726019..2726645] [gbkey=CDS]

MKVGGWDINHENILKIIKSIPYVGAIFIIANFYANSGVLSDRKRIANFKNWVRRVLSGVLFTFVLSLLIV

TFFRDGLYNPNSNTAGLDATLVALSIFPSILGFGIGVFVVVFALPNQFIEKINLIKHNGKNKTFGASLMV

VDMAYPLMVYAVVLMGEFFLKLFQVGFITHVLSIFLLLYGMLMTFDLISMIFMTAYALLATQASRNPK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530194.1\_2656 [locus\_tag=BN49\_RS29110] [protein=HNH endonuclease] [protein\_id=WP\_016530194.1] [location=2727279..2727629] [gbkey=CDS]

MPALIPRVCRKRGCAGTTTDRSGYCEKHRNEGWQQHQQGKSRHERGYGSQWDIKRARILKRDNHLCQNCL

RTGRAVAAKTVDHIKAKAHGGTDDDSNLESLCWPCHRTKTGRERFK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530193.1\_2657 [locus\_tag=BN49\_RS14830] [protein=phage terminase small subunit P27 family] [protein\_id=WP\_016530193.1] [location=2727787..2728284] [gbkey=CDS]

MPGPPKTPTHLALVKGNPSKRPINKNEPKPPSGVPPIPKHFDKQGKYWFKRIGEELDAVGVLTTLDAKAL

ELLIEAYVEYRHHCDTLDREGYTYAVYSEDDSDEGGEREIRMIKPHPAAVMKADAWKRIRAMLSEFGMTP

ASRSKVGAKVPAEADPLEEFLKKRK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530192.1\_2658 [locus\_tag=BN49\_RS14835] [protein=terminase large subunit] [protein\_id=WP\_016530192.1] [location=2728288..2730039] [gbkey=CDS]

MATVADGFRYAERVVSGDIVAGELVRLACQRFFHDLEHGPARGVYFDEGRAQHVLDFYNFVPHVKGHLTG

KPIELMDWHVFILINLFGFVVPLIDEITCEGVLDDDGEPMFVRRFRTAYDEVARKNAKSTLSSGIGLYMA

GADGEGGAEVYSAATTRDQARIVFDDAKRMIKLAPKTLGRLFGSNKLNIHQERTGSKFEPVASDANNLDG

LNIHCGIVDELHAHKTRDVWEVLETATGARLQSLIFAITTAGFNKEGICYEQRDYAIKLLKNFDNPDPLS

PKDDSYFALIYTLDEGDDPFDEANWPKANPGLGVCKRWDDMRRLAKKAKEQVAARVGFFTKHLNIWVQGE

KAWMDMSRWEKCRDTWDDSTTASWSMWLGVDLSNKIDISAAVKVWLAPNGDVYARSRFWIPEGRLEACTK

QQAELYRKWNQAGYLEFTDGDVIDHAVIKEETIEWARGESLNEFAYDPWSATQFALSVAAEGIPIVEVPQ

TVKNLSEAMKEVEAKIYAGRFHHDGNPVMTWMMSNVTVKPDKNENIFPNKATPENKIDGPVAMFITMSRL

LVNGGGEVDFLSTIDPDEDLLLL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530190.1\_2659 [locus\_tag=BN49\_RS14845] [protein=phage portal protein] [protein\_id=WP\_016530190.1] [location=2730187..2731413] [gbkey=CDS]

MLLDALFRSEPLENPATPITSESAETDNVFAQDVFVSPQTAMKLAAVYACIYVISSNIAQMPLHVMRKTN

NKVEAARDHPVFYLVHDEPNMWQTSYKWRELKQRHILGWGNGYTWVKRSRRGEVSGLECCMPWETTLLNT

GGRYTYGVYNEEGAFAVNPDDMVHIRALGNNQKMGLSPIMQHAETIGMGMSGQAYTSSFFNGNARPAGII

SVKSQLNEESWGRLKSMWQKATAALRSQENKTMLLPAELDYKALTVSPVDAQIIDMSKLNRSMIAGIFNV

PAHMINDLEKATFSNITQQAIQFVRYTIMPWVTNWEQELNRRLFTRAELAAGYYVRFNLTGLLRGTPQER

AQFYHFAITDGWMSRNEARAFEDMNPVDGLDEMLVSVNAANPADDFKAPKTDEEKPNE

>lcl|NZ\_FO834906.1\_prot\_WP\_000999827.1\_2660 [locus\_tag=BN49\_RS14850] [protein=HK97 family phage prohead protease] [protein\_id=WP\_000999827.1] [location=2731406..2732005] [gbkey=CDS]

MNDRETRCYSGEVRAEQRTDEPTRILGYGSVFNSRSEPLWGFREIIKPGAFDDVLNDDVRGLFNHDPNFI

LGRSAAGTLSLSVDERGLRYDITAPDTQTIRDLVLAPMMRGDINQSSFAFRVSHDGENWYQDDEGIVIRE

ISKFSRLFDVSPVTYPAYQEADSGVRSMKAWQEARDSGALKNAINQRMARERLLTLLNA

>lcl|NZ\_FO834906.1\_prot\_WP\_004104235.1\_2661 [locus\_tag=BN49\_RS14855] [protein=phage major capsid protein] [protein\_id=WP\_004104235.1] [location=2732015..2733253] [gbkey=CDS]

MKLHEMKQKRNIIAKDMRALHDKIGDTPWTDEQRTQWNAAKSELDALDERIAREEELRRQDQDYIHENEP

EQRQQQNRDPANPEAQANERRAAAFNAFLRRGLGEMSAEERQALKELRAQGTTPDEKGGYTVPTQFRNKI

VEALKDYGGIASVAQILNTANGQDIDWATSDGTTEEGELLGENTETSEEDVSFGGATLGAKKLSSKIIRV

SNELLQDSGVDIEAFLAARIATRIGRGEAKYLVLGTGTGTPLQPKGLAASVTGTKNTAAATTFTWKELNA

LKHSVDPAYRNGPKVRWAFNDATLQLVEEMEDGQGRPLWLPNIIGGAPATVLQVPYVVDQAIPDIAAGAK

FAYFGDFNRFIVRRVTYMTLKRLVERYAEYDQTGFLAFHRFDCVLEDTGAIKALVGKPASGG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530189.1\_2662 [locus\_tag=BN49\_RS14860] [protein=head-tail connector protein] [protein\_id=WP\_016530189.1] [location=2733331..2733648] [gbkey=CDS]

MSTTIEMLRAQCRIDIDDTTEDEVLTLYYGAARRKAESFINRHLYEEEVPETDPDGLVIADDILLALMLL

VGHWYENREESSDAAKTSIPFGFTSLIEPYRYIPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530188.1\_2663 [locus\_tag=BN49\_RS14865] [protein=phage head closure protein] [protein\_id=WP\_016530188.1] [location=2733657..2733995] [gbkey=CDS]

MQAGRLRHRVTIQNFTISKTPSGQPVESWADGKTIWAEVKGISGRELLAAGVERADATIRVWVRFRTDIS

ASSRLKVRTGPFKGAVLNVTGPPVPDIKGTRLEILCKQGTEK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530187.1\_2664 [locus\_tag=BN49\_RS14870] [protein=HK97 gp10 family phage protein] [protein\_id=WP\_016530187.1] [location=2733992..2734441] [gbkey=CDS]

MIDVNLDFSGLQDIAHDLQTLSKAENNKVLRESTRAGAELLREEVIDRAPEKSGKLKKNVVVVTQKSRRS

GEISSGVHIRGVNPRTGNSDNTMKASNKRNAFYWRFVELGTSTAPAHPFVRPAFDTRMEEATQVAMQRMN

QAIDEVLSK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530186.1\_2665 [locus\_tag=BN49\_RS14875] [protein=DUF3168 domain-containing protein] [protein\_id=WP\_016530186.1] [location=2734438..2734785] [gbkey=CDS]

MTEDDLYDLLSTLADGRVYPYVVPLGSDGLPAVSTPYVIFSIPTDVAGDVFCGQAESTLRIQVDVWAETN

DEARALRLDALARLQVLSPVEVTKIPGYDTTTHLHRATLEITVIA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530185.1\_2666 [locus\_tag=BN49\_RS14880] [protein=immunoglobulin domain-containing protein] [protein\_id=WP\_016530185.1] [location=2734842..2735546] [gbkey=CDS]

MSALFERAQKTVVMITSVPVTEAELDTATWLNLSCTIKQASFTAGQKNDIDVTTLCSDETENINGLPAPS

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VYSCVVTDADGTVITSSDCTVTIN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530184.1\_2667 [locus\_tag=BN49\_RS14885] [protein=phage tail assembly chaperone] [protein\_id=WP\_016530184.1] [location=2735577..2735981] [gbkey=CDS]

MSKPCLKALALAPMAGFRKKEVSVPEWDNAKVIIREPSAEAWIRWQGIASPEPPKLPEGQEPQEAPELTP

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530183.1\_2668 [locus\_tag=BN49\_RS14890] [protein=DUF4035 domain-containing protein] [protein\_id=WP\_016530183.1] [location=2735984..2736289] [gbkey=CDS]

MPGMQFLMALALRMGRTLGELRQTMTVGEFRMWAEYDRISPIGDIRGDILNAQLVSAVYGAQGGKVTIED

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530182.1\_2669 [locus\_tag=BN49\_RS14895] [protein=hypothetical protein] [protein\_id=WP\_016530182.1] [location=2736363..2736596] [gbkey=CDS]

MTTTGWILLFVFARLIDLVIWYFLNRGSVRANDQIAMLKEISEKQSAQIDLLIALAHKKEEPEKDYLEEA

RKKAGLI

>lcl|NZ\_FO834906.1\_prot\_WP\_016530181.1\_2670 [locus\_tag=BN49\_RS14900] [protein=phage tail tape measure protein] [protein\_id=WP\_016530181.1] [location=2736657..2740046] [gbkey=CDS]

MATLRELIIKVSANSQSFQTEIARASRMGADYYKTMQNGGRQAAASVRETRRSVAELTDQMESAKATALG

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REYGYSSSQVLDITEAISTGLKLSGANAQESSSVITQFSQALAQGVLRGEEFNAVNESGDRVIRALAAGM

GVARKDLKSMADQGQLTIDKVVPALISQLGKLRNEYGELPQTVSSSATKVENAFMQWVGGANEASGATNT

LTGLLDGVANNIDQIATAAGALVAVGAARYLGNMALGASSATAGIINAAKSEVALAEAQVRGMQVSTARA

RAAVYRAQQALAAARGTDAQAAAEKRLSLAQESLNRNIQARVSAQTALNSVTAVGSRLMGGALSLVGGIP

GLVLLGAGAWYTMYQNQEQARLSAQEYANTIDAVREKTKSMSLPEVSDNETKTRQALEEQNRLVDAQASK

VKSLKEEIAGYQYVLSNPGPTTSGGFMINHLTSVETVTRSLEEATSALAVEQERLTQMQAKSESIQSVLE

GIENRRIALIRQQAAEQNSAYQSLLMMNGEHTEFNRLLGLGNNLLMARQGLVNAPLRLPQVDLTTQQTAA

LEKSRRDLALSKLKGEDKERARLGYAADDLGLTNDPQFQTGRQELINNGLNEWRNNQENKPKPKGRHGKT

EAEKTEDTYTRLIKQQREQIALSSQNTELAKMKYQVTQGELSSLEKSKKETLLHNAALIDQKNIAEQLKT

FREGLADSNAAARERGNIDFLGAGQGDKARDRMTEMADIRADFLRQQRDLQRDFSRGQISEDLYKKQTEA

LKTALAERLDIQEEYYKKTDEQQSDWRAGISDSLMNYADQASDLSSMAATATSEILDATTNSISNNLTNV

LTGAASFKYGMSNIFSSLGETVIKTLIQMATQALITKAIMASFGGGAGGLFGSLFGGASGAASSGTAIQS

AGANFSFNALGGVYDSPSLSAYSNGVYSTPQYFAFAKGAGVFGEAGPEAIMPLTRGADGSLGVKAVGRES

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SNLQPKKPR

>lcl|NZ\_FO834906.1\_prot\_WP\_004177132.1\_2671 [locus\_tag=BN49\_RS14905] [protein=hypothetical protein] [protein\_id=WP\_004177132.1] [location=2740067..2740540] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004864228.1\_2672 [locus\_tag=BN49\_RS14910] [protein=DUF1833 family protein] [protein\_id=WP\_004864228.1] [location=2740527..2741003] [gbkey=CDS]

MTILERLYASSGSEVIHDTLQISAGDDNYWLTSGWDDVSVTLENGQPVTFDASAIDIALPARNADGTQDL

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TAWPRKRYNLAEHPGLRY

>lcl|NZ\_FO834906.1\_prot\_WP\_022615519.1\_2673 [locus\_tag=BN49\_RS14915] [protein=nitrite transporter] [protein\_id=WP\_022615519.1] [location=2741016..2741396] [gbkey=CDS]

MFNPDKYRSVKWQKGGRAYPLLDCFGIVNEIRSDLGLPEWPDFAGVTKDGGGLDREARKLMLSLKRCEPC

EGAGVACYSGSTVSHVGIVVMLDNQLQVAECNPGSGVTFLPLSRFIRRFNRVEFWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530179.1\_2674 [locus\_tag=BN49\_RS14920] [protein=host specificity factor TipJ family phage tail protein] [protein\_id=WP\_016530179.1] [location=2741393..2744470] [gbkey=CDS]

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IYPIPYGTGLEIAAWVSVAVSIASTAYALFFAPKPELGGFSSSNASSLDLNPAKANTAKLGDPVREAFGR

NRIYPDYLVQPVTRFDPADPTRMTVEMFVCLGYGRFSYTGGDFRVGETPALTLGEGFSYKSYGPGDNVAG

DRRSEIWFNSTEVGGTSSGSGLDMAQTAPEASDIVADAMTVSGASVSFSGLDVDDDNDEDEDENKLPPGW

IAGAIVTLKAPVNYQVSIEGGFNVLTGDVVSEIAPFSGMPVTLTFNGTDYDLQISTYIRHQDAVPGTGGA

TAVLRASASPSTYDFTTTSQTFALTWQGITYTISLVANYGTMSGLLTAINGGLNGSGLIAQDDGGVIRIV

EISSPWRGGSLTSSFLPASVFGDSPVFTAGAASSGGSPAVTASVTLAYDSGTAFSGLPEGTQRISLAHRG

NEYQIASTDGPSATVQRVVNGVVDSTWSGFMTRTVVDFAASGINDNETWLGPFLACPQNEVVDAFEVNFA

FPNGICGFQNNGNKRVRHVEYEIQYRVYGSGSGWTSKPGVYALKNINGLGFTERFDLSSPGLVEVRCRRR

NEQGSNNARDSMFWQALRGRLLSRPTSYAGISTIGITVETGGQLAAQSDKRVSVVATRNYDGGGDRTISG

AFLHLARSLGYRDDQIDIAALSTLEETYWTPRGEYFDHQASSDSTSAKDIFDKIAEAGMGYFLLSDGLLS

VGREGVKSWTGIITPQDTVEEMQTSFRVPSEDDFDGVDVKYINPVTWAEETVQCRTPENPFPRKTEAYTI

DVAMTADRAWRIGMRRLMKYLHQRRTYTATTSMLGWCHDFGDHIILSDDIPTGKTQSCLIDAMIYDFQEI

TLHVTEPLDWSYANPRCWIQFQDGRPSSRMLTPQRVDDFTLTVPYNDDLHPGDWIMDDPDIDLPKLLFCD

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>lcl|NZ\_FO834906.1\_prot\_WP\_039108567.1\_2675 [locus\_tag=BN49\_RS14925] [protein=hypothetical protein] [protein\_id=WP\_039108567.1] [location=2744543..2746696] [gbkey=CDS]

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AAQADIANIPESSSTYVRSPDSSALADEYMNVAGTLTATGRKMPSQAAIQAVLDYISSLIATDDADSPLL

TLNDEAGFRLAAFGLNAIQSNAMTAEYDEFIDGFVFRDSVGFVIQQIGTPLLSSVDSVQPVVEQQRLVTE

AFSAESDADISGFVFRDSVGFVLMNLNGEQSDQNNDGVDDISRRNAANLAAAAAARDEINTRIARPVYDY

NILITDGQSLSNGTEGWAALSKDIRATLNINMLGDSVRPKNENGSTFTPLNGAEIRSARAVVQDLIAPPD

GGNLMTDEAVAALPRGANNFGETVDIGAMWMWREMQLQFRGLATDERKIVAVNCGVGGQIIERLSKGHSW

GFYNRIISAVTQIKAIADAEGKTCGVVGFLYLGNEYNYDSTKGGATDRAEYRALLRKLIDDVITDTTAIT

GQTELPLTVLYQTSGSWTRDSTNMSIGEAQLDICAADANVMMASPAYAVTDKGGHLDANGYRWLGMQFGK

VLHRAIDRRQNWRPLQPLSVTLSGTFLRADFLVWSPPLQFRSCYVGSSPTTYAAKGFRVTDDAGDVPVTR

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>lcl|NZ\_FO834906.1\_prot\_WP\_022615521.1\_2676 [locus\_tag=BN49\_RS14930] [protein=hypothetical protein] [protein\_id=WP\_022615521.1] [location=2746709..2747443] [gbkey=CDS]

MGSRIIVPGYFGDKGLGFDPLVRRGLKYLNFYGEADKTGRNLAPDGVAATVLGSPVVQENGVQYTPAGTL

LDTGILQPLDFTFFTIFNCPTLSQILLLSNFNGPRQSGSGTTQGVVLRTQPGSTSMTLNFSVNTLNGSVS

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043215.1\_2677 [locus\_tag=BN49\_RS14935] [protein=hypothetical protein] [protein\_id=WP\_046043215.1] [location=complement(2747499..2748143)] [gbkey=CDS]

MEVFKYFKEKSFKDDYLNGKIRLGTLNYYRGIENEKQGDVLEGISKYKVPYQEFDKTAWDEVIKVQPQFA

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VDLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004214894.1\_2678 [locus\_tag=BN49\_RS14940] [protein=hypothetical protein] [protein\_id=WP\_004214894.1] [location=2748311..2748610] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_2679 [locus\_tag=BN49\_RS14945] [protein=recombinase family protein] [pseudo=true] [location=2748580..2749150] [gbkey=CDS]

MSSDGEDGILILEEFVECELVFEDMVSGKNARRPGLKRALRRLRPGDVLVVWKLDRLGRSVRDLITLVSE

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>lcl|NZ\_FO834906.1\_prot\_2680 [locus\_tag=BN49\_RS14950] [protein=recombinase family protein] [pseudo=true] [partial=5'] [location=<2749455..2749712] [gbkey=CDS]

GHFFFHVMSALAEMERELIVERTRAGLAAAREQGRGGRRRRVMTEEVVERCRRMLENGATRQQIADVIGV

NVKTLYKYLPSKGTI

>lcl|NZ\_FO834906.1\_prot\_WP\_004214887.1\_2681 [locus\_tag=BN49\_RS14955] [protein=site-specific integrase] [protein\_id=WP\_004214887.1] [location=complement(2749811..2750911)] [gbkey=CDS]

MAFFTIEKRLRSDGTARYRCTVAVKQNGKYVHRENKTFSKNTLAKSWGAKRVAYIEEHGLPEPEKEMKEI

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SYLSVALEAAKPLFGAPANLNELSDAKVWLRNMGITGPSQRRSRRASATEVDRLYEVLKVKAETAYTGAP

LHQIFMFSILTCMRVGEVCRLLWEDVDDIQRSVIVRDRKDPRKKIGNHMLVPLLGDAWRILTMQPRVDDR

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>lcl|NZ\_FO834906.1\_prot\_2682 [locus\_tag=BN49\_RS14960] [protein=AbgT family transporter] [pseudo=true] [partial=3'] [location=complement(<2751067..2752158)] [gbkey=CDS]

MSMSSIPSSSPGGKRYGWVEKIGNKVPHPFLLFIYLIAVLIAATAILSALNVGVQNPTDGSRVVVKNLLS

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SDAALVIMPPLGALMFLAVGRHPVAGLLAAIAGVGCGFTANLLIVTTDVLLSGISTEAAKSIDASLHVSV

IDNWYFMATSVIVLTLVGGLITDKLVEPRLGQWQGSRDEKLQTLTPGERFGLRIAGVATLVFVAVIALMV

VPENGILRDPVQHTVMPSPFIKGIVPLIIFFFFVVSLAYGIATGKIRRQADLPQLMIEPMKEMAGFIVMV

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043218.1\_2683 [locus\_tag=BN49\_RS14965] [protein=M20 family metallopeptidase] [protein\_id=WP\_046043218.1] [location=complement(2752278..2753723)] [gbkey=CDS]

MEAIFQFVDEVVEAQRDTYCAIADDIWDHPETRFEEFWSAQRLADALEAEGFQLTRDAGGIPNAFIASVG

EGQPVIALLGEFDALAGLSQQAHSAEPTPLTPGANGHGCGHNLLGTAAFAAAVAAKGWLQQHGDSGTLRF

YGCPGEEGGSGKTFMVREGLFDDVDAALTWHPEVWAGMFSTRTLANIQAAWRFTGTAAHAANSPHLGRSA

LDAVTLMTTGSNFLNEHIIDKARVHYAITDTGGVSPNVVQAQAEVLYLIRAPEMADAEQIFARIEKIAQG

AALMTETQVSCRFEKACSSYLPNRTLEAAMYQAVCHYGTPAWSDEERAFAAAIRATLSANDINNSLNNIA

GTSGEEGKTFARRHRDTLLIDEVAPWAATDNVLAGSTDVGDVSWKAPVAQCFSPCFAVGTPLHSWQLVSQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_004892311.1\_2684 [locus\_tag=BN49\_RS14970] [protein=M20 family metallo-hydrolase] [protein\_id=WP\_004892311.1] [location=complement(2753723..2755033)] [gbkey=CDS]

MPQLDEYLRQLAPSMTQWRRDFHLHAESGWLEFRTASKVADILDGLGYQLALGRDVIDADSRMGLPDEET

LARAFERAREQGAPERWLPAFEGGFAGVVATLDTGRPGPTLAFRVDMDALDLNEQHDDSHRPHRDHFASC

NAGMMHACGHDGHTAIGLGLAHVLKQYAAQLNGVIKLIFQPAEEGTRGARAMVAAGVVDDVDYFTAIHIG

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MQAGTGRNVVPSSALLKVETRGESEAINQYVFERAQHVVAGAAAMYEARYELRMMGAATASAPSPAWVDY

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ETLARVALNFPCQRGV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043221.1\_2685 [locus\_tag=BN49\_RS14975] [protein=LysR family transcriptional regulator] [protein\_id=WP\_046043221.1] [location=2755200..2756108] [gbkey=CDS]

MAFQIKFHQIRAFVEVAREGSIRGASRALAVSQPALTKAIKELEEGLSAQLFVRRSQGVALTDNGESFYQ

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RQGELDFTINTYYPGPYDHEFSFEKLFEKPFAVFARAGHPAAQATSLGELMDHHWTMPTPRGSYFKQLQE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004143055.1\_2686 [gene=smrA] [locus\_tag=BN49\_RS14980] [protein=DNA endonuclease SmrA] [protein\_id=WP\_004143055.1] [location=2756210..2756773] [gbkey=CDS]

MNLDDKSLFLDAMEDVQPLKRNNDVHWHPGRNSRAPQRVDTLQLDNFLTTGYLDIVPLATPLEFKREGLQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151560.1\_2687 [locus\_tag=BN49\_RS14985] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004151560.1] [location=complement(2756770..2757576)] [gbkey=CDS]

MDKHPDDLLTGDGDPFKGDPNFMASLARGLEVIQAFTPQRPLLSISQISQKTGIPRAAVRRCLYTLSKLG

FVYAEDGKNFQLRPRILALGHAWLASTPLARSAQPVLRHLSEMLNESCSIATLDGDDILYIARASSSRIM

TIDLDIGSRLPAWATSMGRVLLSHQPEEKLNDMLARVTMIRYTPQTVDSVAKLRAELKRVHQQGYALNDQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_025368161.1\_2688 [locus\_tag=BN49\_RS14990] [protein=3-oxoacid CoA-transferase subunit A] [protein\_id=WP\_025368161.1] [location=2757746..2758432] [gbkey=CDS]

MIDKSVSTLSEAIAGIHDGATIMIGGFGPAGQPTFLIDALIDQGARDLTIINNNAGNGEVGLAALLKAGR

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530130.1\_2689 [locus\_tag=BN49\_RS14995] [protein=3-oxoacid CoA-transferase subunit B] [protein\_id=WP\_016530130.1] [location=2758443..2759099] [gbkey=CDS]

MQKLTRDEMAQRVARDIPEGAYVNLGIGLPTRIANYLPADKEVFLHSENGLLGMGPKPQPGEEDPELINA

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FQQLAESA

>lcl|NZ\_FO834906.1\_prot\_WP\_025368159.1\_2690 [gene=pcaF] [locus\_tag=BN49\_RS15000] [protein=3-oxoadipyl-CoA thiolase] [protein\_id=WP\_025368159.1] [location=2759110..2760312] [gbkey=CDS]

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MSLLTPMLRSSPLTDWFSDAQRVQGMLDFEAALAQAQAACGMVPPEAVGPIVAACRHEAIDFAALGEAAV

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LAQILGLSLPDTPWHSQRDRLLEAGAWFAGVCGTLGKFANDFSLLMQTEVAEVGEPVAEGRGGSSTMPHK

RNPVACAAILTAAQRTPGLMATLYASQLQQHERALGGWQAEWETLPELITLVGGALAQSEALVRDMQVFP

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>lcl|NZ\_FO834906.1\_prot\_2694 [locus\_tag=BN49\_RS15020] [protein=mechanosensitive ion channel family protein] [pseudo=true] [location=complement(2763417..2765033)] [gbkey=CDS]

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DQVAAGRIQVPGIHPETVSATRRLISVVIWLFALSAAYPFLPGANSLAFKGISVFFGLMLTLGSTGVMTH

AMSGLVLIYSRALRKGDWIRLADNEGQVSEIGVLATKILTRENYIVTVPNAVVVSGKIINLSAESADGGV

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QNLGLGAQFGGKYFAHDIRVIRLPRHGASCPIGMGVSCSADRNIKAKINRDGIWIEKLESNPGKYIPEHL

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NKAAWNTFVWFATLVALADGLSSTGFIAWLGKEGGALMSGISPGMATIVLLLAFYLLHYLFASTTAHTTA

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SGEEVEGMIAKFGDGVRRAILAGFDGVEIHGANTYLIQQFYSPNSNQRDDEWGGSRDNRARFPLAVLDIT

HKMARQYADDAFIIGYRFSPEEMEVPGIRFDDTMYLLEKLAARGVDYLHFSVGATLRPSIVDTSDPTPLI

EKYCAMRSDTLAQVPVMGVGGVVNAADAEQGLDHGYDLIAVGRACIAYPDWASRIAAGEELELFIDSTQR

EALHIPEPLWRFSLVEAMIRDMSMGDAKFKPGTFVETVHDDANELVINVSLENDHIADIELAASPVQTVE

FTTSFEEIRERILTANTPHVDAISGATSQSEAVKKAVAKAMLKSSKALAAEEGGNDAAPKSYDVVVVGSG

GAGLAAAIQAHDEGASVLIVEKMPTIGGNTIKASAGMNAAETRFQRVKGIEDSKELFYQETLKGGHNKNN

PQLLRRFVENAPQAIEWLADRGIMLNDITTTGGMSIDRTHRPRDGSAVGGYLISGLVRNITKRGIDVLLD

TSVEEILMRGDEVSGVRLINDEKEVIEVQTKSIVVATGGFSANSAMVVKYRPDLEGFVTTNHKGATGSGI

ALLERIGAGTVDMGEIQIHPTVEQQTSYLISESIRGGGAILVNQQGNRFFNEMETRDKVSAAIIALPEHY

AYIVFDEHVRAKNKAADEYIAKGFVTSASSPRELAEKLGMDYHAFLATLECYNGAVEKQHDEQFGRTTAL

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FGTLAGHQAAKRARG

>lcl|NZ\_FO834906.1\_prot\_WP\_016531700.1\_2698 [locus\_tag=BN49\_RS15050] [protein=FAD:protein FMN transferase] [protein\_id=WP\_016531700.1] [location=2771902..2772852] [gbkey=CDS]

MSDNRVYSYSAVLMGSPILLKLCSHDEAMASRVFQLIKRYEDLLTVNRAESQVMDINHAAGRHPVTVSRP

VFQLIQCAKAASMVRDSAFNLAIGPLVKLWRIGFHGHSVPDAADIRARLALTRPQEVILDEATCSVFLQQ

PGMELDLGAIAKGYIADRMRDFLRQQQVEKALINLGGNVHTLGEWAIGLKKPFADAQALIGSLTVNGQSV

VTSGTYERYFEQDGKRWHHILDPRSGYPLDNELDSVTVISADSLDGDIWTTLLFGLGVEKGCAALRQRQD

IDAIFVTKNRDIILSSPQRLRFAPLDSGYRVIDCTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176303.1\_2699 [gene=dcuR] [locus\_tag=BN49\_RS15055] [protein=two-component system response regulator DcuR] [protein\_id=WP\_004176303.1] [location=complement(2772833..2773552)] [gbkey=CDS]

MINVLIVDDDAMVAELNRLYVARVPGFRCSGSASTLSQAQEMINDPQQEIDLVLLDVYMQQDSGLDLLPT

IRESGRAIDVIMITSAADAATVQTAMHYGVVDYLIKPFQFPRFEEALTTWREKRKLITGQPYYEQADVDR

LLHGGAPEASDARKLPKGLTAQTLRTLCQWIDAHPDVEFSTDELAAAVNISRVSCRKYLIWLAQINILYT

TIHYGATGRPVYRYRLVAEQYSLLKQYSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043233.1\_2700 [locus\_tag=BN49\_RS15060] [protein=sensor histidine kinase] [protein\_id=WP\_046043233.1] [location=complement(2773549..2775165)] [gbkey=CDS]

MKASEHPPRVRQRALPLKLSTAVSLMIGSVIGAVLLLVYALWYMQISNATRDGLKETALAVARTMADMPQ

VKRGLEAPPQQQIIQPLAQAITHRNDLLYAIVTDMQGIRYSHPDSSIIGKPFIGHDIQPTLQGKENVAIN

HGVLAPALRVFTPVFNERHQQIGVVVVGISLSKVDEQIANSRWDVLLTILFSALVCALGTWSLVRGLKRV

LLGLEPHEISTQFQQRQAMLHALKEGVVAVDAHGEVNLINPAAEEILFSGPDKTLVHSPLLDDLQTVLQS

GEPMFDRELGCNGLLLIGNTVPIRSQGAVVGAICTFRDKTEVSQLLQRLDGMMSYVDALRTTSHEFMNKL

HVILGLLNMKSYGKLEEYVLQTAHRYQADIGDIQHRIKSPVVAGFLISKIQRATECGFTLTLAEESLVPD

CPNEKQVTVLVTVLGNLIENALDAMSGQAEGEIGLLLHYQDGWLSGEVSDDGPGIPENNIDAIFNKGFST

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529947.1\_2701 [locus\_tag=BN49\_RS15065] [protein=hypothetical protein] [protein\_id=WP\_016529947.1] [location=2775321..2775677] [gbkey=CDS]

MELASLVRDILRQRHVERLAQHREQDNEAEAEWEIARWRHRSGVVIQRRYELEIAQQDSASCPECWIDWQ

VIDAADQEINPMRKQFYNLCQQSFWLAMQAGGEDETSDRIAQITDNHP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529946.1\_2702 [locus\_tag=BN49\_RS15070] [protein=N-acetylmuramic acid 6-phosphate etherase] [protein\_id=WP\_016529946.1] [location=2775841..2776761] [gbkey=CDS]

MSSSLTASMQARRHPETTHIDRLATADMLAMLHQDDKQISEAVGACLPDIARLIDIATATISRGGRLVII

GAGASGRTAIEAVSDYSPDEKHALVGLIAGGQTAAMAERETAANNYDLGAFELQSLDFSNRDMLLALTVS

GKTPWVWGAMRHAWSLGAPIAVITQQPTSEAAQLADIIIAPQTGPEAVAGLANPKAQLAQRQIVNMLTTG

LAIRDGRVYSNLRVDVQADNSHWAERQIAIVMAATDCTRSEAKAALASCHQHCRTAILMLLSGLDAWHAR

ELLTKHHDHLRLALREAQRSAVTPAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004190310.1\_2703 [gene=mqo] [locus\_tag=BN49\_RS15075] [protein=malate dehydrogenase (quinone)] [protein\_id=WP\_004190310.1] [location=2777025..2778680] [gbkey=CDS]

MPAMKKTIISLTALAMFVSAATHAEADTSKKTDFLLIGGGIMSASLGTWLQALQPDWDLTMVEKLDGVAL

ESSNGWNNAGTGHSANMELNYTPERADGSIDVSKALDINEQFMISRQFWSAQVKRGILHDPHSFINSTPH

MSFVWGDNVDYLQKRYNALQQTTLFQGMKFSTDHAQIKQWAPLVMEGRDPQQKVAATWTPVGTDVNYGEI

TRQLIGSLKKNNHFTLQTSSEVTDFKRNADNSWHVTIKNVQSGEAQTIDAKYVFIGAGGGALKLLQKTGI

PEADNYAGFPVGGSFLMTENPAVTAQHLEKVYGQASVGAPPMSVPHLDARYLDGKRVVLFGPFATFSTKF

LKNGSFFDLLSTTTTNNVLPMTHVGLDNFDLVKYLVSQVMLSDDDRFAALKEYYPDARKEDWKLIQAGQR

VQIIKKDAEKGGVLKLGTEVVVDQQKTISALLGASPGASTAAPITLNVLKQMFPQQFNSPEWQSRIHAIV

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>lcl|NZ\_FO834906.1\_prot\_WP\_085955508.1\_2704 [locus\_tag=BN49\_RS28075] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_085955508.1] [location=join(2779167..2779425,2779425..2780287)] [gbkey=CDS]

MKKRFSDEQIISILREAEAGVPARELCRKHAISDATFYTWRKKYGGMEVPEVKRLKSLEEENARLKKLLA

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ELVLERRRFGYRRIWQLLRREGLHVNHKRVYRLYHLSGLGVKRRRRRKGLATERLPLLRPAAPNLTWSMD

FVMDALSTGRRIKCLTCVDDFTKECLTVTVAFGISGVQVSRILDSIALFRGYPATIRTDQGPEFTCRALD

QWAFEHGVELRLIQPGKPTQNGFIESFNGRFRDECLNEHWFSDIVHARKIINDWRQDYNECRPHSALNYQ

TPSEFAARWRNGKCEGKQTDLTN

>lcl|NZ\_FO834906.1\_prot\_WP\_129015084.1\_2705 [locus\_tag=BN49\_RS15095] [protein=hypothetical protein] [protein\_id=WP\_129015084.1] [location=complement(2780469..2781692)] [gbkey=CDS]

MLYDAGKDSHLNIEGLMMAVYKLSTRIRSNVPTDSLLYDLCIYRMDSSRNKYCLIDVKQQPFSGTYETQT

HMTGNVDESLSTIYIMEMNLYRKTMLHTVCVTPVPFTKMYTLEAFASGNAWSSVKQENLCYFETKGTMKP

ASEGGETKEIRITIPERPFIAREYPIGSPQDPFKKKKIESEIQDRFYNLSYPSQSGASVCGPAAFFYCLQ

QDRPDVYAQAARELWRYGKTKIGALTISPGEGCRHPTGMFFTSDGQPRILGLDWITLAGLRDSENAALSF

DALDSPVAGITMWPTLAEWFEKAGYEMVFSNVGITQAGVQGIRDLNRYVAQGFKVVTLINDGLLEGSTNN

TTLPTHWVVWDSSVTQDDNGYVNLKLFSWGRSTYWIKKGKDVLFFSTDSLGEWFSSH

>lcl|NZ\_FO834906.1\_prot\_2706 [locus\_tag=BN49\_RS15105] [protein=LysR family transcriptional regulator] [pseudo=true] [partial=5'] [location=<2782110..2782451] [gbkey=CDS]

DYADRKFVSLAEGFATYAGFREAFHIAGFEPEIVTRVNDIFSMISLVQAGVGFALLPGRMKKVYEKDVQL

LKLAEPYQMRQLISIVYSHHRERDADLLALAAEGRMYARSLNR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043234.1\_2707 [gene=mdcH] [locus\_tag=BN49\_RS15110] [protein=malonate decarboxylase subunit epsilon] [protein\_id=WP\_046043234.1] [location=complement(2782441..2783343)] [gbkey=CDS]

MKILFTFPGQGGQRPGMLAMIPDREAFLTQARAVLGDEVDTLDSADALQHTRAVQLCLLIAGVAWARELQ

RQGVDPQMVSGLSIGAFPAAVIAGALDFASALRLVALRGDLMEQAYPEGYGLTAIMGLTRPRVEALMQGH

EVYLANLNAETQFVIAGRDEAMAEVAQLALRAGASKAQRLAVSVPSHCALLDKPAAELAKAFAGASLRRP

RCAYLSGSTARVLWDPQRIADDLAMNMARPVHWQEAMVAADERDARLAIEMPPGGVLTCLTRQAGWRGET

IALERSGMDVARHLAQRLSD

>lcl|NZ\_FO834906.1\_prot\_WP\_016531804.1\_2708 [locus\_tag=BN49\_RS15115] [protein=malonate decarboxylase holo-ACP synthase] [protein\_id=WP\_016531804.1] [location=complement(2783343..2783960)] [gbkey=CDS]

MSATPRPHDLVWLNHASALEDIAEPWVAQQWRAALPVVVRRDVDDLARVPVGVRGMKREQRAAGWVQARN

IVRSVTPEMLVEREALLCSPFVSQPPVQGAIALTLHRWPWGWGVTGSTGYALATEIPVLHAASDLDLLIR

APQPLDREALLEWQTRVAQLPCRADTQVETPYGAFALNEWLRDGRALLKTSRGARLTATPWHREE

>lcl|NZ\_FO834906.1\_prot\_WP\_004148291.1\_2709 [locus\_tag=BN49\_RS15120] [protein=AEC family transporter] [protein\_id=WP\_004148291.1] [location=complement(2783964..2784923)] [gbkey=CDS]

MTYVIIHALAPIFVIMLLGFWAGKAGMVDNKNVSLLNIFVMDFALPATLFSATVQTPWAGIVAQSPLVLV

LTGAMWITYAAIYFLATSVFKRTPQDAAVLTLTVALPNYAALGLPILGSVLGEGASTSLSVAVSIACGSV

LMTPFCLLILEREKARAAGENSGSTLAMLPVLMWRSVKKPIVWGPLLGVVLSAIGIKMPDLLLASIKPLG

LAATAAALFLTGVILSARKLQLNALIATSTIVKLLVQPFIAWGLVMLLGLHGSIAITAILMIALAAGFFG

VVFGNRFGVQSPDAEAVLLLSSVLCILSLPLFISLTSGL

>lcl|NZ\_FO834906.1\_prot\_WP\_004224637.1\_2710 [gene=mdcE] [locus\_tag=BN49\_RS15125] [protein=biotin-independent malonate decarboxylase subunit gamma] [protein\_id=WP\_004224637.1] [location=complement(2785060..2785860)] [gbkey=CDS]

MSQFPNRAALWLNKLAPDAPLMSGLCPSVQVADGQINGENVRFIAVVPDANNHYPRAAGGEVGLLEGWTL

AKVVNETIAADADQPVKRPIVAVIDVPSQAYGRREEAFGIHQALAGAAGAYAKARLAGHPVIGLIVGKAM

SGAFLAHGYQANRLIAFNDSGVLVHAMGKASAARITLRTVEALEKLAATIPPMAYDVSNYATLGLLSALL

DINNPDAPDDHDLSLVSNTLRDAIADARTDASLKCRLGAENRRSSQLVRDRMRASW

>lcl|NZ\_FO834906.1\_prot\_WP\_016529222.1\_2711 [locus\_tag=BN49\_RS15130] [protein=biotin-independent malonate decarboxylase subunit beta] [protein\_id=WP\_016529222.1] [location=complement(2785860..2786693)] [gbkey=CDS]

MRNDRSFIELRARERAHALLDDGSYRELLDPFDGIMSPWLGAQGIVPQSDDGMVVAKGTINGQPAVVIAI

EGTFQGGSMGEVSGAKMAAALELAAEDNRNGIPTQAVLCLETGGVRLQEANLGLAAIADIHAAIVDLRRY

TPVVGIIAGTVGCFGGMSIAAALCSYLIVTREARLGLNGPQVIEQEAGIEEYDSRNRPFIWSMTGGEIRA

ASGLVDALVNDGVNAVKTAMNEAIAKGVPVQHRSDNYDDYLRRLSQFDTRQQADTTQIKQLFAREDK

>lcl|NZ\_FO834906.1\_prot\_WP\_004143106.1\_2712 [gene=mdcC] [locus\_tag=BN49\_RS15135] [protein=malonate decarboxylase acyl carrier protein] [protein\_id=WP\_004143106.1] [location=complement(2786686..2786985)] [gbkey=CDS]

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GQLIIHDFGATPGVARIRIEQVFEEAAHA

>lcl|NZ\_FO834906.1\_prot\_WP\_023283668.1\_2713 [locus\_tag=BN49\_RS15140] [protein=triphosphoribosyl-dephospho-CoA synthase] [protein\_id=WP\_023283668.1] [location=complement(2787003..2787845)] [gbkey=CDS]

MKNLSPLHAESRVSWLAHTASACLIDEARLSPKPGLVDSRGNGAHQDLNLALMERSARSLQPTFHALAEQ

SWRRPADIALRETVGRLGREGEAQMMLATGGVNTHRGAIWALGLLVSAVAMLGGEGQSQAIADAAAALAR

LPDGFAPKSFSKGLRASRRWQVPGAREEAQCGFPHITRLALPQLQQSRARGASEPQAQLDALMAIMTSLS

DTCVLSRAGMAGLQAMQQGACEVLAAGGCASFAGRAALARLDAIMLAQNASPGGAADLLAATLFLDRVAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529225.1\_2714 [gene=mdcA] [locus\_tag=BN49\_RS15145] [protein=malonate decarboxylase subunit alpha] [protein\_id=WP\_016529225.1] [location=complement(2787845..2789500)] [gbkey=CDS]

MNAEQTTGRVWNRRRTEKQRRLAEANMPGKVIPTDQLVSVLENLLAPGDRVVLEGNNQKQADFLSRMLAE

VNPQKIHDLHMIMPSVGRSEHLDLFEKGIARKLDFSFSGTQSLRISQLLEDGLLEIGAIHTYIELYSRLY

VDLSPNVALIAGYKADRKGNLYTGPSTEDTPALVEAAAFHDGIVIAQVNELVDDECDLPRVDIPGSWIDY

VVVADKPFFIEPLFTRDPRLIKQEHILMAMMAIKGIYAEHQVQSLNHGIGFNTVAIELLLPTYGEQLGLK

GKICKHWTLNPHPTLIPAIESGWVESVHCFGGELGMEEYIRARPDIFFTGPDGSMRSNRAFCQLAGQYAV

DMFIGSTLQVDGLANSSTVTRGRLSGFGGAPNMGHDPHGRRHATPAWLNMITEPDPMQRGKKLVVQMVET

FQAGVKPTFVETLDAVEVAKTSGMPLAPVMIYGDDVTHVLTEEGIAYMYRAESLEERRAMVAAVAGITDI

GLGVDAKRVAALRQSGKVVYPEDLGIRRSDATRSLLAAGSVADLVEWSDGLYNPPAKFRSW

>lcl|NZ\_FO834906.1\_prot\_WP\_002903679.1\_2715 [locus\_tag=BN49\_RS15150] [protein=AI-2E family transporter] [protein\_id=WP\_002903679.1] [location=complement(2789725..2790759)] [gbkey=CDS]

MAKPIITLNGLKMVIMLGMLVIILTGIRFAADIIVPFILALFLAVIINPLVQLLVRCRVPRVLAISLLIG

LIVMLAIVLLASLGTSLNELARTLPQYRNYLYEPMQTIAPWLQRMGFTVSVVELNKYIDPNAVMTLVTSL

LTQLSNAMSSIFLLLLTVVFMLLEVPQLPAKLQQLMSRPVEGMGAIQRAIDSVSHYLVLKTAISLITGLV

VWGMLVLLDVRFAFMWGLLAFALNYIPNIGSVLAAIPPILQVLVFGGLYEALVVLAGYLIVNLVFGNILE

PRIMGRGLGLSTLVVFLSLIFWGWLLGPVGMLLSVPLTIIVKIALEQTSGGQSIAFLLSDVSKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529226.1\_2716 [gene=mdtJ] [locus\_tag=BN49\_RS15155] [protein=multidrug/spermidine efflux SMR transporter subunit MdtJ] [protein\_id=WP\_016529226.1] [location=2791202..2791516] [gbkey=CDS]

MFYWILLALAIIAEITGTLSMKWASVSGGHTGFILMLAMIALSYIFLAFAVKKIALGVAYALWGGFGIAA

TIAAGWVLFGQRLNNKGWAGVILLVAGMVLIKLA

>lcl|NZ\_FO834906.1\_prot\_WP\_024623203.1\_2717 [locus\_tag=BN49\_RS15160] [protein=hypothetical protein] [protein\_id=WP\_024623203.1] [location=complement(2791560..2791676)] [gbkey=CDS]

MKNIIIDIVLAEMILRQPKAVNLRSPQRHLTQLQRGQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002903687.1\_2718 [locus\_tag=BN49\_RS15165] [protein=serine protease] [protein\_id=WP\_002903687.1] [location=complement(2791690..2792502)] [gbkey=CDS]

MRRDVLLLLCSFYLLPLGAHADDSGLSAKDIKTLFFGHDDRKAVNRPEESPWDAIGQLETASGNLCTATL

ISPHLALTAGHCLLTPPRGKPDKAVALRFISRKGNWVYEIHGIDGRVDPSLGRRLKADGDGWIVPSAAAP

SDFGLIVLRYAPSGITPIPLFPGSKADLTAALKAADRKVTQSGYPEDHLDNLYSHQDCIVTGWAQTSVLS

HQCDTLPGDSGSPLLLKTEDGWQVIAVQSSAPGPQDRWRADNRAIAVTGFRDKLEALAGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002903693.1\_2719 [gene=asr] [locus\_tag=BN49\_RS15180] [protein=acid resistance repetitive basic protein Asr] [protein\_id=WP\_002903693.1] [location=complement(2793441..2793860)] [gbkey=CDS]

MKKVLALVVAAAMGLSSAAFAADAVSTTQAPAATHSTAAKTTHHKKHHKAAAKPAAEQKAQAAKKHKKAE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004176294.1\_2720 [locus\_tag=BN49\_RS15185] [protein=carboxypeptidase M32] [protein\_id=WP\_004176294.1] [location=complement(2794025..2795512)] [gbkey=CDS]

MTENTPYQQLTRTFQRLSRFSHLAAIAGWDMFAMMPPGGSVARSEALAELGVLQHQILTDKKVGQWLQEA

RQQDLNDVEQANLREMQRQYDQAALLPESLVEAKSLAGSRCEHAWRSQRPANDWTGFADNLREVVRLSRQ

EAQIRADARGGSRYDALLDIFEPDMTSARLDSLFADLKSWLPSLLSQAVEKQAKQTLIAPQGPFPIAEQR

ELGLQAMRILGFDFDGGRLDISAHPFCGGVPQDVRITTRYNENDLLSALFGVIHETGHARYEQNLPRPWV

DQPVGLARSTAIHESQSLFFEMQLGRSERFLNRLLPAVRERFGDRPAFSQDNFVAWNQQVKPGFIRVDAD

EVSYPAHVILRYEIERALIDGEIEVDDIPSLWDEKMQHWLGLSTTGNYRDGCMQDIHWTDGGFGYFPSYT

LGAMYAAQLMAAARRALPTLDRDIEEGDFSALFDWLRQNIWQHGSRFTTSQLIQQATGEDLNSRYFREHL

TTRYL

>lcl|NZ\_FO834906.1\_prot\_WP\_004206050.1\_2721 [locus\_tag=BN49\_RS31455] [protein=hypothetical protein] [protein\_id=WP\_004206050.1] [location=2795729..2795821] [gbkey=CDS]

MNPFTWLFIALLSVDAVRELMGLSSIMGMW

>lcl|NZ\_FO834906.1\_prot\_WP\_002903698.1\_2722 [locus\_tag=BN49\_RS15190] [protein=MFS transporter] [protein\_id=WP\_002903698.1] [location=complement(2795852..2797102)] [gbkey=CDS]

MSRTTTVDTVPAGEVSVAGASRPDPFIKRGTPQFMRVTLALFSAGLATFALLYCVQPILPVLSNEFGVSP

ASSSISLSISTAMLAVGLLFTGPLSDAIGRKPVMVTALLLAACCSLLSTMMTSWHGILIMRALIGLSLSG

VAAVGMTYLSEEIHPSFVAFSMGLYISGNSIGGMSGRLLTGVFTDFFGWRVALAAISGFALAAAIMFWRI

LPESRHFRPTSLRPKTLLINFRLHWRDRGLPLLFIEGFLLMGAFVTLFNYIGYRLMMSPWSLSQAVVGLL

SVAYLTGTWSSPKAGAMTVRFGRGPVMLGFTAVMLCGLLLTLFSSLWLIFIGMLLFSAGFFAAHSVASSW

IGPRARRARGQASSLYLFSYYLGSSLAGTLGGVFWHHYGWNGVGGFIALLLLAALLTGTCLHQRLK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532373.1\_2723 [locus\_tag=BN49\_RS15195] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016532373.1] [location=2797233..2798135] [gbkey=CDS]

MNIELRHLRYFVAVAEELHFGRAAARLNISQPPLSQQIQILEQQTGARLFARTNRSVSLTAAGKQFLADS

RQILAQVDEAAARAARLHHGETGELRIGFTSSAPFIKAVSDTLSMFRQRLPDVHILTRETNTREQIVPLS

EGALDLGLLRNTQLPDTLAWEQVLREPLLAMVPANHPLARQPSVSLAALAREPFVFFDPHVGTGLYDDIL

GLLRRYGHTPKIAQEVGEAMTIIGLVAAGLGVSILPASFQRVQLSEMRWLPIDEQDAVSEMWLVWSKHHE

QGALAKRFREALLSWKSEHN

>lcl|NZ\_FO834906.1\_prot\_WP\_016532374.1\_2724 [locus\_tag=BN49\_RS15200] [protein=ROK family transcriptional regulator] [protein\_id=WP\_016532374.1] [location=2798259..2799479] [gbkey=CDS]

MVADSQPGHIDQIKQTNAGAVYRLIDQLGPVSRIDLSRFAQLAPASITKIVREMLEAHLVQETEIQEPGS

RGRPAVGLMVETEAWHYLAVRISRGEIHLSLRDLSSQLVVEDQLELALTDSTPFLTRVIDHIDRFFIRHQ

KKLERLTSIAMTMPGIIDTENGIIHRMPFYEDVKDVPLGEALANHTGVPVYIQHDISAWTMAESLFGASR

GARDVIQVVIDHNVGAGVITDGRLLHAGSSSLVEIGHTQVDPYGKRCYCGNHGCLETIASVESVLELAQM

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>lcl|NZ\_FO834906.1\_prot\_WP\_016532375.1\_2725 [gene=bioD] [locus\_tag=BN49\_RS15205] [protein=dethiobiotin synthase] [protein\_id=WP\_016532375.1] [location=2799607..2800302] [gbkey=CDS]

MFKRFFITGTDTSVGKTVVSRALLQALAARGKSVAGYKPVAKGSKETPDGLRNKDALVLQSVSTLALPYE

AVNPIALSEDESSVAHSCPINYGLLSDGLQRLAAQVEHVVVEGTGGWRSLMNDLRPLSEWVVQEQLPVLM

VVGIQEGCINHALLTAQAIANDGLPLIGWVANRINPGLAHYAEIIDVLSKKLPAPLFGELPYLPRAEQRE

LSRYVDLDMLGNVMAIDRIPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004148305.1\_2726 [gene=clcB] [locus\_tag=BN49\_RS15210] [protein=voltage-gated ClC-type chloride channel ClcB] [protein\_id=WP\_004148305.1] [location=complement(2800255..2801550)] [gbkey=CDS]

MHRLHPYPDVQVMFRRLLIATLIGLLAALAVALFRHAMVVLETLLLSNDSGSLVNAAQSLPAWRRLVTPA

LGGLTAGTLLWLWQRRSVARPHAATDYMEALETGDGCFDTPASLVKSLASLLVVVTGSAIGREGAMILLA

ALAASLFARRFTPQSEWKLWVACGAAAGMASAYHAPLAGSLFIAEILFGTLMLASLGPVVISAVIALLLT

QFLNGGAAPLYHVVLQQNLSALHYGLMLATGLLAGLCGPLFIWLMDYSHRGFVKLKLAPPWQLALGGLIV

GGLSLITPAVWGNGYSVVQSYLLLPPSGALLVGVFICKLLAVLASSGSGAPGGVFTPTLFVGLAMGMLFA

CFSRLWLPGSEEMAIMMGLTGMAAFLAATTHAPIMSTLMICEMTGQYTLLPGLLITCVVSSVLSRTLRRD

SIYRHHVAEHV

>lcl|NZ\_FO834906.1\_prot\_WP\_029602379.1\_2727 [gene=dmsD] [locus\_tag=BN49\_RS15215] [protein=Tat proofreading chaperone DmsD] [protein\_id=WP\_029602379.1] [location=complement(2801684..2802292)] [gbkey=CDS]

MMPIPNRDAVALSARTLGALFSYAPNSAEIAPLVAAFQDGSWQQQWPFPIAAPLASGFAASAEETLPEAW

QRLFIGPWALPAPPWGSVWLDKESVLFGDSTLALRQWMRENGIALEADGNEPEDHFGTVLLLAAWLCETE

QDALFAQLLAWHLLPWSGRFLSVFIDHAAHPFYQALGQLAQATLAQWQESLPIAVAQKPLYR

>lcl|NZ\_FO834906.1\_prot\_WP\_002903710.1\_2728 [locus\_tag=BN49\_RS15220] [protein=dimethyl sulfoxide reductase anchor subunit] [protein\_id=WP\_002903710.1] [location=complement(2802334..2803191)] [gbkey=CDS]

MGNGWHEWPLVLFTVLGQCVVGATIVSGLGWLALGDQREARRRLVRNMFFIWLLMGIGFLASVMHLGSPL

RAFNSLNRIGASALSNEIASGALFFAVGGFWWLLAVLEKMPATLGKVWLAIAMLLGLLFVLAMTRVYQIN

TVPTWYNGYTTSAFFLTVLLSGPLFAALLLRLAKVDFNGWFFAGLSVAALVISAAVIIMQSAGLSTLHSS

VQQAATLLPDYGKLQALRLVLLALGLGCWLCPLIRRQPPRATGLLIGLLLVLIAECIGRGLFYGLHMTVG

MAVAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004152235.1\_2729 [gene=dmsB] [locus\_tag=BN49\_RS15225] [protein=dimethylsulfoxide reductase subunit B] [protein\_id=WP\_004152235.1] [location=complement(2803193..2803810)] [gbkey=CDS]

MSTQYGFFIDSARCTGCKTCELACKDYKNLTPEVSFRRIYEYAGGDWQEDNGVWQQNVFAYYLSIACNHC

EDPACTKVCPSGAMHKREDGFVVVNEEVCIGCRYCHMACPYGAPQYNADKGHMTKCDGCHERVAEGKKPI

CVESCPLRALDFGPIAELRAKHGQLAAVAPLPSAHFTRPSIVIKPNANARPCGDTTGYLANPKEV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043250.1\_2730 [locus\_tag=BN49\_RS15230] [protein=dimethyl sulfoxide reductase subunit A] [protein\_id=WP\_046043250.1] [location=complement(2803821..2806256)] [gbkey=CDS]

MSNQESPGGVSRRALLKSTALGSLALAAGGLTLPFTLRRAAAAVQQATGDTTRIVWGACSVNCGSRCALR

LHVRDDEVVYVETDNTGDDRYGDHQIRACLRGRSIRRRINHPDRLNYPMKRVGKRGEGKFVRISWQEALD

TLADRLKSVVAQYGNEAVYINYSSGIVGGNITRSSPSASPVARLMNCYGGSLNQYGTYSTAQIACAMPYT

YGSNDGNSTSDIENSKLVVMFGNNPAETRMSGGGITWYLEQARERSNARMIVIDPRYTDTAAGREDEWIP

IRPGTDAALVAGIAWVLINEDLVDQPFLDKYCVGYDEKTLPAGAPANGHYKAYILGEGDDGIAKTPQWAS

RITGIPTERIIKLAREIGMSKPAYICQGWGPQRQANGELTARAIAMLPILTGNVGINGGNSGARESTYTI

TIERLPVLENPVKTAISCFTWTDAIARGPEMTASRDGVRGKEKLDVPIKFLWNYAGNTIINQHSDINKTH

EILQDESKCETIVVIDNFMTSSAKYADLLLPDLMTVEQEDIIPNDYAGNMGYLIFIQPATSAKFERKPIY

WILSEVAKRLGDDVHQRFTEGRTQEQWLQYLYAKMVAKDPALPAYEDLKRMGIYKRKDPNGHFVAYRDFR

RDPEAHPLKTPSGKIEIYSSRLAEIAARWQLEKDEVISPLPVYASTFEGWDDPLRSQYPLQLFGFHYKAR

THSSYGNVDVLQAACRQEVWINPLDAEKRGIKNGDMVRVFNQRGEVRLPAKVTPRIMPGVSAMGQGAWHD

ANMTGDRIDHGACMNTLTTHRPSPLAKGNPQHTNLVDIEKV

>lcl|NZ\_FO834906.1\_prot\_WP\_002903714.1\_2731 [locus\_tag=BN49\_RS15235] [protein=DUF1161 domain-containing protein] [protein\_id=WP\_002903714.1] [location=complement(2806407..2806676)] [gbkey=CDS]

MKLSLCTGAALLLCSTAVLAAPDSCERVKSDIQQKIINNGVPETAFSLAIVPNDQADQPGVQVVGHCAND

TFKITYTRNSDSPAENDAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_042941110.1\_2732 [locus\_tag=BN49\_RS15240] [protein=YnfC family lipoprotein] [protein\_id=WP\_042941110.1] [location=2806778..2807488] [gbkey=CDS]

MKRLYWLIPAALLLTACDRKSAPDAFTPEMASFSNEFEFDPLRGPVKDFSQTLLDEHDVVVKKVSAQLSR

EGCFDLLTLEDVENKTGATLLLDANYYVDGRTHEKRLRLQGKCQLAEMPAAGVSWETDDNGFIISARGKE

TTATYRYDSDGYPLGKTTTAKEERFTVASTPSKDPRKKLDYTAISTFNDRTLGTVRQTCDYDDHHNPLSC

ELQVIDESVQPPLTRHYTIKNRIDYY

>lcl|NZ\_FO834906.1\_prot\_WP\_002903719.1\_2733 [gene=speG] [locus\_tag=BN49\_RS15245] [protein=spermidine N1-acetyltransferase] [protein\_id=WP\_002903719.1] [location=complement(2807482..2808042)] [gbkey=CDS]

MTDALHVKLRPLEREDLRFVHQLDNNASVMRYWFEEPYEAFVELSDLYDKHIHDQSERRFVIECNGDKAG

LVELVEINHVHRRAEFQIIISPDFQGKGLATRAARLAMDYGFTVLNLYKLYLIVDKENEKAIHIYRKLGF

MVEGELIHEFFINGEYRNTIRMCLFQHQYLAEHKTPGPSLLKPTAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002903720.1\_2734 [locus\_tag=BN49\_RS15250] [protein=DUF1283 family protein] [protein\_id=WP\_002903720.1] [location=complement(2808121..2808462)] [gbkey=CDS]

MNMTLNKRWCLTAILALSAVVYTSSSYAATDRLVIESGDSAQSRQQASMEKEQWNDTRSLRQKVNKRAEK

EWDKADVAFDAQDNCQKSANVNAYWEPNTLRCLDRRTGRAINP

>lcl|NZ\_FO834906.1\_prot\_WP\_004219442.1\_2735 [locus\_tag=BN49\_RS15255] [protein=YnfA family protein] [protein\_id=WP\_004219442.1] [location=2808571..2808933] [gbkey=CDS]

MVQRFVSFTNLLMLKTTLLFFATALCEIVGCYLPWLWLKRGATPLLLIPTALALALFVWLLTLHPAASGR

VYAAYGGVYVCTALLWLRVVDGVKLTHYDWAGAAIALCGMLIIVAGWGRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002903724.1\_2736 [locus\_tag=BN49\_RS15260] [protein=MFS transporter] [protein\_id=WP\_002903724.1] [location=2809047..2810330] [gbkey=CDS]

MAIETLAARTGATPLRIRRVQKITLTLLFIAGIVNFLDRSSLSVAGEAIRADLGLSATEFGVLLSAFSLS

YGFAQLPSGILLDRLGPRIVLGAGLIFWSAMQALTGMVNSFSHFILLRIGLGIGEAPFMPAGVKSINDWY

AQRERGTAVGIFNSSTVLGQAIAPPALVIMQLAWGWRTMFVVIGLAGIVVGLCWYVGYRNRRQFTLQEEE

QQYLASEEAARPALKFSEWLALFKRRTTWGMILGFSGVNYTGWLYIAWLPGYLQAQQGLSLARTGWVAAI

PFLAAAVGMWVNGLVVDALARRGYDQAKTRKTAIVIGLVLSALGTLLVVQSSTPAQAVAFISMALFCVHF

AGTSAWGLVQVMVAEHKVASVAAIQNFGSFVFASFAPIVTGWVVDTTHSFNLALVIAAGVTFAGALCYFF

IVKTRID

>lcl|NZ\_FO834906.1\_prot\_WP\_021314212.1\_2737 [locus\_tag=BN49\_RS15265] [protein=fructuronate reductase] [protein\_id=WP\_021314212.1] [location=2810594..2812057] [gbkey=CDS]

MENTLLTANATLPTYDRSALIPRIVHLGFGAFHRAHQAVYADILASEHGSDWGYTEVNLIGGEQQIADLQ

QQDLLYTVAEMSADAWTARVVGVVKQALHAGVDGLEAVLTAMCQPQVAIVSLTITEKGYCHSPASGELQL

DHPLIAADLHNPHQPKSAAGVVVEALSRRRAAGLPAFTVMSCDNMPENGHVMRNVVCAYARALDEDLAAW

IEQNVTFPSTMVDRIVPAVTAETLDKITQLTGVRDPAGVACEPFRQWVIEDNFVAGRPQWEKAGAELVAD

VVPFEEMKLRMLNGSHSFLAYLGYLAGYQHINDCMQDDNYRRAALSLMLDEQAPTLKVQGVDLSRYASLL

IDRYCNPALKHRTWQIAMDGSQKLPQRMLDSIRWHLVHQRDFTLLALGVAGWMRYVGGVDDAGQSIEICD

PLLPVIQQAVAASADGEARVKALLGIEAIFGVELPQESRFVTAVTRAYLALQRQGAKATVAAWAAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002903728.1\_2738 [locus\_tag=BN49\_RS15270] [protein=universal stress protein] [protein\_id=WP\_002903728.1] [location=2812322..2812753] [gbkey=CDS]

MYKKILLPVDVFEMDLSDKAVRHAEFLASAENGEITLLNVLPNSSRSLLRGFTADIRKFEAYMKEESEKK

MREVARLFAIPMTRIHTRVVFGNVRDEILAISNNEEFDVIVIGSRKPGISTHLLGSNAESILRYAKTPVL

VVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002903730.1\_2739 [locus\_tag=BN49\_RS15275] [protein=GntR family transcriptional regulator] [protein\_id=WP\_002903730.1] [location=complement(2812804..2813490)] [gbkey=CDS]

MAAESQLNPTQPVNQQIYRILRRDIVHCLIPPGTPLSEKEVSVRFAVSRQPVREAFIKLAENGLIQIRPQ

RGSYVNKISLSQVRNGCFVRQAIECAVVRRAAGMINEEQLYQLEQNLHQQRIAVDRQQLNDFFLLDDEFH

QKLSIIADCQLAWETVENIKAAIDRVRYMSLDHVTSPEMLLRQHHEIFTALEKRDAEAVEKAMSIHLHEI

SESVLLIRQENRDWFSEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002903733.1\_2740 [gene=ydfG] [locus\_tag=BN49\_RS15280] [protein=bifunctional NADP-dependent 3-hydroxy acid dehydrogenase/3-hydroxypropionate dehydrogenase YdfG] [protein\_id=WP\_002903733.1] [location=complement(2813582..2814331)] [gbkey=CDS]

MIIMVTGATAGFGESITRRFIANGHKVIATGRREERLKTLKDELGDNLYIAQLDVRNRAAIETLIADLPA

EWQAIDVLVNNAGLALGLEPAHRASVEDWEDMIDTNNKGLVYMTRAVLPGMVERNRGHIINIGSTAGSWP

YAGGNVYGATKAFVRQFSLNLRTDLHGTAVRVTDIEPGLVGGTEFSNVRFKGDDAKAEKAYENTQALTPE

DVTEAVWWVATLPKHVNINTLEMMPVSQSFAGLSVHRQG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043253.1\_2741 [gene=dcp] [locus\_tag=BN49\_RS15285] [protein=peptidyl-dipeptidase Dcp] [protein\_id=WP\_046043253.1] [location=2814462..2816507] [gbkey=CDS]

MSERNPFFSVSTLPYQAPPFDVIDDSHYRPAFDEGVRQQRAEIRAIIDNPQPASFANTLEALEQSGQLLA

RVTRVFFAMAGAHTNPYIQSLDEQFSAELAELGNDIWLNAALFQRVNSVYEQRDALALDSESYRLLTLTW

QRFVHAGATLAPEQQAALRTLNTEAATLQSQFQQRLLGAAKSGGLVVDYRHQLAGLSDEEIAAAADAARE

RGLSDRWLLTLTNTTQQPQLLALRDRQTRENLFAAGWTRNQQGDEHDTRDLVLRLAAIRAQQAELLGAAD

YASWALTDQMAASPAEALGFMRQIAPAARARAERELADIQQVIDNEGGGFRATAWDWLYYSEQVRRAAYA

IDDAQLKPYFALERVLHDGVFWTATQLFGLRFVERFDIPVYHPDVRVWEIFDHNGEGMALFYGDYYARDS

KSGGAWMDVFVEQSTLRAQRPVIYNVCNYVRPQAGQSALLSWDEVITLFHEFGHTLHGLFASQRYASLSG

TNTPRDFVEFPSQIFEHWASQPQVFAHYAKHYQSGEPMPQALRDNMLRAATFNKGYDMSELLAAALLDMR

WHSLSTSALPEEVDAFEQQVLREENLDLAAVPPRYRSSYFSHIFGGGYAAGYYAYLWTQMLADDGYQWFV

EQGGLTRENGQRFREAILSRGNSTDLAELYRQWRGHDPQIEPMLKNRGLSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531735.1\_2742 [locus\_tag=BN49\_RS15290] [protein=nuclear transport factor 2 family protein] [protein\_id=WP\_016531735.1] [location=complement(2816585..2816971)] [gbkey=CDS]

MITITRVLDDIINYQQIPLDRILSRYFSPGYRQRTDNKWEGLDGFAQHARRLREIIAFAKIELHDELRNG

NLYATRHRVLCTRRSGEEVDMEVYMFAEIDDSGRFIRIEEATLMLKGRESDRDLGSVR

>lcl|NZ\_FO834906.1\_prot\_WP\_071609162.1\_2743 [locus\_tag=BN49\_RS29130] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_071609162.1] [location=2817071..2817841] [gbkey=CDS]

MHDPLIPFEPVFSPQGPTLLVAVRQSEVIRETPRHHHSCGQLIGAIRGLLTVDGGDCRWVVPATHAVWIP

PGVPHGLRSHGPYSGWSVYVSAKACGELPDKPSVLSMTNLLREAITRAAAWQGVELNASQKRLAGVILDE

IGSLPRVNLGLPMPQDSRLLRIAQALSANPDDGRRLEEWAAWAGMSSRTLTRRFRAETGFSFNEWRQRIR

LLRALELLAAGKPVTAIALDLGYDNVSAFIALFRRMFGTTPGRYKL

>lcl|NZ\_FO834906.1\_prot\_WP\_032419006.1\_2744 [locus\_tag=BN49\_RS15300] [protein=SOS response-associated peptidase] [protein\_id=WP\_032419006.1] [location=complement(2817892..2818566)] [gbkey=CDS]

MCGRFAQAQSREEYLAHLVEAAERDIAWDPAPIGRYNVAPGTKVLLLNERDEQLHLDAVYWGYAPGWWDK

PPLINARVETAASSRMFKPLWEHGRAICFADGWFEWKKEGNTKQPYFIQRKDGQPIFMAAIGRTPFERGD

HAEGFLIVTAAADRGLVDIHDRRPLVLAPEAAREWMRQDVTGAEAAEIASDGAVSADDFTWHPVTRAVGN

VKNQGPELLAPLSP

>lcl|NZ\_FO834906.1\_prot\_WP\_004219446.1\_2745 [locus\_tag=BN49\_RS31050] [protein=hypothetical protein] [protein\_id=WP\_004219446.1] [location=2818738..2818866] [gbkey=CDS]

MLHRYYPNACLIKEIVFTLFIIFQNYRTEFYLCLKWLSLGCI

>lcl|NZ\_FO834906.1\_prot\_WP\_004143611.1\_2746 [locus\_tag=BN49\_RS30720] [protein=small membrane protein] [protein\_id=WP\_004143611.1] [location=2818921..2819043] [gbkey=CDS]

MSNLLLLVLAVVLLFTSLFFGLSYVRERRKMKMRFNKFRR

>lcl|NZ\_FO834906.1\_prot\_WP\_046044052.1\_2747 [locus\_tag=BN49\_RS15315] [protein=LuxR family transcriptional regulator] [protein\_id=WP\_046044052.1] [location=complement(2819040..2819675)] [gbkey=CDS]

MTMPDILINTENIFLNRGICELLSEIAKEEHIRKPYSVVDCSTDILGPIDMLFTEMAAGEHYLCHPFFKK

LPPHTSIFIFVATDSALQVEQLPLCLRDATFISMNSDLRRVKNQIAKRLTESTTSSCGGLEKDSRRCVKC

PWLTLTKSQLYIIDAIRTGMNNQQIAQKMGISHKTIFSHKINIMKKFQIATKQELTRFSSVALALSAGRI

G

>lcl|NZ\_FO834906.1\_prot\_WP\_042941858.1\_2748 [locus\_tag=BN49\_RS31055] [protein=hypothetical protein] [protein\_id=WP\_042941858.1] [location=complement(2819743..2819865)] [gbkey=CDS]

MCQISGHARATLKNKPLINIPLILLASSKSKIRLIAFIDN

>lcl|NZ\_FO834906.1\_prot\_WP\_223174615.1\_2749 [locus\_tag=BN49\_RS31060] [protein=hypothetical protein] [protein\_id=WP\_223174615.1] [location=2820140..2820241] [gbkey=CDS]

MDAKRANRVVEIKMLAMAVPQKVRMQIIRHGVG

>lcl|NZ\_FO834906.1\_prot\_WP\_016531265.1\_2750 [locus\_tag=BN49\_RS15330] [protein=Hsp20 family protein] [protein\_id=WP\_016531265.1] [location=2820687..2821160] [gbkey=CDS]

MALKTLSALPVFADSLFADRFNRIDRLFSQLTGDTPVGTLPAYDLQKVDDSNFLLSVSVPGWKDDELEIE

TVGGNLHISGKRQETDASTDSGERWIYKGIRRANFQLSFSLPEHAQINQAQLDSGILKIAIHQEIPESEK

PRKIAIENQRRVIEHKV

>lcl|NZ\_FO834906.1\_prot\_WP\_002903810.1\_2751 [locus\_tag=BN49\_RS15335] [protein=2-oxo-tetronate isomerase] [protein\_id=WP\_002903810.1] [location=2821326..2821838] [gbkey=CDS]

MTDEIDSDANNTHELTAEVARALIARGWRLTTAESCTGGNLAAALCAQADTAAFYDTGVVTFSDEAKRNV

LQVRAETLAVHSAVSEACVQEMSSGILALAGADIAIAVSGYAGPEGGEDGTPAGTVWFAWNFRGQTETKR

MCFAGDCETVVAKAVRYALAALSEKLAHWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043260.1\_2752 [locus\_tag=BN49\_RS15340] [protein=beta-galactosidase] [protein\_id=WP\_046043260.1] [location=complement(2821859..2825413)] [gbkey=CDS]

MQISDTGRSHTPDFHAVLAREDWQNQTITHLNRLPAHPVFASWRDELAARDNLPSSRRRQLDGEWQFSYA

RSPFAVDAQWLTQDLPDCRGTPVPSNWQMEGYDAPIYTNVRYPIDTTPPRVPEDNPTGCYSLHFTVEDTW

RENGQTQIIFDGVNSAFHLWCNGVWVGYSQDSRLPAAFDLSPFLRPGDNRLCVMVMRWSAGSWLEDQDMW

RMSGIFRSVWLLNKPQQRLCDVQLTPALDALYRDGTLQVQATVEATEAALAGLSVGVSLWRGEEQIAAGR

QPLGTPTVDERGHYAERVDFSLAVATPAHWSAETPNCYRAVVTLWRGDELLEAEAWDIGFRRIEIADGLL

RLNGKPLLIRGVNRHEHHHLRGQVVTEADMVQDILLMKQNNFNAVRCSHYPNAPRWYELCNRYGLYVVDE

ANIETHGMVPMNRLSDDPAWLPAFSARVTRMVQSNRNHPCIIIWSLGNESGGGGNHEALYHWLKRNDPSR

PVQYEGGGADTTATDIICPMYARVERDQPIPAVPKWGIKKWISLPGEQRPLILCEYAHAMGNSLGNFADY

WQAFREYPRLQGGFIWDWADQAIRKTFADGSVGWAYGGDFGDKPNDRQFCMNGLVFPDRTPHPSLVEAKH

AQQYFQFTLLSTSPLRVRIISEYLFRPTDNEVLRWQLQAAGEPLYHGDLTLALPPEGSDEITLLDSLILP

EGARAVWLTLEVTQPQATVWSEAEHRVAWQQFPLPAPLALPAPTVSAGAPDLIVSDEVWQIRAGSQCWTI

DRRTGLLSRWSVGGQEQLLTPLRDQFIRAPLDNDIGVSEVERIDPNAWVERWRSAGLYDLEAHCVQCDAQ

RLANETLVDCRWHYLRGEEVVIVSHWRMHFTADGTLRLAVDGERAETLPPLPRVGLHFPVNDRMFRLLSA

FIADGGRYCLPEPLQPSRWMMMPASGTAAPQHLPGQPCQFALQAIVEPAKKRVSSFEALIRSPTGGSPVE

MFAAIAAEDRYRFDLESKAYAFALAGQLPLGKHQLAINLLPGSLYHHPDAVGWLMDSLLAAGLRPDQVLI

EVTETEVITCFDQFRKVLKALRVAGMKLAIDDFGAGYSGLSLLTRFQPDKIKVDAELVRDIHISGTKQAI

VASVVRCCEDLGITVVAEGVETLEEWCWLQSVGIRLFQGFLFSRPCLNGIGEICWPVARQAMDL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043262.1\_2753 [locus\_tag=BN49\_RS15345] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_046043262.1] [location=2825610..2826674] [gbkey=CDS]

MTRRTATLEDVARAAGVSQQTVSRVLNRPEVVSARTREQVIRAMQALHYVPNRSAQLLAGKAAPSIGLIT

ASLTLHAASQIAAAIKSHASLHQLEVAIAMPAQADFVALQARLDELRAQHIRGVIVSLPLESATAERLVQ

DNPDMACLFLDVSPEADVCCVRFDHRDGCGACVRHLWELGHREFGLLAGPESSVSARLRLASWREALHSL

NIARSTTVFGDWSAASGWQKTFELLHLQPRISAIVVANDQMALGVLSALAQLNRSGSQAVSVTGYDDTAD

SLYFQPPLTTVAQDFDLLGKRAVERLIALMAAPQLRIRELLPTRLIVRQSAWPVAAAEDRQQTLTQLKAL

VEKL

>lcl|NZ\_FO834906.1\_prot\_WP\_004176252.1\_2754 [locus\_tag=BN49\_RS15350] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004176252.1] [location=2826929..2827369] [gbkey=CDS]

MMVIEGKEAIARVDWQRVRTIIAEAGLNERDVQQLEQAFRQSTFCWFGYENGQLIAVARAISDCTWSSYL

ADVAIVPARQGQGYGQQLMLAIREQLLPFGKIFIYAVADKITFYQRFGFAMLTTGMVCASEEGMQKMQEQ

GYIRQP

>lcl|NZ\_FO834906.1\_prot\_WP\_004205985.1\_2755 [locus\_tag=BN49\_RS15355] [protein=DUF4177 domain-containing protein] [protein\_id=WP\_004205985.1] [location=complement(2827422..2827637)] [gbkey=CDS]

MKKECRVVIYKEGLLGSLFFGEAKADPDKMSQFLSSYTREGWEVKTMSVERRRTALFWSREAYLFVLERP

L

>lcl|NZ\_FO834906.1\_prot\_WP\_029602386.1\_2756 [gene=ftrA] [locus\_tag=BN49\_RS15360] [protein=transcriptional regulator FtrA] [protein\_id=WP\_029602386.1] [location=complement(2827606..2828703)] [gbkey=CDS]

MTENANILTTPSVTPSHHQVVALAYDGLCTFEFGVAVEIFGLPRPEMGDNWYQFAVAAVDEGPLCATGGI

RLMTDGGPELLAQADTIVVPGWRGVDAPVPEALCAALASAHARGCRIISICSGVFVLAAAGLLNGRQATT

HWRYTAALQSRFPQIQVVEDVLYVGDALLMTSAGSAAGIDLCLHLVREDFGSEAANVVARRLVVSPHRDG

GQAQQVLRPVARSRESLRLGQLFDYLHQHLAASHTVASLAQRAGMGTRTFLRRFEEATGKTPARWLLEER

LLRARQHLTESTMGIDQIAERCGFASAGTLRHHFRQHFALSPLQYRKQFTPSPIAKSSQPRTIDGHSKPV

ARRVDDEERVSGSDL

>lcl|NZ\_FO834906.1\_prot\_WP\_004183961.1\_2757 [locus\_tag=BN49\_RS15365] [protein=rhodanese-like domain-containing protein] [protein\_id=WP\_004183961.1] [location=2828771..2829169] [gbkey=CDS]

MSVVTQFPPATSAEAIRWFSHKLHLETDCADVHSAQRAGEVDFVLLHVVGSEEAFARRHLPGAQHLPHSQ

ITAERMAAWPADTLFVVYCAGPHCNGADVAALKLAELGRPVKMMLGGLTGWEDEGYAFASGD

>lcl|NZ\_FO834906.1\_prot\_WP\_004148338.1\_2758 [locus\_tag=BN49\_RS15370] [protein=cobalamin-independent methionine synthase II family protein] [protein\_id=WP\_004148338.1] [location=2829318..2830421] [gbkey=CDS]

MQRQQAPFRADIVGSFLRPDSIKQARQQLAEGIIDAAQLREIENNAIRHLVQQQCDCGLHVVTDGEFRRA

WWHFDFFDGLQGVERYDAEQGIQFNGVQTKAHGVRVTGKLAFGDHPMLEDFRYLKSISGDAQPKMTIPSP

SVLHFRGGRKDIDATVYPDLSDYFDDLATTWRDAIRAFYDAGCRYLQLDDTVWAYLCSDAQRQQVRERGE

DPDALARIYARVLNQALEGKPADLTVGLHVCRGNFRSTWISEGGYEPVAEVLFGSVNVDAFFLEYDNDRS

GDFAPLRFIRPGHQQVVLGLITTKNGELENPQGVKARLAEAAQYVPLEQICLSPQCGFASTEEGNALSED

QQWQKVRLVTSIAADVW

>lcl|NZ\_FO834906.1\_prot\_WP\_004176249.1\_2759 [gene=urtA] [locus\_tag=BN49\_RS15375] [protein=urea ABC transporter substrate-binding protein] [protein\_id=WP\_004176249.1] [location=2830593..2831864] [gbkey=CDS]

MQRRTLLKAFALSASVMAMGLSFQAYAADTIKVGIMHSLSGTMAISETPLKDVALMAIDDINAKGGVLGK

KLEPVVVDPASNWPLFAEKARQLLAQDKVAVVFGCWTSVSRKSVLPVFEELNGLLFYPVQYEGEEMSPNV

FYTGAAPNQQAIPAVEYLLSEDGGGAKRFFLLGTDYVYPRTTNKILRAFLHAKGIQDKDIEEVYTPFGYS

DYQTIVANIKKFAAGGKTAVVSTINGDSNVPFYKELANQGLKATDVPVVAFSVGEEELRGIDTKPLVGNL

AAWNYFESVDNPTNKAFVADYRAYAKAHKLPNADTVVTNDPMEATWVGLHMWAQAVTKAGTTDVDKVREA

MAGQTFNAPSGFTLTMDATNHHLHKPVMIGEIEGNGQFNVVWQTDKPVRAQPWSPWIPGNDKKPDHPVKT

VSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530306.1\_2760 [gene=urtB] [locus\_tag=BN49\_RS15380] [protein=urea ABC transporter permease subunit UrtB] [protein\_id=WP\_016530306.1] [location=2831926..2833500] [gbkey=CDS]

MNALRLMNVLALLLILLPWRAQAAEADDFVAASRSQQAQLLTQWAAAPQADRLPLLRALTTESLVMDDGK

HAFRTRQGGLQPLGAVAAPQGETRPVRLTNRLGNLAAGALASHLILSDNVTERASAARTLQREATPAMAA

LLQQRLQAETNDKVRGLLEVALARLQLAQPEASARLAAVTLLGHSADPETQALLIPFTDAQHEPDAAVRE

AASDSLQKIKHRLLLGDLLGQAFMGLSLGSVLLLAALGLAITYGLLGVINMAHGEMLMIGAYSCWLVQQA

LAQLAPQWLAFYPLVALPVAFLVTAGIGMALERTIIRHLYGRPLETLLATWGISLMLIQLVRMLFGAQNV

EVANPAWLSGGVQVLPNLILPWNRLAVLAFVLLVLCFTWLILNRTRLGMHVRAVTQNRAMAACCGVPTGR

VDMLAFGLGSGIAGLGGVALSQLGNVGPELGQGYIIDSFLVVVLGGVGQLAGSVAAAFGLGIFNKILEPQ

MGAVLGKILILVMIILFIQKRPQGLFALKGRVID

>lcl|NZ\_FO834906.1\_prot\_WP\_004151617.1\_2761 [gene=urtC] [locus\_tag=BN49\_RS15385] [protein=urea ABC transporter permease subunit UrtC] [protein\_id=WP\_004151617.1] [location=2833500..2834573] [gbkey=CDS]

MSQPITLTLAQRAPRPLRWLGILLVLGLLCMPFLALLPASHPLAVPSWLLTLSGKILCYAIVAVALDLVW

GYAGMLSLGHGIFFALGGYAMGMYLMRQAAGDGLPAFMSFLSWSELPWFWWGTQHFAWAMALVVLVPGLL

ALVFGWFAFRSKIKGVYFSIMTQALTYAGMLLFFRNETGFGGNNGFTGFTTLLGFPVTATGTRASLFMAT

VLLLLLTLWLGAALAQSKFGRILTAVRDAENRLMFCGYDPRGFKLLVWTLSAVLCGLAGALYVPQVGIIN

PSEMSPTNSIEAAIWVALGGRGTLIGPVLGAGLVNGAKSIFTVAMPEYWQLFLGLIFIIVTLFLPRGVMG

LLRRGDR

>lcl|NZ\_FO834906.1\_prot\_WP\_004190223.1\_2762 [gene=urtD] [locus\_tag=BN49\_RS15390] [protein=urea ABC transporter ATP-binding protein UrtD] [protein\_id=WP\_004190223.1] [location=2834573..2835370] [gbkey=CDS]

MQPDEGLFTRQLPGDRFREQTDPVLQLENINVSFDGFRALTDLSLAIGVGELRCVIGPNGAGKTTLMDVI

TGKTRPQSGKALYDQSVDLTTLDPVAIARQGIGRKFQKPTVFEALTVAENLALAMKGDKSVWASLRARMS

SEQDDRLNEVLRLLRLDGERYRQAGLLSHGQKQFLEIGMLLVQEPHLLLLDEPAAGMTDAETEYTAELFR

TLAGQHSLMVVEHDMGFVETIADRVTVLHQGQVLAEGSLREVQANEQVIEVYLGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004176246.1\_2763 [gene=urtE] [locus\_tag=BN49\_RS15395] [protein=urea ABC transporter ATP-binding subunit UrtE] [protein\_id=WP\_004176246.1] [location=2835380..2836078] [gbkey=CDS]

MLQVSQLHQYYGGSHILRGVDFSARQGEVTCLLGRNGVGKTTLLKCLMGLIPARSGEVRWQDQNITHRKP

HQRVQAGVAYVPQGREIFPRLTVEENLLMGLSRFPAREAQQVPEEIYQLFPVLRTMKQRRGGDLSGGQQQ

QLAIGRALASRPQLLILDEPTEGIQPSVIKEIGEVIRQLASRGDMAILLVEQFYDFAAGLADHYLVMSRG

AIVQQGKGGDMESDGVRAMVTI

>lcl|NZ\_FO834906.1\_prot\_WP\_002904389.1\_2764 [locus\_tag=BN49\_RS15400] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_002904389.1] [location=complement(2836114..2836596)] [gbkey=CDS]

MNSNNQVKQLRLQRAWSQEQLAEMAGLSVRTIQRIENGERPGLETLSALAAVFEVTVAEIGGEARREDAP

GQEASLDLRIEEAKARVHQESRFFRSLSVALVVCVLLAVLNRFTNPQYYWSGWVALIWGALLVVRGLRLF

VFGEWIKNWRQARLQRLLRK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530303.1\_2765 [gene=ydeE] [locus\_tag=BN49\_RS15405] [protein=efflux MFS transporter YdeE] [protein\_id=WP\_016530303.1] [location=complement(2836726..2837922)] [gbkey=CDS]

MITTLRRSTIALLASSLLLTIGRGATLPFMTIYLTRRFQLEVDVIGYALSLALVVGVLFSMGFGILADRF

DKKRYMVWSVLVFILGFSAIPLVNNAPLVVIFFALINCAYSVFSTVLKAWFADRLTAEKKARIFSLNYTI

LNIGWTVGPPIGTLLVMHSINLPFWLAAACAAFPLVFIQLFLQRDGAAAAQPGAAPWSPSVLLRDRALLW

FTCSGLLASFVGGAFASCLSQYVLVVASSEFAEKVVAVVLPVNAAVVVALQYAVGRRLSARNIRPLMTFG

TVCFVIGLVGFMFSGASLWAWGISAAIFTLGEVIYAPGEYMLIDHIAPPGMKASYFSAQSLGWLGAAFNP

MLTGLILTHLPHWSLFVILIVAIVAAWLMIFRGINARPWQPDSPLANA

>lcl|NZ\_FO834906.1\_prot\_WP\_004143566.1\_2766 [gene=eamA] [locus\_tag=BN49\_RS15410] [protein=O-acetylserine/cysteine exporter] [protein\_id=WP\_004143566.1] [location=2838117..2839016] [gbkey=CDS]

MTRKDGLLALLVVVVWGLNFVVIKLGLHNMPPLMLAGLRFMLVAFPALLFVARPAIPLRLLLGYGLTISF

GQFAFLFCAIGLGMPAGLASLVLQAQAFFTIILGAFVFGERLQGKQLAGIALAIFGVLVLVEGSLGGEHV

PLVGFMLTLAAALSWACGNIFNKKIMSQASRPPIMSLVVWSALIPVLPFMLASLLIDGPQTMLASLQHID

LLTILSLLYLAFIATIVGYGIWGSLLGRYETWRVAPLSLLVPVVGMASAALLLGETLSGLQLTGAVLIMA

GLYINVFGLRLVRPGMARG

>lcl|NZ\_FO834906.1\_prot\_WP\_002904394.1\_2767 [gene=marB] [locus\_tag=BN49\_RS15415] [protein=multiple antibiotic resistance protein MarB] [protein\_id=WP\_002904394.1] [location=complement(2839065..2839283)] [gbkey=CDS]

MKLFAAAAIVLLSLASSLSYAEQNTTPVRQNQRDTMIIPSEHNDSPFDFNHMAAGNDKSDELGVPYYQQH

DL

>lcl|NZ\_FO834906.1\_prot\_WP\_002904397.1\_2768 [gene=marA] [locus\_tag=BN49\_RS15420] [protein=MDR efflux pump AcrAB transcriptional activator MarA] [protein\_id=WP\_002904397.1] [location=complement(2839324..2839698)] [gbkey=CDS]

MSRRNNDAITIHSILSWIEDNLESPLSLEKVSERSGYSKWHLQRMFKKETGHSLGQYIRSRKLTEIAQKL

KQSNEPILYLAERYGFESQQTLTRTFKNYFDVPPHKYRITNVPGESRYLHPLNN

>lcl|NZ\_FO834906.1\_prot\_WP\_004143563.1\_2769 [gene=marR] [locus\_tag=BN49\_RS15425] [protein=multiple antibiotic resistance transcriptional regulator MarR] [protein\_id=WP\_004143563.1] [location=complement(2839719..2840153)] [gbkey=CDS]

MKSTSDLFNEMIPLGRLIQMVNQKKDRLLNDYLSPMDITATQFRVLCSIRCEVCITPVELKTVLSVDPGA

MTRMLDRLACKGWIERLPNPADKRGVLVQLTPDGAALCEQCHQVVGQKLHQELTKNLSADEVAMLEQLLK

KVLP

>lcl|NZ\_FO834906.1\_prot\_WP\_004217987.1\_2770 [locus\_tag=BN49\_RS31065] [protein=hypothetical protein] [protein\_id=WP\_004217987.1] [location=2840243..2840371] [gbkey=CDS]

MLKWKSTMWVTLYDFSNACYFFAEVIYQQAGVKFVEADILTE

>lcl|NZ\_FO834906.1\_prot\_WP\_002904403.1\_2771 [locus\_tag=BN49\_RS15435] [protein=MarC family NAAT transporter] [protein\_id=WP\_002904403.1] [location=2840415..2841083] [gbkey=CDS]

MFDLFKAIGLGLAVLLPLANPLTTVALFLGLAGNMNNAERNKQALMASVYVFAILMVSWYAGQVVMNTFG

ISIPGLRIAGGLIVAFIGFRMLFPQQKAHDSMEAKIKSEELQDEPTANIAFVPLAMPSTAGPGTIAMIIS

SASTVKHGVDFPEWVVLAAPPIIFLLLGVILWACLRSSGAIMRLVGKGGIEAISRLMGFLLVCMGVQFII

NGVLEIISTWHP

>lcl|NZ\_FO834906.1\_prot\_WP\_002904407.1\_2772 [locus\_tag=BN49\_RS15440] [protein=sugar transporter] [protein\_id=WP\_002904407.1] [location=complement(2841152..2842351)] [gbkey=CDS]

MTTNTVSRKVAWLRVVTLAIAAFIFNTTEFAPVGLLSDIADSFGMETAQVGMMLTIYAWVVALMSLPFML

LTSKVERRRLLIGLFILFIASHVLSFFAWNFDVLVISRIGIAFAHAVFWSITSALAIRMAPPGKRAQALS

LIATGTALAMVFGIPIGRIIGQYFGWRMTFLAIGLGALATLACLVKLLPTLPSEHSGSLKSLPVLFRRPA

LVSVYILTVVVVTAHYTAYSYIEPFVQTVAGLSGNFATVLLLILGGAGIIGSILFGKLGNQHASGLISLA

IALLLACLLLLLPASHNPQHLMLLSIFWGVAIMIIGLGMQVKVLASAPDATDVAMSLFSGIFNIGIGAGA

LVGSQVSLHLSMASVGYVGAIPALVALVWSLMIFRRWPVSLEDHQPHHS

>lcl|NZ\_FO834906.1\_prot\_WP\_004179766.1\_2773 [locus\_tag=BN49\_RS15445] [protein=PhzF family phenazine biosynthesis protein] [protein\_id=WP\_004179766.1] [location=2842553..2843347] [gbkey=CDS]

MQEIQFYLVDAFSDKNFGGNAAAVCPLSEWLADDVLLKMAQQHNQSETAFFVRTDEGYELRWFTTLAEIN

LCGHATLAAAHVIFEYLDHPSATILFSTRFVGELRVTRNGDWLTLDFPAWSTSPVENPPADLLTGLGLEA

AVEVREGRDYLVVLADRQQVEAVRPDMARLRTLGKMICVSAPDEEYDFVSRFFCPGEGVPEDPVTGSAHS

MLIPWWGEKLGKTTMMARQVSARGGDLRCQWQGDRVLISGQATTYMRGTVYLRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004179768.1\_2774 [locus\_tag=BN49\_RS15450] [protein=MFS transporter] [protein\_id=WP\_004179768.1] [location=complement(2843393..2844712)] [gbkey=CDS]

MNTTANTTRIRWWIAGLMWLAIAINYIDRTVLSAAAPHLIDELKLDPEMMGFIMAAFFWSYSLLQIPAGW

FADRFGQKKGLGLAVAWWSIATSMMGVATGFKSLLALRLALGVGEAAAYPSNAGIAARWFPDKERATVSG

LFDSASKFGGAIAMPLIVWMIYTFDWRLTFLIIGSVGILWVIAWYFIYAENPEEHKRISPSEVRIIRDGQ

KQHHGDKTVLPMKWYKLLRYRNIWAMCIGFFTINYTSYFFITWLPTYLVKEKGMDFIKMGMVAALPLLCG

MVIEVFAGWASDRLVHKKVLSLTATRKLFLTIGLLMALCIGFAPFTDSVFMTVFLLCVAKSGTTVAASQV

WALPGDVAPKNSVSIVAGLQNTVSNMGGAVGPIITGAIVAATGSFNWALIFSAILVVIGIINYLFLMGKI

EPINDKGGKSPVLNAAEQH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529129.1\_2775 [locus\_tag=BN49\_RS15455] [protein=phosphoglycerate dehydrogenase] [protein\_id=WP\_016529129.1] [location=complement(2844776..2845726)] [gbkey=CDS]

MKVICTSPSFAKYDDASISALKEADLELVMLPADASIEMLAQHLPDAIAMIVAFTDINESLLAKAPRLKI

VCKHGVGVDNIDLNATRQRKIFVTNVPDANKHAVADFAFGLILNTARQIYQAISETKAGNWPRIFATDVY

GKTLGIVGLGHIGKEVARRARGFNMRVLATDAWPDREFAQQHQIEYVSLDTLTAQSDFISLHTPLTPETE

NMFNAARLQQMKSGAFLINVSRGGIVDEQALYEALKSGHLAGAAADVFLEEPCATHPLFTLANFAPTSHI

AGYTDGAISNISARCVNNIITCVCRGERPENIMNSL

>lcl|NZ\_FO834906.1\_prot\_WP\_014907630.1\_2776 [locus\_tag=BN49\_RS15460] [protein=dihydrodipicolinate synthase family protein] [protein\_id=WP\_014907630.1] [location=complement(2845812..2846696)] [gbkey=CDS]

MRKAISGVLTAIVTPFTAEGALNLPALRQQVQRQLAAGNGIFCGGTNGEFFVLNEEEKIAIARTCVEEAA

GRAPVVAHIGEVSTRETRRLGQQIARLGVDAVSAITPWFVPLKQEELINHYTAIADALSVPLFLYNIPAR

TGNTIAPETARQLARHENIVGIKDSAGSYDSLKGFLDAVRDIDGFDVLNGPDSLIHQGFVDGCSACISGL

ANVAPAEINAIWSRFHAGDIAGSRQAQEQVTGLRTDLYKVAFSPAAVKKALQLMGHEVGDSRYAVQFSDH

QLQQIKNIINTYLH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529130.1\_2777 [locus\_tag=BN49\_RS15465] [protein=iron-containing alcohol dehydrogenase] [protein\_id=WP\_016529130.1] [location=complement(2846711..2847859)] [gbkey=CDS]

MATIHSTIISGAGASSALLPLLASKTSILLVTDKNVGALEATQAIHRLLAAEGREVEVIDSVPAEPNHHD

VTQIVSQLGASQPQMVVGIGGGSVLDVAKLLSVLLHPEAPSLTALLAGEQPQRRICSLLIPATAGTGSEA

TPNAILAIPEQQTKVGLISPVLLPDYVALLPELTTSMPPSIAASTGIDALCHLLECFTSTVANPVSDNAA

LIGLHKLVRHIERSVNQPQDLTAKLEMLWASWYGGAAINYAGTHLVHALSYPLGGTWHLPHGVANAILLA

PCMRVVRPHAVAKFAQVWDLIPDADRTLSAEEKSHALVAWLAALVKRLPLPDNLAALGVPQESISALSAA

AQNVKRLMNNAPCSVSREEIAAIYQTLYPEHA

>lcl|NZ\_FO834906.1\_prot\_WP\_032434503.1\_2778 [locus\_tag=BN49\_RS15470] [protein=four-carbon acid sugar kinase family protein] [protein\_id=WP\_032434503.1] [location=2848034..2849269] [gbkey=CDS]

MNDGNNRVLVLADDFTGANDAGVSLAEAGMSVEVAFTAGQPSTARALILNSDSRAMTAAAAADKVAALLR

GAATFVPHWQVKKIDSTLRGNPGGELEAMMAAQGCRMAVVAPAYPAAGRHTRDGRCYVHGVPLDQTEFAS

DPKTPVSRAEISEIIAMQSRLPCLTLNAGQLPAALATAGEEKRVLIVDAWEDSHLDQVIDAVAPHARETL

LVGSAGLCEALARRLRRNEQGPLLAVVGSMSEMAQRQVAALQVHSRVRVIEIDVEQAFSGSPKEEASRIA

GALREGQHCVVTTRPNHAVRHGIEARCRERGLSRAAYGEHICAWLADVTAQAVAQSSPGALYLSGGDVAI

AVAHALGATGFQIRGRVAECVPYGHFLGGRWSRPVMTKAGGFGTDTTLLHVVNFIEEKLSV

>lcl|NZ\_FO834906.1\_prot\_WP\_016532445.1\_2779 [locus\_tag=BN49\_RS15475] [protein=D-threonate 4-phosphate dehydrogenase] [protein\_id=WP\_016532445.1] [location=2849262..2850248] [gbkey=CDS]

MSKMIAVTMGDPAGIGPEIIIKSLAEGALSGAPVVVVGCAQTLRRILALNITPRAELRIINHPAEASFSP

ATINVIDEPLSDPQGLRPGEVQAQAGDLAFRCIRRATALALEGAVAAIATAPLNKEALHLAGHAYPGHTE

LLAHLTQTTDYAMVLYTEKLKVIHITTHISLRQFLDTLNQPRIETVIGVADRFLRRVGYPRPRIAVAGVN

PHAGENGLFGDEEIRIVAPAVAAMRAKGVEVTGPCPPDTVFMQCHEGMYDMVVAMYHDQGHIPLKLLGFY

DGVNITAGLPFIRTSADHGTAFDIAWTGKAKSESMATSIELAMHIAQE

>lcl|NZ\_FO834906.1\_prot\_WP\_002904489.1\_2780 [locus\_tag=BN49\_RS15480] [protein=DeoR/GlpR family DNA-binding transcription regulator] [protein\_id=WP\_002904489.1] [location=2850250..2851011] [gbkey=CDS]

MKGYNRLEQIMDFLKSHNLVTVDQLVAATNASPATIRRDLIKLDQEGVISRTHGGVTLNRFIPSQPTTLE

KAQRSPLEKQAIASAAAALVKAGDAIVLDAGTTMIELARQITHLPLRVITSDLHIALFLSEFKQIEVTII

GGRIDDSSQSCIGDHGRRLLQTIWPDLAFVSCNGWDLEKGITAPTEEKAALKRDLMANARRRILLADSSK

YGAWSLFNIAPLASLTDIVTDAHLPDKTREALETLSPQLIIAD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043270.1\_2781 [locus\_tag=BN49\_RS15485] [protein=L-lactate dehydrogenase] [protein\_id=WP\_046043270.1] [location=complement(2851026..2851970)] [gbkey=CDS]

MHTKARKVRIIGAGNVGASAAYALLNQSICEELILVDLNQQRAEAHAQDLSDAAAYLPGMMTISTREASD

CADVDIAVITVSSGALRPGQSRLDELTSTAKIVKSIVPTMMANGFNGIFLVATNPCDIITWQVWQLSSLP

RSQVLGTGVWLDTTRLRRLLAQELEIGAQSIDAFILGEHGDTQFPVWSHSSVYGTPIADLYQQRTGLPLD

REAMADKVRKLGFEIYAGKGCTEYGVAGTIAEICRNIFTGSHRALAVSCILDGEYGVSGAAAGVPAVLAQ

GGVKQIIELQLAGEEQAKFSQSIAVIKANIARLP

>lcl|NZ\_FO834906.1\_prot\_WP\_002904493.1\_2782 [locus\_tag=BN49\_RS15490] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002904493.1] [location=2852115..2852597] [gbkey=CDS]

MYTITDIAPTDAEFIALIAALDAWQETLYPAESNHLLDLSQLPPQTVIALAIRSPQGEAVGCGAIVLSEE

GFGEMKRVYIDPQHRGQQLGEKLLAALEAKARQRDCHTLRLETGIHQHAAIALYTRNGYQTRCAFAPYQP

DPLSVFMEKPLFADLRSAAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002904495.1\_2783 [locus\_tag=BN49\_RS15495] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002904495.1] [location=complement(2852551..2853429)] [gbkey=CDS]

MDLTQLEMFNAVASTGSITQAAQKVHRVPSNLTTRIRQLEADLGVELFIRENQRLRLSPAGHSFLRYSQQ

ILALVDEARMVVAGDEPQGLFSLGSLESTAAVRIPSTLAHFNQRYPKIHLALSTGPSGTMIDGVLEGALS

AAFVDGPLVHPGLEGLPVFPEEMMIVAPYGHAPITRASEVNGANVYAFRANCSYRRHFESWFHADRATPG

RIHEMESYHGMLACVIAGAGLALIPRSMLESMPGHQQVSAWPLAEEWRWLTTWLVWRRGAKTRQLEAFIA

LLNEDRQTVVSP

>lcl|NZ\_FO834906.1\_prot\_WP\_004179780.1\_2784 [gene=sad] [locus\_tag=BN49\_RS15500] [protein=succinate-semialdehyde dehydrogenase] [protein\_id=WP\_004179780.1] [location=2853531..2854919] [gbkey=CDS]

MMNLSATHAVSVNPTTGEVVSSLPWASEREVDAAIALAAAGYRQWRQTPLADRADALRRIGAALRARGEE

VAQMITLEMGKPIAQARGEVAKSANLCDWYAEHGPAMLATEATLVENNQAVIEYRPLGAILAVMPWNFPV

WQVMRGAVPILLAGNSYLLKHAPNVMGSARLLGEIFAAAGLPDGVFGWVNATNDGVSQIINDDRIAAVTV

TGSVRAGKAIGAQAGAALKKCVLELGGSDPFIVLNDADLDEAVKAAVTGRYQNSGQVCAASKRFILEAGI

AEAFTRKFVDAVAALKMGDPRDEQNYVGPMARFDLRDELHQQVTATLDEGATLLLGAEKIEGAGNYYAPT

VLGNVTAGMTGFRQELFGPVATLTTARDADHALALANDSEFGLSATVYTTDEAQAQRFARELECGGVFLN

GYCASDARVAFGGVKKSGFGRELSHFGLHEFCNAQTVWKDRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179782.1\_2785 [gene=glsB] [locus\_tag=BN49\_RS15505] [protein=glutaminase B] [protein\_id=WP\_004179782.1] [location=2855000..2855926] [gbkey=CDS]

MATVINNAMLEAILAEIRPLIGRGKVADYIPALASVSGDKLGIAISTVDGQHFAAGDAHERFSIQSISKV

LSLVVAMNHYQEEEIWQRVGKDPSGQPFNSLLQLEIEQGKPRNPFINAGALVVCDMLQSRLSAPRQRMLE

IVRRLSGVADIAYDPVVARSEFEHSARNAAIAWLMKSFGNFHNDVATVLQNYFHYCSLEMSCVELARTFL

FLADRGIAPHLDAPVIAPIQSRQVNALMMTSGMYQNAGEFAWRVGLPAKSGVGGGIVAIVPQEMAIAVWS

PELDDAGNSLAGVAMLEKLTQRMGRSVF

>lcl|NZ\_FO834906.1\_prot\_WP\_002904598.1\_2786 [locus\_tag=BN49\_RS15510] [protein=DUF4186 domain-containing protein] [protein\_id=WP\_002904598.1] [location=2855926..2856294] [gbkey=CDS]

MVDQDRLFARLARSTFRSRFRLGGKERQYCLDKGPEVIDRHAADFIRQRLAPAAPINDGKQTPMRGHPVF

IAQHATATCCRGCLEKWHAIPHGRALSEPEQDYIVQVIHRWLVLQMNAPSVR

>lcl|NZ\_FO834906.1\_prot\_WP\_004148352.1\_2787 [locus\_tag=BN49\_RS15515] [protein=sensor domain-containing diguanylate cyclase] [protein\_id=WP\_004148352.1] [location=2856409..2857833] [gbkey=CDS]

MSSLSIRSFTLFREEQPVRDALVLFTLTLLLHFLGAMLRLVQELSFFWPLNAVMAGIFARYVWLNRSYFY

AVCFAAMLVYDGLTSRWGMGFASLLINFSNIVFIVTLAQLVLWDKRRADSMPGPINALNLFCFCLLAALL

CAAVGALGSVDVERATFVPQLADWFSEQFSTAVLILPFILTLTLPSALSGFRFRQLLPVLALVLSIALGV

AVGGAGSITFPLPALIWCAVRYPLPLTCLLTFLTGIGEILLVANSLIHFSPDARMQPWQLFSTRLGIAAM

LISPVIVASSVEAINTLVKQLALRADFDFQTRVYSRSGLSEALKRQTLPADKLLTVMVLDIDGFKRVNDA

LGHEGGDCVLTQFAQQVRQLVGEQGMVARIGGEEFAVAAVVDSAQQGYLLAEKIRHGVESQPFGLGQNPI

HLTISLGLETREVGHARITELFNQLLLAADDEMVKAKQSGRNQICMPTLTESAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002904601.1\_2788 [locus\_tag=BN49\_RS15520] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002904601.1] [location=2857911..2858441] [gbkey=CDS]

MTTSFSLRTLSRDDILHHLPALSEILASCVNGGASVSFMLPFAPQTAITFWQRTADSVAAGERIVLAAFD

AEERPVGTVQLITSQPENQPHRADVAKLLVHQNVRRQGIAQALMSELERIARRERKTVLVLDTATGSGAE

QFYARCGWEKVGEIPRYALMPDGEMTATSLFYKFLP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529709.1\_2789 [locus\_tag=BN49\_RS15525] [protein=tagaturonate reductase] [protein\_id=WP\_016529709.1] [location=2858555..2860006] [gbkey=CDS]

MKTLNRRDFPGAQYPDRIIQFGEGNFLRAFVDWQIDLLNEHTDLNAGIVVVRPIATDFPPSLNTQDGLYT

TIIRGLNEQGEAVSDARLIRSVNREISAYADFDAFLRLAHNPEMRFVFSNTTEAGISYHAGDRFDDAPPV

SYPAKLTRLLFERYQHFAGAADKGWVIIPCELIDYNGEALQALVLRYASEWELPQAFITWLTSANTFCST

LVDRIVTGYPRDEVAALEAQTGYKDAFLDTAEHFYLFVIQGPASLEAELRLDKLPLNVRIVDDIKPYKER

KVAILNGAHTALVPVAFLAGIDTVGEAMNDAEICAFVEKAIYDEIIPVLDLPRDELVSFASAVTGRFRNP

YIKHQLLSIALNGMTKYRTRILPQLLAGQKAHGALPPRLTFALAALIAFYRGERDGESYPVQDDADWISR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002904604.1\_2790 [locus\_tag=BN49\_RS15530] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002904604.1] [location=2860260..2860706] [gbkey=CDS]

MVIDIREVRPHDKAEWLQLWQGYTRFYGSPQPEEVTECTWQRMLDVNSSVLGRVAVVDDAVVGFAICVLH

EGTWVTTPICYLEDLFVDPAFRGQGIARTMIKSLQSEGADKGWSRLYWHTRRDNPARHLYDEFTPADDYV

RYRITLES

>lcl|NZ\_FO834906.1\_prot\_2791 [locus\_tag=BN49\_RS15535] [protein=tautomerase family protein] [pseudo=true] [partial=5'] [location=complement(2860917..>2861102)] [gbkey=CDS]

FVLFHIFAGKPRNRAQKQGLYRRLCARLDDEMAVSPQDVMVVIQFNQLEDWSFSPGKMADE

>lcl|NZ\_FO834906.1\_prot\_2792 [locus\_tag=BN49\_RS31460] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=<2861249..2861344] [gbkey=CDS]

MI\*SVITGVPYLNPMIISDDELAELLIKLMR

>lcl|NZ\_FO834906.1\_prot\_WP\_002904612.1\_2793 [locus\_tag=BN49\_RS15540] [protein=hypothetical protein] [protein\_id=WP\_002904612.1] [location=2861349..2861543] [gbkey=CDS]

MDFLKRWLKEEFILFLWGWGIVLLIIIFSMIAVSLFPDIAINLIGLFVLLIIGFHVVVWFKVKN

>lcl|NZ\_FO834906.1\_prot\_WP\_016531260.1\_2794 [gene=hcp] [locus\_tag=BN49\_RS15545] [protein=type VI secretion system tube protein Hcp] [protein\_id=WP\_016531260.1] [location=2861562..2862044] [gbkey=CDS]

MSNPAYLWLTDENDSPIIGSCLMPTRTGSIELRAVNHHVWLPTDNNTGKLTGTRLHTPVKIEKEFDRTTP

LLFRALCEGRTLRSATLKMYRINEAGLEVEYFNIAMANIKITAITPNLHPAGMTSTHLEDIDFRYETITW

IYTEGNIMYRDSWNDRCCAW

>lcl|NZ\_FO834906.1\_prot\_WP\_046043276.1\_2795 [locus\_tag=BN49\_RS15550] [protein=tautomerase family protein] [protein\_id=WP\_046043276.1] [location=complement(2862093..2862473)] [gbkey=CDS]

MPLTRISLGTAWRPAEFAQLSALFHECLVAEFDVPSADRFQFIERAADEQRIYDPRYLSEGRSARFVLFH

IFAGKPRCRAQKQGLYRRLCARLDDEMAVSPQDVMVVIQFNQLEDWSFSAGKMADE

>lcl|NZ\_FO834906.1\_prot\_WP\_004143517.1\_2796 [locus\_tag=BN49\_RS15555] [protein=carboxymuconolactone decarboxylase family protein] [protein\_id=WP\_004143517.1] [location=complement(2862464..2862784)] [gbkey=CDS]

MSTPPVDRRTLAAIAPKLAELTETVLFGDIWARSELSPRERSLITLSALTAQGKTEQLPWHIALGYQNGL

SREEIVELFTHLAFYAGWPAAASALTCLNAQEASCP

>lcl|NZ\_FO834906.1\_prot\_WP\_016528935.1\_2797 [gene=tam] [locus\_tag=BN49\_RS15560] [protein=trans-aconitate 2-methyltransferase] [protein\_id=WP\_016528935.1] [location=complement(2862945..2863706)] [gbkey=CDS]

MADWNPSLYLQFDAERTRPAADLLSRIAHLQVEHAVDLGCGPGNSTRLLRAAWPLATIVGIDNSPAMLVQ

AAQALPDCEFIDADIARWRPAQPPDVIYANASLQWLTDHETLFPHLVNQLADNGTLAVQMPDNWQEPSHT

LMRQVASEMGLPDRGRQPLLPPAAWYDLLSRQGCEVDIWRTTYFHPLASHQAIVDWLQGTGLRPYMAGLD

EQAGSAFLTRYLALLAAHYPLQCNGKVLLRFPRLFIVARKIAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002904624.1\_2798 [locus\_tag=BN49\_RS15565] [protein=hypothetical protein] [protein\_id=WP\_002904624.1] [location=complement(2863915..2864205)] [gbkey=CDS]

MHQSFNQRVHFYYCVLVALKMHGKSKKAGGIRGKNNFLLKWLRRAQDNNIFPPDITSEIEWLRGKIIQAG

YDTDLEPMLDFVYATASRAEALKNAE

>lcl|NZ\_FO834906.1\_prot\_WP\_042937467.1\_2799 [locus\_tag=BN49\_RS15570] [protein=MFS transporter] [protein\_id=WP\_042937467.1] [location=complement(2864434..2865621)] [gbkey=CDS]

MSTSVSTTQLNLRIISIVVFTCICYLSIGLPLAVLPGYIHYQLGYSTFVAGIVISLQYISTLISRPHAGR

YTDIWGPKKVVSLGIVCCLLSGAFTLLAVVLQATPMLAIAALLAGRVFLGVGESFTATGATLWGIKTVGA

IHTSRVISWNGVATYVAMAVGAPLGVTLNHYFGISGFATVVVLVAAIGLLFARTRQDVKVTAGARAPFHA

VVRKIWPYGLGLAFGTVGFGVIATFITLYFAAHSWQGAAFTLSLFSVGFICVRLVLGNTITRFGGVPVSL

ACFIIESLGLLLIWLAPSAWMAGVGAFLTGSGFSLVFPALGVEAVKQVEEQNQGTALGTYSAFLDLALGL

TGPLAGWVAGFYDLATLYLLAAIVVALAFLLIFRVHRQQQLVARE

>lcl|NZ\_FO834906.1\_prot\_WP\_004213413.1\_2800 [locus\_tag=BN49\_RS15575] [protein=prolyl endopeptidase] [protein\_id=WP\_004213413.1] [location=complement(2865777..2866199)] [gbkey=CDS]

MSFCHMRIARPVSELDTTASMYCAGLGLEQLGSFTDHEGFSGIMLGAPEAGWHLEFTHCRHHPVTPSPGD

EDLLVLYYPQQAAWEAQCAAMDAAGFLRVTAFNPYWEVNGVTFVDRDGYRTVLQNRAWGMVCDSSGMAAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176218.1\_2801 [locus\_tag=BN49\_RS15580] [protein=YbfB/YjiJ family MFS transporter] [protein\_id=WP\_004176218.1] [location=2866406..2867563] [gbkey=CDS]

MNNQSRQALWLALAGSIVLMIGMGYGRFAFTGVLPLMLNEGLLTLHEGNLAASANYAGYLVGALLLARVQ

PGAATRLSIISAGLTIASLALLAWVSSPWTIITLRAVAGALSAITLIAGSLWLLEHMGHHHGAPLLYAGV

GLGIFISAEGIALGHALSLTSQQIWLLSALCAGLLLALAIRWLLTPPAALVRVSHVETSSPASGSDTRRA

AWRLLMVYGLAGFGYIITATYLPLFLSGSLQSVDPVHLWALFGLAAAPSCLIWHKLVLKWGYRQALTRNL

LVQALGVILPACSASLLFCVLSALLVGFTFMGTVTIALPKAKSLSHQVSFNMIAAMTALYGVGQIAGPLI

AGALYQIAASFNPALYAAALALLIAAGLVFTERQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004143508.1\_2802 [locus\_tag=BN49\_RS15585] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004143508.1] [location=complement(2867560..2868405)] [gbkey=CDS]

MNHSTLEIFIQVAETQSVTQAAKRLGRAQSNITTRIQQLEEELAVELFVRGNKKMVLSPAGVQFLSYARR

ILSLAEEAKQALHPTTPGGSLRLGAMEATAASRLPPLLTRFQQQCPQVDITLITQPTRQLTEGVLTAALD

AALVCLPPGADGQPACPAELAFTPVFYETLMLVRPQTPGPLRFAAFASGCSYRALGERWLAEQQAAVEVH

EVNSYHSMLACVASGRYACLLPQSVLSLMTLPENCLSEPLCEATTQLIWRSGLSAPALSEWRKLLQSVAI

G

>lcl|NZ\_FO834906.1\_prot\_WP\_042941527.1\_2803 [locus\_tag=BN49\_RS15590] [protein=nitronate monooxygenase] [protein\_id=WP\_042941527.1] [location=2868495..2869553] [gbkey=CDS]

MSNPLLSLLDIDYPLIQAPMAGVSTPALAAAVSNAGALGSLGLGASTVAQAEAMIVATRQLTDRPFNVNL

FCHAPPRRDARREADWATTLRPHFARYGSTPPDSLSEIYQTFIGHAPMLELLLDISPAVVSFHFGLPEGE

TIQRLRRQGIVTLATATSLLEALLIEQQGIDVVVAQGYEAGGHRGIFAPQAPDAQLSTFTLVQLLRRRLT

IPVVAAGGIMDGAGIASVMQLGAQGVQLGTAFLLCPESAADAGYRAAIHNSLDGRTVLTSAISGRPARCL

ANAFCALGEGYPASAVPDYPLAYDIGKALAAAAKAQGVHEYGAHWAGQGVGLIRECDAATLVRQLAAESG

WN

>lcl|NZ\_FO834906.1\_prot\_WP\_004217626.1\_2804 [locus\_tag=BN49\_RS15595] [protein=ABC transporter permease] [protein\_id=WP\_004217626.1] [location=complement(2869564..2870223)] [gbkey=CDS]

MSWEDLWPLLLDGTLDTLYMVGLAALFTVLIGLPTGVLLFISRANGLAPMPKLNALLGAVINIGRSLPFI

VLLIALIPFTRLIVGTTLGSTAAIVPVTIGAFPFFARLTENALDEVDYGRIEAILSMGGNVWHVIFKSLL

PEALPTLLAGITLTIVMLIGFSSMAGVIGGGGLGDLAIRYGYQRFNNEVMFGTVLILVAMVQGVQMAGDR

LVRSLAHRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530805.1\_2805 [locus\_tag=BN49\_RS15600] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_016530805.1] [location=complement(2870220..2871011)] [gbkey=CDS]

MITIEGLSKTYAGTGRPALNDIALQIPKGAIYGILGRSGAGKSTLIRCLNLLERPTSGRILVNGQDITQL

NKPALRDYRLRTGMIFQHFNLLHARTVADNVAVPLEIAGVPRAAREARVRELLALVDLSEKAAAFPSQLS

GGQKQRVGIARALAARPEVLLCDEATSALDPETTASVLALLADINQRLNLTIVLITHQLEVVKTICDHAA

LLEQGEIVESGKLADLLVTPWSRLRQSLLHDPQAEQEFLTRHGVQGRPLCGVA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530804.1\_2806 [locus\_tag=BN49\_RS15605] [protein=MetQ/NlpA family ABC transporter substrate-binding protein] [protein\_id=WP\_016530804.1] [location=complement(2871008..2871814)] [gbkey=CDS]

MKYAAFKLAGVALSLSLAWTSAQAAALRVAADPVPHAEILNYIKKIDPSLDLKVVELTSGVNANELLASG

DVDANYFQHVPYLKDQEKALGKTFTVAATVHIEPLGIYSHKHKNFSSLPENATVAVPNNTTNLSRALFLL

QAQKLIKLDPKFTDPATTLATPKDIVENPKHLKILEIESPQIPRSLDDVDLAVINGNYALEAGLVPAKDA

LGLESAEHNPYANILVTTPALANDPRIKALAKDLTSPQVAEFIRKTYNGSVIPVAPQS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530803.1\_2807 [locus\_tag=BN49\_RS15610] [protein=isopenicillin N synthase family oxygenase] [protein\_id=WP\_016530803.1] [location=complement(2871838..2872866)] [gbkey=CDS]

MNATTLPILDLARYADPADKAAFLADLRHAARDIGFFYLINHGVDDALQYEVQRQSQRFFALDEAQKQQV

AMIHSPHFRGYNRAASELTRGQPDWREQFDIGAERPALTLSDDAPRWQRLQGPNLWPAALPSLKPVLLHW

QQQMTQVGIRLLRAFAEALQLPENAFDRLYGEKPNEHIKLIRYPGQQETQSSQGVGAHNDSGFLSFLLQD

EQKGLQVEVAPGEWIDAVPLAGSFVVNIGELLELATNGYLRATVHRVVSPPAQQQRLSIAFFLGAQLDAV

VPVYTLPPELAREARGPDSDPHNPLLRDVGWNYLKGRLRSHPDVAERYYQDVFRERAEQLIV

>lcl|NZ\_FO834906.1\_prot\_2808 [locus\_tag=BN49\_RS29140] [protein=VF530 family protein] [pseudo=true] [location=2873149..2873412] [gbkey=CDS]

MHSSKDLLHGVTLEALLNALVARYGWAEMAR\*VNINCFKSDPSIKSSLKFLRRTPWARKEVEAMYLASLD

DDAPVEKADPWANWQKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002904646.1\_2809 [locus\_tag=BN49\_RS15615] [protein=cupin] [protein\_id=WP\_002904646.1] [location=2873434..2873745] [gbkey=CDS]

MQSWSSKDFTADRAWGALDIANFSGTTVRLHWTDQPYIWHINDGQEVFAVMDGQVAMHVKVDGEEQIIML

NAGDIFYAGVGCEHVAHPQGAARILVIEKEGSV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529433.1\_2810 [locus\_tag=BN49\_RS15620] [protein=VOC family protein] [protein\_id=WP\_016529433.1] [location=2873922..2874677] [gbkey=CDS]

MATLQWDHAVQFVNQPEAAIQTFADQQLRAVAGGRHPGWGTRNALSYFGLTYIEFLAIADPDELRAATDK

FLLSRDAARLLPENEALFRVALRSDDIDATHNQLRRTGVTVSPIVDGQRNDPQGNIIRWRIFTIDGDTAG

LVYPFVLQWGEDDATRLTRLRAQRLDVPHPLGDITLEQAVFEVVNPQAVRDRWQALLGFPPLGEQGLDVG

GQQFIFREGAANQLTELVFRVANPALKGQRFRVGNGVYRFT

>lcl|NZ\_FO834906.1\_prot\_WP\_004190181.1\_2811 [locus\_tag=BN49\_RS15625] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004190181.1] [location=complement(2874687..2875631)] [gbkey=CDS]

MSQPAIDLTSELLRGMRLSGVNYRRIETARPFGVGFSAVAGKAQFHFISRGPVLLRMASGEQFTLESGDA

LFIPNGDGHALLSDPQATVVNVAQLPSETVCSTVSCINAGDQPDCPERAVIFSGCMDFELGGMQPLVKAM

PEVMRVSSLLNTWPEIQPLLVAMERESLTRQAGYAGILARLADVVAALIVRGWVACGCGNATGWVQVLRD

PRLAKAIYAMHQRPGVNWKVEDLAREAGLSRSLFAERFLAATGTTPARYLTELRMRLAVQYITHEGQALE

KVAFSLGYQSLAAFSRAFKRITGQPPGALRATAR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529021.1\_2812 [locus\_tag=BN49\_RS15630] [protein=MFS transporter] [protein\_id=WP\_016529021.1] [location=2875737..2876975] [gbkey=CDS]

MSSCIAADASLSSAKPAWRAVYALALGVFGLIVAEFLPASLLTPMASSLGVSEGMAGQAVTATALVALVT

GLLIATATRNIDRRWVLMFFSILQIVSSLMVAFADSLAFLLLGRLLLGIAIGGFWAMSTATAMRLVPAAH

VPKALAIIFSAVSVATVVAAPLGSYLGELIGWRNVFILCAIPSLLALLWQLWVLPSMRPESVGTFSTLFR

VLRRPGMLGGMLATILIFSGHFAFFTYLRPFLETVAQASVEGVSLILLGFGIANFIGTSVASYLLNRSLR

LTLALVPLMMSVLALLMVTFGHLTVLDGLLVALWGFAFGLVPVAWSTWLATTVPDEAESAGGLLVASIQL

AISAGAAGGGAVFDLRGASGVFTGSGLLLLSAMVIVFAAVRVKPVARADQPVTGRLSREIDN

>lcl|NZ\_FO834906.1\_prot\_WP\_032414905.1\_2813 [gene=hpxE] [locus\_tag=BN49\_RS15635] [protein=molybdenum cofactor-independent xanthine hydroxylase subunit HpxE] [protein\_id=WP\_032414905.1] [location=complement(2876952..2877935)] [gbkey=CDS]

MRDILPVVVDGLWRQGAKNLAVSLVSAEGQPLPAWTPGAHIDLHLPCGLIRQYSLTGSPAEQDRYLLCIA

RESQSRGGSRYIHDTLRPGQPLMISAPRNHFPLHEGGHVVLLAAGIGITPLLAMAHARAASGASFTLHYY

VSRAQEAAFATEIARQLSGGICQIHCSDEGQSPRQRLAQDLGAPDADTRVYFCGPPGFMARVRDTARAVG

WEEAQLHSEAFQPPAPTAAASASAADGTFTITLASTGERWPVPGDKTIAQVLQEHGVAVPLSCEMGICGA

CLTPVREGTVDHRDTVQSEAEKQAAEQHIALCCSRSLSANLVIDLAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002904779.1\_2814 [gene=hpxD] [locus\_tag=BN49\_RS15640] [protein=molybdenum cofactor-independent xanthine hydroxylase subunit HpxD] [protein\_id=WP\_002904779.1] [location=complement(2877947..2878984)] [gbkey=CDS]

MKTTTPTPPAHCTFDPEDWLRLARCWHPVARACDIAGAPVKATLLDEQLVIYRIKGQVVVARDVCPHRGV

PLTLGFHEEEGIVCPYHGLRFGEDGRCNRIPSSPGQPIPAKLHLTSFAVEERYGLIWTCLACDPDNPPPL

PTMPHWDDAGFQQINCPAFEVKGFAGRQVEGFLDVAHFAWIHTDTFADPDNQQVPDYTPQETPFGFVADY

WSSVGNYPASSDFRAPEGFQWLRHFEMHLPFTATLTIHFPADARLVIMNAASPVSSRVTRMFAPIARNFD

LHVPVEDVHAFNLRVFEEDRLMVETQRPERLPLDLTLEAHIPADRSSIAYRRGLKKMGFGDFFLV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529218.1\_2815 [gene=hpxR] [locus\_tag=BN49\_RS15645] [protein=LysR family hpxDE operon transcriptional regulator HpxR] [protein\_id=WP\_016529218.1] [location=2879110..2880033] [gbkey=CDS]

MSPFSRFAHYFIAVARCGSLRRAAEQLHISASAINRQILQAEEAFGTPLFERLPEGLRMTTAGELLYDNL

LRWQKEFRQTRQKFDELQGMKRGSVSVGMVQALAEGGFAAALAEIIASWPWLELDLQVADSHTVSQKVRQ

ADLDVGLSLDPQGQAGLSVLAFAELEVGIVMRPDHPLAGAKALSLGELSLERHIVPGAPLIVHERVALLY

RHHDFAPENTISCNDIRLIKSLVLRGSGVTLLSLLDVLDEVQRGQLAFVPLRSTLLRPLTLALCTAPSRQ

LSRPAQMAIQTLSAVIESMATVSPAAR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043281.1\_2816 [gene=hpxO] [locus\_tag=BN49\_RS15650] [protein=FAD-dependent urate hydroxylase HpxO] [protein\_id=WP\_046043281.1] [location=complement(2880014..2881168)] [gbkey=CDS]

MKAIVIGAGIGGLSAAVALKQSGIDCDVYEAVKEIKPVGAAISVWPNGVKCMAHLGMGDIMETFGGPLRR

MAYRDFRSGENMTQFSLAPLIERTGSRPCPVSRAELQREMLDYWGRDSVQFGKRVTRCEEDADGVTVWFT

DGSSASGDLLIAADGSHSALRPWVLGFTPQRRYAGYVNWNGLVEIDEALAPGDQWTTFVGEGKRVSLMPV

SAGRFYFFFDVPLPAGLAEERDTLRADLSRYFAGWAPPVQKLIAALDPQTTNRIEIHDIEPFSRLVRGRV

ALLGDAGHSTTPDIGQGGCAAMEDAVVLGAVFRQTRDIAAALREYEAQRCDRVRDLVLKARKRCDITHGK

DMQLTEAWYQELREETGERIINGMCDTILSGPLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004176204.1\_2817 [locus\_tag=BN49\_RS15655] [protein=purine permease] [protein\_id=WP\_004176204.1] [location=2881514..2882893] [gbkey=CDS]

MSDEHHSGLLYGLEQRIPPLPAFFSALQHVLAGLVGIITPPLIIGATLGLGDWLPYLISMSLLASGIGTF

LQSNRVWGIGAGMICMQGTSFAFLGVTVAGGMWVKAQGGGPQDMMAMLFGVNFVAALVPVIVSRFIEPLK

KIFTPIITGSVIALIGISLIKVSVINWCGGEKAEDFASMSNIALGAGTLGVIVLLSCAKNRWLRLSSVVV

GIAVGCIAAGLSGQFHLHSLGDTLFRLPTLFPFGFQFNSAIFLPVALVSLVCILEAVGDLTANSLISQQS

VDDRAFRNRLKGGILADGVSCMVAAMLCAFPNTTFAQNNGVIQMTGVASRYVGRYIGVILILLGLFPPVG

ELLRQIPAPVLGGATMVMFGCVVAAGIRIITQTPLSRRDVLIVGLAFGAGLGVESVPAFLSHFPPMVGDL

FGSAATSGGLVAIALNLILPQEQAATKTIRSQDDRAESV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043283.1\_2818 [gene=uraD] [locus\_tag=BN49\_RS15660] [protein=2-oxo-4-hydroxy-4-carboxy-5-ureidoimidazoline decarboxylase] [protein\_id=WP\_046043283.1] [location=2882871..2883371] [gbkey=CDS]

MIALSQFNSLSKDEAAGLLAPCVAIPAWGEMLVSLRPFASRHTLLQTAREAMANWGEDELNAALSAHPRI

GEKPTGSQAHAALSRQEQSAVDSENERLAQALREGNARYESRFGRVFLIRAKGRSGDEMLQALTRRLQHT

ADEEVAEALAQLREITMLRLEGVIGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002904788.1\_2819 [gene=uraH] [locus\_tag=BN49\_RS15665] [protein=hydroxyisourate hydrolase] [protein\_id=WP\_002904788.1] [location=2883368..2883694] [gbkey=CDS]

MSTLSTHILDISTGTPAEGVTVSLSREGETLANLVTNAQGRIATFSAAPLPAGRYCLTAETGAWFARAGR

ESVFTRAQIDFVIGEAAEDHFHLPFLIAPGGWSTYRGS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176198.1\_2820 [gene=hipB] [locus\_tag=BN49\_RS15670] [protein=type II toxin-antitoxin system antitoxin HipB] [protein\_id=WP\_004176198.1] [location=2883987..2884253] [gbkey=CDS]

MNSPQIYSPVQLANYLKLLRQQNHWTQDALARRIGIKQATLSNFENHPDKTTLTTLFKILQSLGVVMMLN

AKAAETAPAPDNNTDLDW

>lcl|NZ\_FO834906.1\_prot\_WP\_016529318.1\_2821 [locus\_tag=BN49\_RS15675] [protein=type II toxin-antitoxin system HipA family toxin] [protein\_id=WP\_016529318.1] [location=2884253..2885575] [gbkey=CDS]

MATLTTWMNNVRVGTLTRQANGAHSFRYDEEWLRSPRARPLSLSLPLQYGNITADAVYHYFDNLLPDSPQ

VRDRIVRRYQARSKQPFDLLAEVGRDSVGAVTLLPPGEEAHLEGLRWQTLDEAQLTALLTAYQSDIPLGM

ITGQDDFRISVAGAQEKTALLRMGEQWCIPQGATPTTHIIKLPIGEIKQPNATLDLRESVDNEFLCLALA

RELGLAVPEAEIITTPRIRALAVTRFDRRWAQEGRVLLRLPQEDLCQAFGLPSAMKYESDGGPGIAAIMT

FLLGSSEALKDRYDFMKFMVFQWLTGATDGHAKNFSIYLLPGGSYRLTPFYDIISAFPVLGGTGLHLRDL

KLSMGLNATKGRKTEINAIYPRHFLATAKAVNFPREQMLAILQEFAGHVPQAIESARRTLPADFSSHVWQ

AITENMLKLHARLQQGLQAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002904794.1\_2822 [locus\_tag=BN49\_RS15680] [protein=glycoside hydrolase family 10 protein] [protein\_id=WP\_002904794.1] [location=complement(2885592..2886884)] [gbkey=CDS]

MALAGAALIAAGMLFSCTSKAPKSLVTPPNAAAVKAGQAHREPVRGVWLTTVSRLDWPPVGSIIASTPES

RITQQKLALIAKLDNLQRLGINTVFFQVKPDGTALWRSDILPWSDMLTGKIGEYPGYDPLQFMLDEAHKR

GMKVHAWFNPYRVSVNTKPSTIAELNNTLTQVPASVFVLHRNWIRTASDRFVLDPGIPEARDWITSIVAE

VVQNYPIDGVQFDDYFYTETASSPLNDNETFRRYGQGYASKGDWRRHNTQQLIAQVSTTIKKLNPNVEFG

VSPAGVWRNRSHDPAGSDTRGAAAYDESYADTRSWVQQGLLDYIAPQIYWPFARDAARYDVLANWWAEVV

KPTHTRLYIGVALYKVGEPSKNEPDWTVDGGVPELKKQLDLNETLPQIQGTILFRENNLNQPQTRQAVNY

LRSRWGQPQS

>lcl|NZ\_FO834906.1\_prot\_WP\_009308876.1\_2823 [locus\_tag=BN49\_RS15685] [protein=type 1 fimbrial protein] [protein\_id=WP\_009308876.1] [location=complement(2887026..2888030)] [gbkey=CDS]

MSFLTLLRRVAMTLLFILLPAASGWACTPVFVRGQASTLRLNVGQLTVPADARPGTPLYHKSFAWNRLSD

GGEQWIRCADDPHGLSPLLLDSLLSGGVTRPTVYQTNLAGIGVRVSLRAIGGYGGFPDRPTPSPFSQRVD

NPAALPDAVWKLGYFRLTIELIKTGPAATPGELEYHSERFLMAEHTPLAALDLTGRISTAGCSVNDATPA

LIKLPAAMLDHFGGVGKTTGDTPFALQLDCNSAVTVSLRVDGAEPFSARGHGVLRNDATDDRAQGIGVQL

LYHRQPVVLNHEMTLGSASAGRFTLPLTARYYQTRSRITAGQVSAVATYTLHYD

>lcl|NZ\_FO834906.1\_prot\_2824 [locus\_tag=BN49\_RS15690] [protein=fimbrial biogenesis outer membrane usher protein] [pseudo=true] [location=complement(2888018..2890519)] [gbkey=CDS]

MRHGPAHTVTIVSLSILLGGQSALLHAQATFNMDLLEKNDHLPAVDLQRFNQQAGQPPGAYPVSWQVNGV

TLDARKTVTFRQNDRGQLTPCLKPEDLLQAGVNPAVLS\*APGATSRSCPELNALLSGSTVNFDFAHQRLV

MTIPQALMTHRARDNVPSALWDEGISAFQSNYRYSGASQRTREGSTERDNYLMLKSGVNVGAWRLRASNS

LTANSDDKPQWTTSGAWLERDLTRWQSELTLGDTFTSGDVFDAVQFQGISLASSDAMLPDSQKGFAPTIR

GIARTNAQVTVRQNGYVLYQTYVTPGAFVIDDLYPTASSGNLEVAVKESDGEIRRFTQPYASVTSMQREG

SLKYNLVAGRYHSDDASQRPLMMQLSLMRGFAHNLTLFGGLQSAAQYHNLSLGAGQGLGEAGALSLQLLN

ARDRHQQDPIDGRAWQLQYSKGFDRLGTQLTFTGWRYSHQRYATLSEAFSSPGSDDDLQDSDNKKATLQI

TASQSLPYDITLYLSLDQDSYWSGGATQRTANMGISSQVHGIAWSLSYSDSRSSHGDEEDDEPHSDKVVT

LSLSVPLSHLLPGSYAGYTLTSSRHSVGSQMVSLNGTLLDNHALSYAVSQTRDRQNGSSGSLTAGYSSGR

GDLNLGYSHDSQAARLNYGASGGILIHRHGVVFTPEMNGAVVLIDAGGAGGVTLANQKTIATNGDGYAVL

PFATAYHRNDVSLDSHSLPENVDLANSTVTLVPTKDAVVLARFHTHVGYKALFTLQSRGQPLPFGSEVRA

KDTNSIVASEGQVYLAGLAPKGTLYAQWGPGPQQRCSARYDLTPTLAQTPHPLILQQTLSCPF

>lcl|NZ\_FO834906.1\_prot\_WP\_025861922.1\_2825 [locus\_tag=BN49\_RS15700] [protein=molecular chaperone] [protein\_id=WP\_025861922.1] [location=complement(2890535..2891230)] [gbkey=CDS]

MQCYKAAFILSLLFCPFLASAAGVAIAGTRVIYNEQSHEADITVKNTNPHDPVLIQSWVDDLADNNKSPF

IVTPPLFRLDAGDSNDLRVLLTSAQLPNDRESLFTLNIKVIPANTAPAGENILQFAIKNQLKLIYRPAGL

PGSALDAAQHLRWRISGNHLQAENASPYYVTITTLTCAGQNQKTPLERSVIAPHSREEYALPGEACAREV

SWRILDDFGAVQTFSAPVSAH

>lcl|NZ\_FO834906.1\_prot\_WP\_004143457.1\_2826 [locus\_tag=BN49\_RS15705] [protein=type 1 fimbrial protein] [protein\_id=WP\_004143457.1] [location=complement(2891307..2891870)] [gbkey=CDS]

MKEKGTLLVVGSLLALSLATVTTARAAGTLNFTGKIINESCQIANNGGDVNVDFGNVDMSALKSHEAKTA

ETPFTINLTGCPLAQNISISLEGTPDTNANGTSAAVLALSDAADTAKGVGIEVFSSPDGSTEGTQLTFDK

QSKTAVSQADENGDIAFNFIADLKSDSSQDVTAGNINATANIDIVYE

>lcl|NZ\_FO834906.1\_prot\_WP\_004176193.1\_2827 [locus\_tag=BN49\_RS15710] [protein=hypothetical protein] [protein\_id=WP\_004176193.1] [location=2892316..2892603] [gbkey=CDS]

MSPFRLALLCLCLAPLASSAALSGQVHFSGRVINPACVIAPRHDRIDVSCQHHSPEQVALTNNRPRYAMP

DNRGEVSIHWRNAQHSEADVIIRYR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531240.1\_2828 [gene=map] [locus\_tag=BN49\_RS15715] [protein=type I methionyl aminopeptidase] [protein\_id=WP\_016531240.1] [location=complement(2892831..2893613)] [gbkey=CDS]

MPSIIIKTADELARQRHAGQLLASVFDMLDTFIIPGVTTMAINDRVEDFIVNQLHARPASKGQYDFPYVL

NTSINDVVCHGIPKATEHLRSGMIVNVDITLEKAGMIADSSKMYLIGDVSPLARRLVKTTYEAMWKGIEV

VKPGATLGDIGHAIQRWVEEHGYSVVREYCGHGVGQEMHEEPQVLHYGRPGEGAVLQEGMVFTIEPMVNQ

GDSRIKTKKDGWTVVTRDKKLSAQWEHTVAVTANGFEVLTLRDDEQSRIR

>lcl|NZ\_FO834906.1\_prot\_WP\_002904808.1\_2829 [locus\_tag=BN49\_RS15720] [protein=ParD-like family protein] [protein\_id=WP\_002904808.1] [location=complement(2893594..2893812)] [gbkey=CDS]

MGIVKISDLLHDDIRDASKAMSRSVNAQAEYWIRLGMMSELYPELNHQQIKLLMLKSGSDRLLEVINAIN

NH

>lcl|NZ\_FO834906.1\_prot\_WP\_002904810.1\_2830 [locus\_tag=BN49\_RS15725] [protein=hypothetical protein] [protein\_id=WP\_002904810.1] [location=complement(2894102..2894350)] [gbkey=CDS]

MLRDYLKVEKEDQLVEQQSRHDNSQHYSSVTEWVILSKDGQRKGRVSLFDRFTTRRSWSDSFRITQFDNA

GKVVVDKLTDAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004143447.1\_2831 [locus\_tag=BN49\_RS15730] [protein=EAL domain-containing protein] [protein\_id=WP\_004143447.1] [location=2894647..2896302] [gbkey=CDS]

MSNDHLTDIAYRHFIESVKDYAIYMLSADGTVISWNEGARRAKGYLSDEIIGRYFGLFYSEAEQLSGVPA

KNLEIALRSGQFEGEGWRYRKDGSRFWAHVMIDTIRDEQNTLLGFAKITRDISEQKAINDRIAWMARYDA

LTGLPNRVEFFERVEKLITGNDARRFAIFTIDLDKFKEINDLQGHLIGDQLLQRVAGAVLKTLQKEEMVA

RFGGDEFVAVKPFSDEGEVDAFAARLWHCFSGKQTFAATEVVLSASIGISVYPEDGTDINTILSNSDLAM

YRAKSSLDHKICWYEREMDDKTRQRNMMAADIRRGIHAGEFSLHYQAIRNIKDRSITGYEALLRWQHPQL

GTIPPDVFIPIAEESGAIVPLGYWVLEQVCNESLENGLNRKVSVNISPVQLRHRSFIEKVREILMRTAYP

VSLLEFEVTETAFVINKQLAFSVLHHLQKMGISIALDDFGTGYSSLSMLRDFHFDVIKLDRSFMTDVESN

PQVRSFVRAIISLGNSINTPLIAEGVETAGQLQILEEEGCDEMQGFLFGEPVDIKHLPDRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004148380.1\_2832 [gene=iroE] [locus\_tag=BN49\_RS15735] [protein=siderophore esterase IroE] [protein\_id=WP\_004148380.1] [location=complement(2896336..2897271)] [gbkey=CDS]

MKLSSGSITTGRTSGLLTLAIGALFYSSGSIARPDLQPLGPNIADKGSAFYHFTQRQYDSADGERHYRVW

TAVPDKAPPAAGYPVLYMLDGNAVMDKLDDAFLQQLFAGSPPVIVAIGYQTALPFDTAARAWDYTPPLKT

HEPRAGKPALPPRKTGGNDVFRQLLTETMVPQTEANLKIDPHQRAIWGHSYGGLFVLDAWRKASPFGIYY

SASPSLGQALQSPLQASQSLDAVRFRGKSLYLLEGDGKARGEPSGHEASLEVLRQTQQQLASKGLTVAFW

RYPGLTHGQMFEVSLRSALLHLSGQAALAHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002904814.1\_2833 [locus\_tag=BN49\_RS31070] [protein=hypothetical protein] [protein\_id=WP\_002904814.1] [location=complement(2897458..2897598)] [gbkey=CDS]

MTLAMLLVLISHHKGLTLLLIVIIALLFIALTPLVKKLLSHLHDRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002904816.1\_2834 [locus\_tag=BN49\_RS15745] [protein=hypothetical protein] [protein\_id=WP\_002904816.1] [location=complement(2897623..2897862)] [gbkey=CDS]

MCNAFNGIAIVLCFRGISSVTGFSEAIWQVIITLAIIISTWYSANYFAALEARRDKRRYLLLAWVVMTIL

LNFIHLGGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002904819.1\_2835 [locus\_tag=BN49\_RS15755] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_002904819.1] [location=complement(2898279..2898722)] [gbkey=CDS]

MIDNITLDNLHIGCKASNKAEVIAMIGAEFKAKGYVNQECVHFLLEREHQVSTFLGNGITLPHLPKSATD

IILKTGIEIYQFPDGVIWDRSNVMFIAIGVIAKEKEHIDVLKEIASIFSDELIANALSLISDKHDFLKIL

QHNALPH

>lcl|NZ\_FO834906.1\_prot\_WP\_004143440.1\_2836 [locus\_tag=BN49\_RS15760] [protein=sugar porter family MFS transporter] [protein\_id=WP\_004143440.1] [location=complement(2898712..2900157)] [gbkey=CDS]

MSFITNLNQQQRKRLHQITLVATFGGLLFGYDTGVINGAFSSLKQYMALTPTTEGLVMSVLLVGAALGSV

FGGKFADYFGRRKYLLFLSFVFLIGALLSAAAPDITTLLIARALLGYAVGGASVTAPTFISEVAPTEMRG

KLTGLNEVAIVIGQLAAFAINAIIGIIWGHLPDVWRYMLLVQAIPAICLFVGMWRAPESPRWLISKNRHD

EALHILKQIRPAERAQKEYDDISTLIKIEAGNKYSAQSTFATIVKTPWILKILLVGITWAALQQTTGVNV

IMYYGTEILSAAGFSERTSLICNVLNGVFSVGGMLIGVLFLVDRFKRKTIIIYGFAIMATLHLIIAAVDY

TLVGDLKATAIWLLGALFVGVMQGSMGFITWVVLAELFPLKFRGLSMGISVFFMWIMNAVVSYLFPLLQA

KLGLGPVFFIFAAINYLAILFVVFALPETSNKSLEQLEAELSANHEDKKSTRLTREVGYDR

>lcl|NZ\_FO834906.1\_prot\_WP\_016528925.1\_2837 [locus\_tag=BN49\_RS15770] [protein=6-phospho-alpha-glucosidase] [protein\_id=WP\_016528925.1] [location=complement(2900903..2902231)] [gbkey=CDS]

MKDNFVVTIAGGGSTYTPGIVMMLLENMSRFPLREIRLYDNHHQRQKTIGDACAILVAERFPQVKFSYTT

DPQAAFTDVDFVMAHIRVGLYEMREKDEKIPLKYGVPGQETCGPGGIAYGMRSIAGVLELVDYMQQYAPG

AWMLNYSNPAAIVAEATRRLRPDARIINICDMPVAIEGLFADILGLPSRKALNVRYYGLNHFGWWTSITD

KAGNDLMPALKRHVAEQGYSSPKEDFQHKAPSWIETFKKVKDVFALDPSTLPNTYLKYYLYPDYEVAHSD

PEFTRANEVMAGREKEVFDMAREITRRGTAEGAHFHAGAHATFIVDLACAIAFNTQERMLLIVENNGAIA

NFDETAMVEVPCLVGVNGPEPLAMGKIPSFQKGLMEQQVAVEKLVVDAWIEGSYQKLWQAIALSKTVPSA

SVAKAILDELIVVNEGYWPALH

>lcl|NZ\_FO834906.1\_prot\_WP\_016528926.1\_2838 [locus\_tag=BN49\_RS15775] [protein=PTS transporter subunit EIIC] [protein\_id=WP\_016528926.1] [location=complement(2902243..2903775)] [gbkey=CDS]

MIGVKKLQDFSKAMIGPVLYLPAIGLLIALFSMTTNRLWVDESSGLYLMGKFVSSMLWALMNHLGFLFCL

GLASGLAKTRKAEAAFVAAMTWLMYLAANNSWLTLTHRLATGATNAQLYGSGQTFIFGFQVIDMGVFLGI

ILGCAVAFVHNRVVGIEFRGALSIYGNSKLVLIVMLPLVGMFAIATVYLWPVVELGISALTGFMKSFGAI

GVFLYGFLNRFLIPTGLHHLIWSPFVFTSIGGQLLIDGQTVIGAKPIFLAEIARHPVDALSDSARFLTYG

MVKIFGTAGMALAFYRTAKPENKQRLKVTLIPLIVTSVLVGITEPFEFLFIFTAPLLWLIYSLLDGFFQM

LAWLLHVRVCATNGLIDFVVYNLPAGVSATRWPVFVALGLLETATMYLVGTFCITRLRLLTPGRETAAED

EHSQQANSEHPDKGALVIAGLGGKENVCAVGNCFTRLRVDVRDPALIQQTLLKESGGSSVLIKGNHVQVI

YGLGVNKIRTAVNASLGVIE

>lcl|NZ\_FO834906.1\_prot\_WP\_002904825.1\_2839 [locus\_tag=BN49\_RS15780] [protein=GntR family transcriptional regulator] [protein\_id=WP\_002904825.1] [location=2904043..2904741] [gbkey=CDS]

MIYKKIATELRTRINSDDYAVGDMLPSEKALAAELKVSVMTLRKALALLEEEKLIARRHGSGTCIVRKSN

YHGGELEGFNYQMQVVGVTNYRNKVIEFTLLDAPPAIAQQLKIQPGEKVYYVRRLRLIDEVPILVENSYI

PFATFPWLSVGNLEQSKFNYFKKECHITIIESHRSYTPVLATREQAELLQVAPNSLLLRVQSISYAQNRA

IVDFSEIYQNTSKYNVKHITRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016528927.1\_2840 [locus\_tag=BN49\_RS15785] [protein=sulfite exporter TauE/SafE family protein] [protein\_id=WP\_016528927.1] [location=complement(2904747..2905490)] [gbkey=CDS]

MFDLHTISFLLIFIAAGLVKGVTGMGLPTVAMGLLGLLMPPQAAAALLLLPSLLTNLWQLLAGPALAQIV

RRLWLMMTGIIIGTLAGSSLLIGLNPRWSALALGAALIVYAGYALCSPVFQVSGRVEKWLSPLMGGLTGV

ITGATGVFVIPAVPWLQALGFRRDELVQALGLSFTLSTLALAAGLALHDGWHDDAWLLSALALLPALLGM

WLGQRIRSRLSPQRFRQGFLLFLLALGIELIARGWLV

>lcl|NZ\_FO834906.1\_prot\_WP\_032411477.1\_2841 [locus\_tag=BN49\_RS15790] [protein=LysR family transcriptional regulator] [protein\_id=WP\_032411477.1] [location=2905602..2906486] [gbkey=CDS]

MRLDLADLRLFIAIVDTGSITGGAANAHLALASASERLRKMEAEIGVPLLHRHARGVAMTEAGEVLARHA

RPLLAQQQRLRQAMHAFACGQRGTLRLFANTSAMSAFLPGKLAAWMAAHPAVQIETEERTSADIVSCILA

GVAQAGVVSDAVDPGPLRLEPVADDPLVLIVPPARPLAEKQEVAFAAVLNEPLVALYQTSALQQHIEQHA

AELGQALNVRVRMSHFAGLCEMVAHGAGGAILPRVIAERYRQRYSFAVIGLQDRWAQRRLCLCYQDDASL

SPAMRRLLEWLRQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002904832.1\_2842 [locus\_tag=BN49\_RS15795] [protein=NAD(P)-dependent oxidoreductase] [protein\_id=WP\_002904832.1] [location=2906597..2907472] [gbkey=CDS]

MSTLPKVAVLGLGAMGHAFASNLLKNGFTVAGWNRSPARGEDLQAHGLSLHATPQQAVADAEVIISMLAD

GEATLEVLAQIAPACQPQAIYCQMGTIGLPETRQAIALLRELQPAMTYIDAPVSGTKAPAEKAQILVLAS

GDREKGAAAEPVFAAISRGTQWFGEAGNSQKMKLVLNAWLISMMQGIAESAQLAKTLGFTPDQLWSALEG

GPLAAPYVKVKLDAIASEQFTPQMQLAHALKDARLALSLAEPHTMPGLENIAELWQQAADAGYAGEDLSA

VYQWLSPSSKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016528974.1\_2843 [locus\_tag=BN49\_RS15800] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_016528974.1] [location=complement(2907555..2908712)] [gbkey=CDS]

MIITTALANEIVARAMAIIHHNVNVIDHHGQIIASGERHRIGEQHEVAREVIRTGKRICINNAAEAARFH

NVHPGINHPIIYDDRVVMVVGISGDPAAISRYAELAVLTAELLVRQAIEMRETNWRQRLRDTLFCQYLEQ

GATPAGQEALHRLLELGFDFDTPRVPIVVTVQVEQHQLSDILSTLLREFSQLSGVSDVILLCSHEILILN

ALSEAQETLLRGIEFVLSNQISHYHIGIGVQADSAPDIREAIRFARSVIEVGSKVQPQRQIYYFREMAML

CLFRVLEDSYMVNFFINNVRQLLEHDSGEVLLDTLSSFIANNAEPGKTSLLLGIHRNTLTYRLQQIKKHI

QLDPMVFTDLTQLAVSVHCYRRLNPRQSEWIDSLS

>lcl|NZ\_FO834906.1\_prot\_WP\_015958409.1\_2844 [locus\_tag=BN49\_RS15805] [protein=glycerate kinase] [protein\_id=WP\_015958409.1] [location=complement(2908709..2909884)] [gbkey=CDS]

MKIVIALDSFKGSCSAQAACAAVAQGLRRVDQTLELVEMPVSDGGEGLLSTLADSPLLEGAVWQQQRCTS

PYGLSLQADFLILPGERAIIEMAQSCGLELTPPAQRDVRQASSYGLGEQVKAALDAGCRHLIIGLGGSAT

NDGGIGFAQALGARFWRKDGTLLPAPAAGQDLAHIQRIDLSGLDPRLQQSEIQASCDVTNPLLGEHGATW

VYGAQKGADEAALCELEAGMAHYSQLLTQTLGFDVSGRPGAGAAGGMGAALIAYTGATLRPGIDLVLELL

NADDHLRDAALTIVGEGWLDRQSAFGKAPVGVAGKAARHGVPVVALCGGRDESSRQLYQHHIDAMWSICQ

RPMALAESMNTCEPLLADAAENVLRTFLSGWRGEAHKRITV

>lcl|NZ\_FO834906.1\_prot\_WP\_004176181.1\_2845 [locus\_tag=BN49\_RS15810] [protein=MFS transporter] [protein\_id=WP\_004176181.1] [location=complement(2909898..2911268)] [gbkey=CDS]

MLSRRRGVNTTMTTINHTPAGEQRGKKRLIHRFSWVSLLVCWLIWVLNAYDREMILRLGPVISKEFSLSP

EQWGNIVALIMVALAVLDIPGSIWSDRYGSGWKRARFQVPLVLGYTALSFISGIKAISHGLTAFVLLRVG

VNLGAGWGEPVGVSNTAEWWPKEKRGFALGVHHTGYPIGALLSGVVASLVLATFGEGSWRYCFLLALLVA

IPLMIFWAKYSTADRINTLYQHIDSQGLTRPATQESSHVAKGEGMKTFLRTLRNRNISLTAGNTLLTQIV

YMGINVVLPPYLYHVSGLSLAASAGLSIIFTLTGTLGQVIWPWLSDSFGRKRTLIVCGLWMSIGIALFYF

ATNMPRLIAIQLFFGLVANAVWPIYYAMASDSAEERATSTANGIITTAMFIGGGISPLLMGWLIQFGGGW

ENPAGYIYAFFTMAGCALLGMLLQLMTTDKTPRKAH

>lcl|NZ\_FO834906.1\_prot\_WP\_009308862.1\_2846 [locus\_tag=BN49\_RS15815] [protein=SMP-30/gluconolactonase/LRE family protein] [protein\_id=WP\_009308862.1] [location=complement(2911345..2912223)] [gbkey=CDS]

MRIEVLLDLKTRLGESPVWDVEQQRLWWVDSLDGRLFACNAQGGAIKSWDVRQKIGSFALRQNGEGAVVA

LQNGVHLLDFASGELTLLHHPEADRPFNRLNDGKVDRQGRFLFGSMDMREEEPSGALYRLDADLSLHVLK

KDIIVSNAPCWSPSGETFYFADTWTGEICAWDYNTATGDLSGERVFCHVDRSEGGAADGATVDSEGYLWN

ALVYAGKLVRYTPEGKVDRIIEMPVKKVTSVMFGGENLDVLYVTSMAQPPLPRFPEDNQLRGSLFAIYDL

GVTGVAERRFAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004199866.1\_2847 [locus\_tag=BN49\_RS15820] [protein=MFS transporter] [protein\_id=WP\_004199866.1] [location=complement(2912237..2913574)] [gbkey=CDS]

MSAINEKAVNGTQLQRTHKKIYRHLMPLLIVAYIISFIDRTNIGMAKATMSVDIGLSATAFGLGAGLFFL

TYAVLEIPSNLFLTRIGARRWIARIMITWGILSCGMAFVTGPTSFYVMRLLLGAAEAGLYPGIIYYLTLW

FGREERAKATGLFLLGVCLANIIGAPLGGLLLSLDGMSGWHGWQWMFFIEGLPAIALAFVVWRRLPDKPA

DARWLDSDDVQAINAVLAKEAEETRHTPSRFSLKTALSTRVFLLLVLIYFTHQFSVYGLSYFLPGIIGSW

GQLTPLQVGLLTAIPWIAAAAGGILLPRFARTEQRSRSMLMAGYLVMATGMAIGAIAGHGVALLGFSLAA

FMFFAMQSIIFNWLPSIMSGHMLAGSFGLLNCLGLCGGFLGPFILGAFEDRTGAATSGLWFAVALLIIGA

LVSLFLKSSSSPGSVSAKQAHGEKV

>lcl|NZ\_FO834906.1\_prot\_WP\_004179834.1\_2848 [locus\_tag=BN49\_RS15825] [protein=thiolase family protein] [protein\_id=WP\_004179834.1] [location=complement(2913710..2914900)] [gbkey=CDS]

MTQANDIVIVSGVRTAIGTFNGSLKHTHQHDLGAAVIREAIARAGIAPQDIDETIVGNVGQIAESGFIAR

ICQLRAGIPQESTAYSVNRQCGSGLQALADGMMQLQSGQAEVVVACGTENMTQLPYYLRKARDGYRMGHG

ELEDGLISILTWPEGPYHNGITAENVAQRFGITREAMDDFAWSSQQKALKAIAEGRFREQILALEVPDGK

KATRLFATDEHPRDTPREKLATLRPAFKADGVVTAANSSGINDGAAALVMMTRQQAEKRGLTPRMRIRGW

AVAGCGAEIMGFGPSPATRRLMDRLNIDVQSIDLIELNEAFAAQALAVMNDLRLDPARVNVNGGAIALGH

PVGASGAILPVKLMYEMARSGARTGLVTMCIGGGQGISMLFEREGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002904841.1\_2849 [gene=fabG] [locus\_tag=BN49\_RS15830] [protein=3-oxoacyl-ACP reductase FabG] [protein\_id=WP\_002904841.1] [location=complement(2914912..2915646)] [gbkey=CDS]

MKLASKTAIVTGAARGIGFGIAQVLAREGARVIIADRDAHGEAAAASLRESGAQALFISCNIAEKTQVEA

LFSQAEEAFGPVDILVNNAGINRDAMLHKLTEADWDTVIDVNLKGTFLCMQQAAIRMRERGAGRIINIAS

ASWLGNVGQTNYSASKAGVVGMTKTACRELAKKGVTVNAICPGFIDTDMTRGVPENVWQIMISKIPAGYA

GEAKDVGECVAFLASDGARYINGEVINVGGGMVL

>lcl|NZ\_FO834906.1\_prot\_WP\_004143421.1\_2850 [locus\_tag=BN49\_RS15835] [protein=acyl CoA:acetate/3-ketoacid CoA transferase] [protein\_id=WP\_004143421.1] [location=complement(2915658..2917250)] [gbkey=CDS]

MSSKFIDAHEAARWVASGDTVCTVGMTLIGAAESILSAIEARFLTAGEPRDLTLLHAAGQSDRQRGIQHF

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RMNARTRERPNLIEHVTFRGDEYLFYPALPLDVVIVRGTHADEDGNLTTDEEVMKLEVLHAVLAARRYGA

KVLAQVKYRVAKGSLHPKSITVPGNLIDAIVVCEEPQTDHRQTSSWAFDPALCGDIQLPAAQNAPLPLDL

RKLIGRIACRYLTPGCVINLGTGIPNDVIGAIIHEEQLGEQVTITVESGIYGGQQAGGVDFGIGRNLSAM

ISHQDQMLYYNGAGVDITFMGAGEMDPHGHVNATRLGASCPGAGGFIDITQNARHVVFCSSFTAKGLEIA

CEHGALHIRREGEVRKFVAGVNQISYNGELARAKGQTMHYVTERAVFELRPEGPVLTEIAPGIDLERDIL

AHMDFHPAIAADLQVMDSRLFTPPPCGLAEHLSRNSSSDS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043293.1\_2851 [locus\_tag=BN49\_RS15840] [protein=acyl--CoA ligase] [protein\_id=WP\_046043293.1] [location=complement(2917247..2918803)] [gbkey=CDS]

MNSTSADFQNLYQALSHSAARSPDALALAFEDRRYLYRDFHLRVQRAMAQLDRGWSLRKGDRILLAWGNH

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PEPLTRPPVPVNRDDTAVMMFTSGTTGEPKGAIITHNNLLCAIDAYAQKLNLTAADSTILAVPIYHITGL

SALLALFISLGASIWLQHRFNAPQVITTLREQNITFLHGSPTIFILLCQAAREQSASHPGDFPALRTIAC

GAGHLSDGLIKELKTLFPHTAIQPIYGLTETTSPATIFPGDVWGSDKCGSSGQAIPGLAITIRNDRQQPL

PAGQIGHIWLKGDVVIREYWQHSERRPSCDAQGWFCTGDLGYLDDEGWLYIKDRSKDMINRGGEKIYSLE

LENILSTYRGVREVAVIPTPSPVYGEEPVAFIVPDGQHHLTSEEILDWLKVKIARFKLPARIIFTRALPR

THNGKVSKQQLKTRLAESIITLSTEDKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176179.1\_2852 [locus\_tag=BN49\_RS15845] [protein=VOC family protein] [protein\_id=WP\_004176179.1] [location=complement(2919052..2919441)] [gbkey=CDS]

MRELINTIAHIGYQVSDLTRSLAFYEPLGFQRQQRFSKPSPQGTIEVAFLEMAGAVLELYQLPAGTPFDA

PRCGIDHLALEVSDLDAVQQRLAALGYPLDEGPIEEDNVRFLLIRGPDGERLEFDACKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004143414.1\_2853 [gene=fucP] [locus\_tag=BN49\_RS15850] [protein=L-fucose:H+ symporter permease] [protein\_id=WP\_004143414.1] [location=complement(2919443..2920777)] [gbkey=CDS]

MSTLITDKVENAAVQKEKLDTSAYLPHTPWLQFLLVCCLFALWGMAGNLNDILIAQFKKGFDLTDTQTAL

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TSANTYSSLLGPIQSSTQRINFSQIFNSLGVISGVLIGQLMVFGENDPSHEQLLAMPAAAADVARHQMVG

QVVGPYLIIGSVLVVLALVFVFIKFPSCKGAPAQQQQLPTESMGPTLKRLFAIPRFRLGILSQFLYVGAQ

VGVWSFTIRFVQLVQQGTSEHSATYWLLASLVIYAVGKTVATWLMNRLNPAMLLGTFALAATALLLIAVF

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AFIAPLLCFVYVAFYGFWCVRKGV

>lcl|NZ\_FO834906.1\_prot\_WP\_042940771.1\_2854 [locus\_tag=BN49\_RS15855] [protein=ribokinase] [protein\_id=WP\_042940771.1] [location=complement(2920814..2921755)] [gbkey=CDS]

MSGKVCVFGSFNFDMVARVDRFPVPGESLVACGSMTSAGGKGANQATAALKAGANVHYIGKIGNDTFGHF

ARRHLKGVGFNAVTLLVAEEIPTGNALIYVAGNDAENMIAVDPGANMTVTDDEIAGCIPAIGCADVVLVQ

LENNLSAIEQVIDAGKQAGALVILNPAPWQPVEHAVLSKVDLLTPNATEAGLMTGRRVDSLTAAAEAADV

LHAQGARNVIITLGASGALLSEHGVKSPIPCFPSHPRDTTGAGDAFNGALAARLACGEPLQASARFAAAY

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151641.1\_2855 [locus\_tag=BN49\_RS15860] [protein=D-allulose 6-phosphate 3-epimerase] [protein\_id=WP\_004151641.1] [location=complement(2921767..2922456)] [gbkey=CDS]

MRYYLSPSLMCMDMMKLTEQLRFLNSKADRLHVDIMDGHYVKNLALSASFVAQIRPYTSLPIDVHLMVEA

PASFIPALLDAGADAFSLHPETICREAFRVINMLRQAGKEVGMVLNPATPVESIQHYLHLLDKVTVMTVD

PGYAGQPFIPEMLAKITQLHQLKETGSLRFLLEVDGSCNRNTYRALLGAGAQILVMGSSGLFRADMPLEL

AWETMSRELSAALHSPELV

>lcl|NZ\_FO834906.1\_prot\_WP\_004143408.1\_2856 [locus\_tag=BN49\_RS15865] [protein=DeoR/GlpR family DNA-binding transcription regulator] [protein\_id=WP\_004143408.1] [location=complement(2922566..2923366)] [gbkey=CDS]

MLPLERHRLIVELLGQHGVMRVNEIAQATRVSRETIRRDLSELERKGILTRSHGGALAAENPLPATRAAA

SALPVEDSQGSFQHRTLLHSEGKMRVARKALQFLQPGQTIVLDGSSTSWFLARQMPEMALTVITPSIRIL

QTLMSRRSLHLVGLGGDFSPTEESFFGETASRTLREYAIDTLFFSCQGLERDSGLYAGTQAHAALLKQML

LAARQTVALVDGSKLGRTGVARIGGLGELDCLVTERFVDPLLEKEMTWHNVSLQIA

>lcl|NZ\_FO834906.1\_prot\_WP\_004891965.1\_2857 [gene=deoC] [locus\_tag=BN49\_RS15870] [protein=deoxyribose-phosphate aldolase] [protein\_id=WP\_004891965.1] [location=2923729..2924478] [gbkey=CDS]

MKAIKNKGQDKTMNETTHRFARLVDLSAVQATSTEADVRACAELAARYNIISVHVLPCWTRFLSTLLPQQ

GTGEVMIGGPVGFPGGGHTTDTKVQEVRQLIADGAREVDMVVNIGKVLSGDYDYVREDLRRVVEAAAPVP

AKVILETHYLNEEQIRRVCEIAVEVGMKWVKTSTGWAPTGATVEKVSIIADQLKGRIDIKGAGGIRDLAT

VRALYQLGVRRFGMSHGAVTKVLAELEQHPERFPELNAD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043298.1\_2858 [locus\_tag=BN49\_RS15875] [protein=FGGY family carbohydrate kinase] [protein\_id=WP\_046043298.1] [location=2924532..2926037] [gbkey=CDS]

MKDKILTIDVGTGSTRAAIVRIDGAMIGFAQREYEQTTPRAGWSEQAPSLWWQAACDCIREVLYRYPETA

AQIAVIGACGQMHGTVLLDDRGELVEDRALLWNDKRSQPQVDAFNAREGWEKWLAHLNNPPAAAWPAFKL

AWWRENHPDRWSQLAKVLMPKDYINFMLTGAMATDYSEASCYFLMDSETRSWSSQACETFGLRVDQLPEL

KLSSDIIGQVTQRAADLTGLPAGIPVVAGTSDMAASLLGSGVYEPGMASDSTGTSTLMTVVSPRPLHHPL

VNNLHLANAAWGGFTILDAGGDAVRWARLALADNQITHPQLLQEAAAVPAGAEGLLFLPYLTGERLAEHT

NSRAQFFGLQRKHRRGHLFRAVLGGVAFASWRNLRQLQKCGQYPQQMIASGGGARSSLWLEIKAAAYNLP

ILSTRNQENGVTGCGIIAGVGVGLYADFASGVRQTVQFDKLISPDPRLRDYYHACCELFDTLYRQSAALY

DRLDALSVGPD

>lcl|NZ\_FO834906.1\_prot\_WP\_002904899.1\_2859 [gene=pgtA] [locus\_tag=BN49\_RS15880] [protein=two-component system response regulator PgtA] [protein\_id=WP\_002904899.1] [location=complement(2926402..2927652)] [gbkey=CDS]

MLSNNCSILLIDDDADVLDAYTQLLEQAGYHVSACNNPFDAREQVPKDWPGIVLSDVCMPGCSGIDLMTL

FHQDDDLLPILLITGHGDVPMAVEAVKKGAWDFLQKPIDPGKLLTLVDAALRQRQSVIARRQYCQQKLQV

ELIGRSQWTVRYRQRLQQLAETDIAVWLYGEPGTGRMTGARYLHQLGRHAEGPFIACELTPANAHTLNEL

IAQAQGGTLVLSHPEHLTHEQQHQLVQLQSHEKRPFRLIGIGSASLVELAASSQIVAELYYCFAMTQIGC

QPLSKRPDDIEPLFHHYLQKTCQRLNHPVPEVDAGLLKGMMRRVWPNNVRELANAAELFAVGVLPLAETV

NPLMHIGEPTPLDQRVEDVERQIITEALNIHQGRINEVAEYLLIPRKKLYLRMKKYGLNKEHYKGV

>lcl|NZ\_FO834906.1\_prot\_WP\_164876875.1\_2860 [gene=pgtB] [locus\_tag=BN49\_RS15885] [protein=two-component system sensor histidine kinase PgtB] [protein\_id=WP\_164876875.1] [location=complement(2927642..2929636)] [gbkey=CDS]

MLQRLRQISISSSLRGAFLTGALLTLIVSSVSLYSWHEQSSQIRYSLDEYFPRIHAAFLIEGNLNLVVDQ

LNEFLLAPNTTVRLQLRNQIIQHLDKIERLSQGLSPAERQQLGVILQDSRALLAELDRVLYNMFLVREKV

GELAARIDWLHDDFTTELNSLVQDFTWQQGTLLDQIEARQGDARQYLKRAREVQNEQQQVYTLARIENQI

VDDLRDRLNELKSGNDDGMLVETHIRYLENLKKTADENIRALDDWPSTITLRQTIDELLEIGMVKNNMPD

TMRDYVSAQKALVEASRSREATLGRFRTLLEAQLGSSHQQMQMFNQRMAQIVRVSGGLILVATMLALLLA

WGLNHYFIRSRLVKRFTALNQAVVQIGLGRTEATIPVYGRDELGRIAGLLRHTLGQLNAQKQQLEQEIGE

RKAIEADLRATQDELIQTAKLAVVGQTMTTLAHEINQPLNALSMYLFTAGRAIEQGQAEQARTTLSKAEG

LINRIDAIIRSLRQFTRRAELETPLHPVDLRQTFTVAWELLEMRHKPQQGTLVIPDDTVWIQGDEVRVHQ

VLVNVLSNALDACPHAAQITVSWQIQGGRLCVLIADNGPGWPAALLPSLLKPFTTSKTVGLGIGLSICVS

LMTQMEGALRLASTFTRSACVVLEFNLTDVKDVE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530122.1\_2861 [gene=pgtC] [locus\_tag=BN49\_RS15890] [protein=phosphoglycerate transport regulator PgtC] [protein\_id=WP\_016530122.1] [location=complement(2929648..2930868)] [gbkey=CDS]

MLALLLLTAWLRPCAAQGNELVMATTFSPSATVWIIDRWQKEPGSVMIRTLNRTSASLEQLLDTANAENV

DLILTSSPMLLQHLQEHQKLAPFSGAPAVSQHLVPESIRSTSVAVAISGFGLLMNRSALMTRHLPAPADW

DDLTDPRYQGALLMSSPSRSDTNHLMVESLLQQKGWIKGWETLLTTAGNLVTISSRSFGVADKIKSGLGV

AGPVIDNYANLLLNDPHLAFTYFPQSAVSPTYVAVLKNSQHASEARRFIRYLLSPEGQTILADANTGKYP

VTPLAPGNPRAAQQAMLMNQPPLNYRLILKRQRLVQRMFDTAISFRLAQLKDAWRALHSAEVRLKRPLPE

IRALLTRVPVDPASSEDEAWLAQFDNKSFAEQQMMEWQLWFLNNQRQAITKLEELK

>lcl|NZ\_FO834906.1\_prot\_WP\_004184088.1\_2862 [gene=pgtP] [locus\_tag=BN49\_RS15895] [protein=phosphoglycerate transporter PgtP] [protein\_id=WP\_004184088.1] [location=2931274..2932665] [gbkey=CDS]

MLSLLKKGPSANKVPAEKIQATYGRYRMQALLSVFLGYLAYYIVRNNFTLSTPYLKEQLDLSATQIGLLS

SCMLIAYGISKGVMSSLADKASPKVFMACGLVLCAIVNVGLGFSTAFWVFAALVVLNGLFQGMGVGPSFI

TIANWFPRRERGRVGAFWNISHNVGGGIVAPIVGAAFAILGTEHWQSASYIVPACVAVVFAISVLVLGKG

SPREEGLPSLAEMMPEEKVVLKTKHGQKAPENMSAFQIFCTYVLRNKNAWYVSFVDVFVYMVRFGMISWL

PIYLLTVKHFSKEQMSVAFLFFEWAAIPSTLLAGWLSDKLFKGRRMPLAIICMTLIFICLIGYWKSESLL

MVTVFAAIVGCLIYVPQFLASVQTMEIVPSFAVGSAVGLRGFMSYIFGASLGTSLFGVMVDKMGWHGGFY

LLMGGIVCCILFCYLSHRGALELEQQRKITEQEEARLALADAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002904908.1\_2863 [gene=lysM] [locus\_tag=BN49\_RS15900] [protein=peptidoglycan-binding protein LysM] [protein\_id=WP\_002904908.1] [location=complement(2932802..2933251)] [gbkey=CDS]

MGLLNFVKEAGEKIWDAVSGDSKEDRAEKLKKHIDGLNLPGAEKVNIDVAEDGTATVTGDVASQEDKEKI

LVAVGNVTGVGQVSDGVKVTQSGAESRFYTVKSGDTLSAISKAMYGSANEYQRIFEANKPMLTHPDKIYP

GQVLIIPAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004151646.1\_2864 [locus\_tag=BN49\_RS15905] [protein=alpha/beta fold hydrolase] [protein\_id=WP\_004151646.1] [location=2933705..2934577] [gbkey=CDS]

MESVIIPVSQGGFVAATLWQRHKAKALVIVHPATAVVQGFYKGFAEYLYKRGFSVITYDYRGTGLSKSGR

VRHNKNTMSDWIEQDVGCITAWAKARAPGLTLLAIGHSIGGHAVLLSSASTDLRAAVMVASHAGVTSTIS

QTKEKLRVWCLLRVLGPALCRLFGYMPARRLGLGEDLPAPAMLQWGRWSAMPEYFYDDPEWDARQRAGKI

TLPILVLGFDDDPWANTEAISRLLAPAQNAKIERREIRRADYGLSSIGHMGFFRTRNAEKLWPLVAQWLE

RHCPDKRRTT

>lcl|NZ\_FO834906.1\_prot\_WP\_002904912.1\_2865 [locus\_tag=BN49\_RS15910] [protein=TenA family protein] [protein\_id=WP\_002904912.1] [location=complement(2934630..2935274)] [gbkey=CDS]

MEAFSERLLREHQPAWQAMQQHPFVTDIEQDRLPTVVFNRYLVFEGNFVATAIAIFALGVSKAPGIQQQR

WLIGVLNALVDIQIAWFEQVLSARQIDPAEYPDDLPGVRRFRDGMLRTAHEGSYEQIVTLMFGAEWMYYF

WCRRASEHYQSDADLRRWVEMHAEDEFYQQALWLKNELDRCAMALSEDEKQALSALYGEVLQWEIDFHHA

AYEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002904914.1\_2866 [locus\_tag=BN49\_RS15915] [protein=BtpA/SgcQ family protein] [protein\_id=WP\_002904914.1] [location=complement(2935274..2936119)] [gbkey=CDS]

MVAISAEKTNAIQAIFSRSKAVIGVIHCDPFPGSPKYRGKSVSDIVERALRDAENYISGGVHGLIIENHG

DIPFSKPEDIGHETSALMAVITEKVRERFAVPLGINVLANAAIPAMAIALAGGADFVRVNQWANAYIANE

GFIEGAAAKTLRYRSMLRAEHIRVFADSHVKHGSHAIVADRSIQELTRDVDFFEADAVIATGQRTGDSAT

MAEIDEIRAATELPLLVGSGVTPANVKQILGRTQGVIVASTMKVDGVWWNDVELARVKHFMSVAQAALEE

A

>lcl|NZ\_FO834906.1\_prot\_WP\_004213032.1\_2867 [locus\_tag=BN49\_RS15920] [protein=PfkB family carbohydrate kinase] [protein\_id=WP\_004213032.1] [location=2936146..2937018] [gbkey=CDS]

MRVYVTGNITVDETWSIPDIPKKGASIHGVKVSQDIGGKGANQAIILSRCGIETRLIAATGNDSNGAWIR

QQIKNEPLTLLPDGHFNQHSDTSIILNSADGDNAIITTTAAADTFSLDEMIPHMADAVAGDILLQQGNFS

LDKTRALFQYARSRGMTTVFNPSPVNPDFCHLWPLIDIAVVNESEAELLQPYGVKTLVITQGAAGAWLVQ

EGQRQFCPAVPAEALDTTGAGDTFLAVMLASALLRGVAPDALALAHASRAAAITVSRRGTLSAFPGSREL

AALLTTDGAR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529100.1\_2868 [locus\_tag=BN49\_RS15925] [protein=substrate-binding domain-containing protein] [protein\_id=WP\_016529100.1] [location=complement(2937020..2937973)] [gbkey=CDS]

MMLFHTGKLRFLAVATTMLASMSFISAASAAGPTYALVQINQQALFFNLMNKGAQDAAKASGKDLVIFNS

NDNPVAQNDAIENYIQQGVKGILVAAIDVNGIMPAVKEAAAANIPVIAIDAVLPAGPQAAQVGVDNIEGG

RIIGQYFVDYVQKEMGGQARLGIVGALNSAIQNQRQKGFEETLKSNPKITIANVVDGQNVQDKAMTAAEN

LITGNPDLTAIYATGEPALLGAIAAVENQGRQMDIKVFGWDLTAKAISGIDGGYVTAVLQQDPEKMGAEA

LNALNSITSGKTVPKTILVPATVVTKANVDSYRPLFK

>lcl|NZ\_FO834906.1\_prot\_WP\_004176158.1\_2869 [locus\_tag=BN49\_RS15935] [protein=LacI family transcriptional regulator] [protein\_id=WP\_004176158.1] [location=2938319..2939341] [gbkey=CDS]

MAQEMSIKRVLLSDVAKLAGLSKATLSRYMNNSIVLPQDTIDRIETAIRELDYRGNSLARRLSKGGSETL

GLVLPDITNPFFAELADAAEEAASASGYSLVLCITRNNPEKECQFIRWLDTCQVDGLLFTTNRPDNGLLR

KEVQRHERIVLLDEDIPGSKVPKVFADNVQGGRIATEKLIAAGHRHIAFVGGPDKLMSVRERYQGFCTAM

EQAGLSWPPEWVMYGDYQREFGQQALRYLFSQQVRPTAVFAASDYLVLGLLDGLRASGLQAPEALSLVGF

DDANYADFTQPRISTIRQPARELGRTAVNIMMRLLNDDPDIPAETRLPVEWIGRDSIKIC

>lcl|NZ\_FO834906.1\_prot\_WP\_004198552.1\_2870 [locus\_tag=BN49\_RS15940] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_004198552.1] [location=2939722..2940468] [gbkey=CDS]

MINITKTYGSIRSLRGVNLELAPGEVLGLVGDNGAGKSTLTKVLSGAVIPSSGTIRIDGEQQQFTNPADS

RRCHIEMVYQDLSLCDTVDVAGNLFMGREPMKSVLGIPFLDEAKMHADAREMLKGLGISIPDTRLLVRNL

SGGQRQAIAIARAAAFDPKVLIMDEPTAALAVAEVEAVLELIRRVSARGVSVILITHRLQDLFLVCDRIM

VMYEGTNVADRRVSDTSLSDIVNLIVGEKFTARSAAAH

>lcl|NZ\_FO834906.1\_prot\_WP\_171819475.1\_2871 [locus\_tag=BN49\_RS15945] [protein=ABC transporter permease] [protein\_id=WP\_171819475.1] [location=2940487..2941350] [gbkey=CDS]

MNLSSSRMIQHSLPRRLLHNHSGVVSIALFFVFCCVVFSLITSNFLTGTNWLNIIRQSAPLLIVATAMTL

VITTGGIDLSVGSTLALVGALATLAVVRGIALLVTQGYSIPVPADSLFTFIGRAWVVGIPMPALLGILIL

LIGHIVLNHMRFGRYVTAIGANAEGARRSGINTKAVTMKVYIISGMAAALAGMSITARLGSGSSNQGEGF

ELQVIAAVVLGSTSLFGGFGTIIGTLLGALSIAVIQNGLILSHISPFYTQIATGTIILLAIWLNTRILNP

TRSAAKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004176149.1\_2872 [locus\_tag=BN49\_RS15950] [protein=phosphotriesterase-related protein] [protein\_id=WP\_004176149.1] [location=2941354..2942433] [gbkey=CDS]

MKGSIFRHPSPLPVGVSSGYVMTVLGPLPINEMGVTLMHEHILLDASGKWVPPCCCSDRHLAEMPVKMEN

LGELSLNPLMSRDNCQLFDVDVAIDELTKYRALGGETVVDPTNIGIGRDPKALARIARLTGLNIIMGTGL

YLEPSHPEWVKISSVEQLTERLIYDLGGAEEKPEVLAGLIGEIGISSRFTPDEEKSLRAAGRASAATGVP

IEVHLPGWERLGHRVLDILEQEGADLRHTVLCHMNPSFADKRYQRELAQRGAFLEYDMIGMSYYYADESA

QSPSDEENARAIRELIDDGYIQQILLSQDVFLKTMLTRYGGHGYGYILKHFVPRLRRHGVSGEQLETLMI

GNPQRVFGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002904983.1\_2873 [locus\_tag=BN49\_RS15955] [protein=glutamine amidotransferase] [protein\_id=WP\_002904983.1] [location=2942448..2943203] [gbkey=CDS]

MQKKILLVGESWTSTSTHVKGFDQFATATWHTGATDFLAALADSPYAITYMPAHAAATDFPLTLEALQEW

DAIILSDIGANTLLLHPDTWLKSRRTANRLTLLHDYVAGGGALMMIGGYYSFQGINGGARYRHTEVEKVL

PVRCLAWDDRIETPEGCYAEVTESHPLFNDIPGEWPWLLGYNEVEMHPEGKLLATVAGTGHPLLAVREYQ

QGRSLVWTSDMSAHWLPEEFAKWPGYRQLWINCLDWLTERR

>lcl|NZ\_FO834906.1\_prot\_WP\_004199916.1\_2874 [locus\_tag=BN49\_RS15960] [protein=M20 family metallopeptidase] [protein\_id=WP\_004199916.1] [location=2943203..2944345] [gbkey=CDS]

MTATLELARQLLGFNTINPPGSEADCMRFFADWLDDSGFEVSLSSFGEGRCNLIASLPGAKSGKPLAFTG

HLDTVPLGNARWQYDPFGSQMEDGRLYGRGSSDMKAAIAAFAVACVHQREAILAGRGAVLLITGGEETGC

DGARALIASATLPEVGALIVGEPTANYPVIGHKGALWLRCETRGKTAHGAMPELGINAIYLAADALGKIQ

HFSPGAPHPLMKQPTLNVGRIEGGLNINSVPDRTRFDVDIRSAPNLQHATIRERLTTLLGESVTVSTLVD

LPAVLSREDHAWIKQVYQRCQPLHAEPIAPRVVPYFTDASLLLPALGDPPCIILGPGEPSMAHQTDEYCL

LSRLAEAEQLYGDIIRDWMASPPATKVKNE

>lcl|NZ\_FO834906.1\_prot\_WP\_014599166.1\_2875 [locus\_tag=BN49\_RS15965] [protein=cell envelope integrity protein TolA] [protein\_id=WP\_014599166.1] [location=2944458..2944886] [gbkey=CDS]

MSVKTNAVLVCTLSLLLSACSGRASAPGSAEDAKISAEVDKILRDYQTGSDTSPQANASRYLARIQAAIF

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KP

>lcl|NZ\_FO834906.1\_prot\_WP\_004218740.1\_2876 [locus\_tag=BN49\_RS15970] [protein=N-acyl homoserine lactonase family protein] [protein\_id=WP\_004218740.1] [location=complement(2944991..2945785)] [gbkey=CDS]

MMPEIKLFMFQSGTQHCRYQHIRMNQGVGEHYEIPVPWFLLTHPDGFTLIDGGLAVEGLKDPSGYWGSAV

EQFKPVMSEEQGCVEQLKRIGIAPEDIRYVVLSHLHSDHTGAIGRFPHATHVVQRQEYEYAFAPDWFTSG

AYCRRDFDRPQLNWLFLNGLSDDHYDLYGDGTLQCIFTPGHSPGHQSFLIRLPGGTNFTLAIDAAYTLDH

YHEKALPGLMTSATDVAQSVRKLRQLTERYHAVFIPGHDPEEWKKNRLAPACYY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529922.1\_2877 [locus\_tag=BN49\_RS15975] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016529922.1] [location=2945946..2946833] [gbkey=CDS]

MRIFIRVVERGSMSAAARDLGIGQPAVSERIEKLEAHLGTRLLRRNTRNMSLTQSGNVFYERSKTAVQAA

EHALSVNEENQGLQGKIRIAAPYSAGESLLMPALLQLQNEHPELQVDVIFNDRVINPVTEGVDLSLRLGD

VSEGFFVARPLGTVRRVLLASPALLAKMGHPDTPDALTDYPFAAVSGVFASNRIQLVASEDQLINVPVNI

QFQSTHWRSVLSWLLTGHAIGVLQSPVCRKEMADGALIPLLSHYPIPPFSAWLLHPPAGMMSYETRICAS

LLEGYIRDLLLEPAG

>lcl|NZ\_FO834906.1\_prot\_WP\_009307847.1\_2878 [locus\_tag=BN49\_RS15980] [protein=LysR family transcriptional regulator] [protein\_id=WP\_009307847.1] [location=complement(2946875..2947777)] [gbkey=CDS]

MRPVLDFNALKIFIAVVERDSFVGASKALEMPTSNVSRCISQLEDKLNLQLIERSTRHMKLTQAGHLLYT

RAKPLLEALEQTETELTLRQMQFKGPLRICIPNEIGPVLLGSVVADFACQHPDLEISCVTNLSGYESLRD

DLDLAVIVSRGKMDDSDYIARHLVTIPCTIVAAPSVIQRYGTPSRIQQFEELPCITTVNALKGAPWQFVN

KKGGFETIKVNGRYRVNSGEMAGRAAISGVGFAILSKQACQPYIDDGRLIEIEFEQSAAPLQLFALYSDR

RYLPAKTRALIDFMHQRLSH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529923.1\_2879 [locus\_tag=BN49\_RS15985] [protein=MFS transporter] [protein\_id=WP\_016529923.1] [location=2947881..2949089] [gbkey=CDS]

MPLVTTTFNQKTLIRIAMVIAFVQFTNALEYMMFSPVFTFMAADFAVPVTFSGYVSGMYTSGAVLSGIIA

FYWIDRCNKKHFLIANMVLLAMATLLTTFTNSFPLLLTLRFFAGLVGGTTMAVGITILINHTPADLRGKM

LATVIASFSMVSIVGMPAVLFLCTHYGWHVALWLICTLCWLALPLIVSIIPQDPVTFDTSHALPLDVDTL

LFASGNALVQFSPMLIIPVLAPLMTQLLGASQGLLPWLFFGGGLAGYLSTRMTGALTSRVSALSLATGST

LVFILSLLIPVMGYPHPALFITLFLGAAYSRLVSSSAVTIQFPDNKQRAGFSSLQTSMMYLMTTAAFFLS

AFLLPDHRMALQNMDTLLAVCAITASGTPIIVIVLQKKLAKRTFEPDRFTTE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043309.1\_2880 [locus\_tag=BN49\_RS15990] [protein=LysE family translocator] [protein\_id=WP\_046043309.1] [location=complement(2949147..2949767)] [gbkey=CDS]

MLVTDSLLAYTLAATLLTLTPGLDTALILRTATTEGGRKALHAALGIDLGCFIWGALVAFGLGALLAVSE

LAYTLLKWCGAGYLCWLGIQLLLRPRQQFNTHPAESDSTSNWFLRGMLGNVLNPKMGVFYVSFLPQFIPA

GHSPISWTFLLVTIHVLIGTLWSLTLITATRYAAGILKKPAVVKWMDRTTGCLFLLFAAKLAMSRR

>lcl|NZ\_FO834906.1\_prot\_WP\_023287651.1\_2881 [locus\_tag=BN49\_RS15995] [protein=PTS fructose transporter subunit IIC] [protein\_id=WP\_023287651.1] [location=complement(2949973..2951079)] [gbkey=CDS]

MSLKQIWQAANPKGHLLTAISFLIPIVCGSGFIIAIGMGLGGTVQDTLTPGQFDVWQAMATLGAKALGLL

PVVIAVGISGSIAGKPGIAPGFVVGLAANTISAGFIGGMIGGYIAGYIALAIIKNVKVPDWARGLMPTLI

VPFFASIISCLIMVYIIGTPIGIFTEALTSFLRSMGTSSNLVLGAVIGALCIIDFGGPLNKTCFAFVLTL

QAQGINEPITALQLVNTATPIGFGLAFFIAKLLRKNIYNREEVETLKSAVPMGIVNIVEGSIPIVMNDIV

RGIAAAAIGGACGGAVTMVYGADATVPFGGVLMIPTMSHPMAGIMALLVNIVVTATVYAVIKKDIPRDVI

IDNDYEEEDIDLDDIKVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004176139.1\_2882 [locus\_tag=BN49\_RS16000] [protein=PTS fructose transporter subunit IIB] [protein\_id=WP\_004176139.1] [location=complement(2951122..2951433)] [gbkey=CDS]

MNIVGVTACTVGIAHTYIAQKKIETAAKKAGHNVKIETQGTIGIENPLTADEIAAADIVLLAADVKVTGE

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>lcl|NZ\_FO834906.1\_prot\_WP\_016532074.1\_2883 [locus\_tag=BN49\_RS16005] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_016532074.1] [location=complement(2951490..2951960)] [gbkey=CDS]

MDISTVLNVKNIKLNMTARTKEEVIEELTDLLIQDGAVTNKEDFIRDVWLREELGSTGFENHIAIPHGKS

SGVSRTALAIGRTQHAIPWETMDGSDVRCVILFAVCLVDQNATHIRLLAQVSGSLADEDIIAKLLVESDP

HKIIALFNSETENADS

>lcl|NZ\_FO834906.1\_prot\_WP\_014907576.1\_2884 [locus\_tag=BN49\_RS16010] [protein=D-allulose 6-phosphate 3-epimerase] [protein\_id=WP\_014907576.1] [location=complement(2952077..2952757)] [gbkey=CDS]

MSAKFSPSLMCMDLTQFKEQITAMNKKADFYHVDIMDGNYVRNITLSPFFIENLKKITTVPIDVHLMVNH

PEDIIPMCLEAGADIISFHPETANNKIFRLLNQIKDAGKKCGVVLNPATPAESIAEYAHLLDKVTVMSVD

PGYAGQKFIPESLNKIRKLINMRKNNGYRYLTEIDGSCNEKTFGQIAESGVDVFIVGTSGLFSLHEDVSQ

AWDRMIEIFQRETVAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532075.1\_2885 [locus\_tag=BN49\_RS16015] [protein=PTS ascorbate transporter subunit IIC] [protein\_id=WP\_016532075.1] [location=complement(2952778..2954040)] [gbkey=CDS]

MLHFLIYDVLGTPAILVGLFSLIGLLLQKKGISDVISGTLKTIMGFVILTAGAGIIAYTLTIFSQLFEHS

FHIQGVVPNTDAMAALAQKNYGTETATIMVLGMLINIALARLTPLKYIFLTGHHTLYMAAMLAVILSVGG

LSGGWVVAIGAVILGAMMVISPAILQPFTRKITNTDDLALGHFGSIGYLLSTLVGKIIGKGSPSIEEIKV

PKSLNFLRDSSVAISLTMMILFLVLVLVAGKSFVEETLSAGQNFIIFAIIQSLTFAAGVYIILAGVRMVI

AEIVPAFKGIADKLVKDAKPALDCPTVFPFAPNAVIVGFLASFVAGLVSMFLCPLFGLSVIVPGLVPHFF

CGATAGVYGNITGGRRGAVVGAFAHGLLISFLPAILLPMMGDMGLGSTTFGDADFGVVGIVLGHIIAMFN

>lcl|NZ\_FO834906.1\_prot\_WP\_004176134.1\_2886 [locus\_tag=BN49\_RS16020] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_004176134.1] [location=complement(2954071..2954337)] [gbkey=CDS]

MKKVLIVCGNGLGSSFIVEMNVKKILAEMNKEAEVAHTDLTSAKSETADLILSAKDIAEHLSSHSAKVVG

LSNLLDNNKIKEILAENI

>lcl|NZ\_FO834906.1\_prot\_WP\_004179927.1\_2887 [locus\_tag=BN49\_RS16025] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_004179927.1] [location=complement(2954349..2954786)] [gbkey=CDS]

MIRDWLTPDKIKVINSIDSWENAVRLAAEPLLMQGYIAGSYIEAILQSHKELGPYYVLAPGLAMPHARPE

QGVLRNGLSLLHIKEGVSFGSEENDPIYVVIMLCARSGNEHITMIGELAEIFSDQQKLHRLLNADDSKAI

QAVID

>lcl|NZ\_FO834906.1\_prot\_WP\_004151868.1\_2888 [locus\_tag=BN49\_RS16030] [protein=LacI family transcriptional regulator] [protein\_id=WP\_004151868.1] [location=2955004..2956056] [gbkey=CDS]

MVKSLDADGSPKEKRRKGTGKITLTEVAEFVGVSAMTVSRALRMPEKVNPELRDRIDAAVSQLGYVPNLQ

ARNLASVHSDLILAVVPTFSSPGFLPVSEALQKVLTERGYTMMFMESGHDGQSEQKTFEKMLAYNPAAII

QFNIDTIESCTQLLANVDVPILEIGALNTHPVGMCIGVDYGKAVKQIVTHLADASLKNIALLCTPANNTM

FRQLLSGWNTAMLALNRSPHRVVTTHLPSTIATGVNIFKDMMITWGDLDALICTSDEMACGCMMACHSAG

IKVPNTVAIASLGGGVLSTVCSPALTTVEFPWHDIGVKAGKALLELLNDKPGEKFIEIPSVLKVRASTAA

>lcl|NZ\_FO834906.1\_prot\_2889 [locus\_tag=BN49\_RS16035] [protein=MFS transporter] [pseudo=true] [partial=3'] [location=complement(<2956149..2956991)] [gbkey=CDS]

MHGWTSRQRNAAIASFLSWTLDAFDFFLLVFLLSDIAHSFHVDLEEVTLAILLTLAVRPVGALIFGRAAE

KFGRKPILMLNIVFFSAFELLSAAAPSLMLFFLLRVLYGVAMGGIWGVASSLAMETIPDRSRGLMSGLFQ

AGYPFGYLLAAVAYGLLFEQLGWRGMFVIGAAPVLLLPFIYFCVEESPVWQAARQNKESTALLPVLRSHW

KLCLYLVVLMAAFNFFSHGTQDLYPVFLKVQHGFEPKTVSIIAVCYNIASIIGGVFFGSLSEKIGRRKAI

I

>lcl|NZ\_FO834906.1\_prot\_WP\_046043317.1\_2890 [locus\_tag=BN49\_RS16040] [protein=FAD-NAD(P)-binding protein] [protein\_id=WP\_046043317.1] [location=2957267..2958874] [gbkey=CDS]

MKRIAIVGVGPTGIYTFYELVKRGEPLAITLFEKEAQAGVGMPYSDDNTAAQMLANIASIEIPPIDLTYL

QWLQQQSDDWLAARGLERHALHERQFLPRVILGEYYRDRFLYLVERARDVGFVISVCESCEVTDIAVQST

GIAIHTDSAADPVIVDLVAIATGHLWPEEERASRQYFPSPWTGLMEARIAPCRVGILGTSLSAIDAAVAV

VARHGVFHTEDDKTTHFSLHPGSEALEITLMSRHGVLPEADFYCPIPWEPLEIATPAALEAAIAEGSDAL

LDRIFELIVKELEYAAPDWSEAIGLRQLTPDSIADAWFADRLTHDPFQWAQRNLQEVERNKREHHTVPWR

YAILRLHEAIETLVPQFNDADSRRFRQGLARVFIDNYAAIPPESIRRLLALHRAGILRILTLGEDYELQR

EPDRTLIVHHRQRCEFDVFIDARGQKALKTRDLPFPSLRQQLLACGDDIPDVGDDYTLQAPETVRGRVAF

GALPWLMHDRPFVQGLTASAEIGSAMARAVSQQAAGRRRRLWYIE

>lcl|NZ\_FO834906.1\_prot\_WP\_002905225.1\_2891 [locus\_tag=BN49\_RS16045] [protein=NADH:flavin oxidoreductase/NADH oxidase] [protein\_id=WP\_002905225.1] [location=2958982..2960082] [gbkey=CDS]

MSHLFSATRIGQLTLDNRIVIAPMCQYSADEGKATSWHRIHLGQLAFSGAGLLILEATAVEPAGRISPGD

LGLWDDETENALRGVVEDIRAWSPIRLGIQLGHAGRKASCAAPWQGGHQLALNDGGWQTVAPSAVAFHDG

DRAPAELSHADLARIKAAFVASALRAQRLGFELIELHAAHGYLLHQFLSPLSNQRRDEYGGSLENRMRYP

LEVFKAIREAVGNTMAVGVRLSATDWVEGGWDCEQSIKFSQQLETLGSDYIHVSSGGLSPQQAITVGPGY

QLPFARDIRQQVAIPVIGVGLITDPQQAEAALENGDADLIALARAVLYDPHWPWHAAASLGAQVRVPSQY

LRSEPHGLKGTLLPNR

>lcl|NZ\_FO834906.1\_prot\_WP\_004179939.1\_2892 [locus\_tag=BN49\_RS16050] [protein=hypothetical protein] [protein\_id=WP\_004179939.1] [location=complement(2960314..2960847)] [gbkey=CDS]

MQRITKLDNDLTCKGMLMKLWNKTLLASALCLTLFGCDDASKVDNKLDKAKDNAEQMKDAAADKAQAIKQ

DADKQIDTLKSQADAEADRLKDQASAIKAEADKKADAIAQQAKAQADAVKQNAKQESDRIVKEAGQIKDN

AIGDANQLSAEAASKTKAIQDSIAKDKQNAAPPAAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_072196415.1\_2893 [locus\_tag=BN49\_RS16055] [protein=LysR family transcriptional regulator] [protein\_id=WP\_072196415.1] [location=complement(2960912..2961802)] [gbkey=CDS]

MNLFENIKIFIEIVDAGSFAQAAENLQIHRPAVTKALQQLEQESGVRLLQRTTRRLYLTPEGEEFYRRSK

PLLSQADDLLESFAPDRPIRGQLRVDMPIAFARLLVIPHLPDFYQAHPEVEIVLSSSDVRRDMLRDGLDC

LLRVGDLEDGDYVARSLGEVALTTCASPGYLVRYGAPATLEDLQSHLAVNWVNSSSRQIMPWRFQTPEGI

RQIAIPGKLVLDNSEVFTAAGLAGLGMLQGMRFFLQPYIDSGQLVEVLPDFPAPRRPLSLLYPHRHLSHK

VRVFADWLQGLVATLD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043325.1\_2894 [locus\_tag=BN49\_RS16060] [protein=nitronate monooxygenase] [protein\_id=WP\_046043325.1] [location=2961977..2962954] [gbkey=CDS]

MQPNRVARILGIEKPVVQGPLSWLTDARLVAAVGNAGGLGVLGPNAGLTAATAVSTPEATAEKMREEIRK

TKQLTEKPFGVNLIPTAENDIWTPAILPVIKEEGVKVVVYTGYGDGSLKPALFDELKAAGITIIYRDINP

TPENSRRAEQAGADIIVATGFDEGGTLPGTALGTFTIVPLIVDAVQRVPVMATGGITDARGARAVHALGA

EGVFAGSVFISTIESRVPDSVKAKIVAANGLDLRLFRTLPDYYRALPGKLSDTLVAMDRAGASRTELAQA

MGGLRGMRLGMLEGNTDEGYISVGAGIGNIHAITSVAEVVNQLAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004190018.1\_2895 [gene=hpxK] [locus\_tag=BN49\_RS16065] [protein=allantoate amidohydrolase] [protein\_id=WP\_004190018.1] [location=complement(2962987..2964246)] [gbkey=CDS]

MSDTVRQQAEREAAASRVMARADRLAAFSETADALTRVYLSPEHLQANQLVGQWMQAAGMMVWQDSVGNI

CGRYEGQQEGAPAVLLGSHLDTVRNAGRYDGMLGVLAAIEVVQRLHQQGRRLAKAIEIVGFGDEEGTRFG

ITLLGSRGVTGTWPESWLSQCDTDGVSVAQALVNAGLDPARIAHAARHPRDIAAYLELHIEQGPCLEQAG

LALGVVEAINGARRLNCRFTGEAGHAGTVPMLHRKDALAAAAEWMVQVENLTRQRGGNLVATVGTLRCAP

GAVNVIPGEVQLTLDIRGPQDAPLTALLEELLGQAQAIAGRRQLSFAAEEYYRIAATACDSHLQAVLSEA

VVAVQGRSLTLPSGAGHDAIAIAERWPSAMLFVRCLGGVSHHPAESVTAADVGLAIDAFSRAVEKVADA

>lcl|NZ\_FO834906.1\_prot\_WP\_004190015.1\_2896 [locus\_tag=BN49\_RS16070] [protein=alanine--glyoxylate aminotransferase family protein] [protein\_id=WP\_004190015.1] [location=complement(2964243..2965484)] [gbkey=CDS]

MDITQFSQINPPQRLLMGPGPINADPRVLRAMSSQLVGQYDPAMTHYMNEVMALYRGVFRTENRWTMLVD

GTSRAGIEAILVSAIRPGDKVLVPVFGRFGHLLCEIARRCRAEVHTIEVPWGEVFKPDQVEDAIKRVRPR

LLLTVQGDTSTTMLQPLAELGEICRRHDVLFYTDATASLGGNPLETDAWQLDAVSAGMQKCLGGPSGTSP

ITLSPRMEEVIRRRRCIEQGIRTDAHHDGVDEMIYSNYFDLGMVMDYWGPERLNHHTEATSALFAARECA

RLILQEGLDNGIARHKLHGDALLKGIQAMGLETFGDLRHKMNNVLGVVIPNGVNGDQVRKLMLEDFGIEI

GTSFGPLHGKVWRIGTMGYNARKDCVMQTLSALEAVLNYLRFTTTQGAAMQAAWDHYRTEATL

>lcl|NZ\_FO834906.1\_prot\_WP\_004179947.1\_2897 [locus\_tag=BN49\_RS16075] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_004179947.1] [location=complement(2965500..2966237)] [gbkey=CDS]

MPLITINQMQKYYGDNHVLKGVDLDIDMGEVISIIGRSGSGKSTLLRCINGLEGYQEGSIKLGGMTITDR

DSQAREISRSIGMVFQNFNLFPHMTALENVMLAPRRVLKKSQAECRELAQRMLEKVGLGDRLDYYPANLS

GGQQQRVAIARALAMSPKVLLCDEITSALDPELVGEVLKVLEQLAAEGMTLILVTHEMNFAREVGDRVVF

MHQGRVWEQGDSKTLFASPQTSELKQFISSVRGLN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529165.1\_2898 [locus\_tag=BN49\_RS16080] [protein=amino acid ABC transporter permease] [protein\_id=WP\_016529165.1] [location=complement(2966218..2966874)] [gbkey=CDS]

MTTFTDWDIIRNLLLAGCWTVLLSLVAFTGGALVTLPLLLLRLTGGRQVKRLIRGYIELFQGTPLLMQLF

LAFFGVALFGVDVSAWTAASVALTLYTSAFLLDIWFGSIRALPKGQWEASRCLGLSFGQTLYRVVAPQAL

RIAIAPTVGFAVQVIKGTALASIIGFVELTKAGTMLTNVTYQPFKVFALVALGYFILCYPLSRYSRYLEN

KFNASHHH

>lcl|NZ\_FO834906.1\_prot\_WP\_004176117.1\_2899 [locus\_tag=BN49\_RS16085] [protein=amino acid ABC transporter permease] [protein\_id=WP\_004176117.1] [location=complement(2966874..2967539)] [gbkey=CDS]

MTEQLHFSELWPHWPELLAGLWVTVQLTVLATIGGLAIGILGAAIRSGRPGMLSRVWGGYVEIIRNTPFV

VQLFFIVFGLPNLGLKMTAGEAALLAMVVNLGAYSTEIVRAGIQVTPKGQWEAGRVLGLSRTQTFVRVVL

PPALQRIYPALVSQCIIVMLGSSVVSQVSYEELTFAANLIQSRTFLSFEVYLVTTGIYLALSIAMRQLLM

AAGRKWLGVQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004143665.1\_2900 [locus\_tag=BN49\_RS16090] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_004143665.1] [location=complement(2967549..2968334)] [gbkey=CDS]

MKKLLIALAGAACLLSSVSAAQADQLQDIEKRGVIRIAVPQDFPPFGSVGTDLQPQGYDIDMARYLAKSM

KLKLQLVPVTSANRVPYLQTDKVDLVISSLGKNAEREKVIDFSRAYAPFFLGVFGPKGAELKDAAALSGK

SIGVTRGAVEDMVLTSVAPQAAQIKRYEDNNTTLSAYLSGQVQYVATGNLVVAAISRQNADKAPVPSFML

KDSPCFIGLKKNEPALKAKVDTLIEQGIKDGTLNGLSEKWLKAPLPASLGA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176115.1\_2901 [gene=hpxU] [locus\_tag=BN49\_RS16095] [protein=MurR/RpiR family transcriptional regulator HpxU] [protein\_id=WP\_004176115.1] [location=complement(2968549..2969388)] [gbkey=CDS]

MQQLDERLKGQYASLSPQEQRVADFIFDHFDDLISYNSAELAQLSGVSKATVSRLFKRLGYDKYKDMRDE

LRTLRQSGMPLTDQRDAVQGNTLLARHYKQEMANLTQWVNALDARQFAEALTAMVAARRIVVIGMRNAYP

AALHLRQQLLQARGQVLVLPQPGQSLSEELVDLTADDLVVMMAFRRRPRIVRPLLQQLQRDGVPVLLMCE

PQAHSLFPLSRWQLCAPLDSVSAYDSYASVNSLINLLANAFLHETLDSGRPRIHDIATLYQQLDELEQR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043329.1\_2902 [gene=hpxW] [locus\_tag=BN49\_RS16100] [protein=oxamate amidohydrolase] [protein\_id=WP\_046043329.1] [location=2969568..2971154] [gbkey=CDS]

MHSSNVSAHGMAVAPHHLASQSALAILREGGSAIEAMVAAAAAIAVVYPHMNGLGGDGFWLIVPPEGDPI

AIDASGAAGSLATLEAYAGQRHIPHRGPQAALTVAGTVSGWDEALRISRDLTGRALPVARLLADAIGYAE

DGIPVTASQAHATASKLEELRHQPGFSETWLVAGEAPRPGSRFRQPALAGTLRMLASDGLDSFYRGPLAE

RLAQGMAALGMPVTLGDLQAHRARRPGPLTLQHQQGTLWNLAPPTQGLVSLAILGITDRLKMADADDAQT

VHRIVEATKRAFALRDAHITDPRHLDVDVQQLLTPEALQPLADSIDDASASPWGGGKGPGDTVWMGVVDN

SGLAVSFIQSIYHEFGSGVVLPDTGIVWQNRGAAFSLDPQHLLALAPGKQPFHTLNPAAARLNDGRVMVY

GSMGGDGQPQTQAALFTRYILQGVPLQESISRPRWLLGRTWGQSSDSLKLEGRFAPACIARLRELGHDVE

VLADFSEAMGHAGAIVRHPNGLLEGATDPRSNGAAAGY

>lcl|NZ\_FO834906.1\_prot\_WP\_004176113.1\_2903 [gene=hpxX] [locus\_tag=BN49\_RS16105] [protein=oxalurate catabolism protein HpxX] [protein\_id=WP\_004176113.1] [location=2971165..2971350] [gbkey=CDS]

MTTQPDWSEYLTQMTHLLDMELDAPRRKELERQFARIAAMAQPLMDYPLGPREEIAGVYKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043331.1\_2904 [locus\_tag=BN49\_RS16110] [protein=AtzE family amidohydrolase] [protein\_id=WP\_046043331.1] [location=2971347..2972744] [gbkey=CDS]

MTLQHFTIADLQRALHDGELSAREIARQTLDDIARVNPQINAWTEVTAQRMLAEADSIDALRREKRPLPP

LAGIPYAVKNLFDVAGHTTLAGAELLSDRPPAASDSWAVRQLHSAGALLSGMLNMDAYAYGFTTENSYYG

ATRNPHDLSRIAGGSSGGSAAAVAAGLVHFSLGSDTNGSIRVPASLCGIFGLKPTFGRLSRSGSHPFVAS

LDHIGPFARRVADLAAVYDALQGRDPADDFQADKASERTGNLLERGLEGLRCARLGGYFTTWCDDDARAA

VERVAHALSADSELQFADAALARSAAFIISASEGGNQYLADLRHSPERFEPHSRERLLAGAMIPSAWYLQ

AQRFRRHARQAMKSLFSQADVLIAPATPCSATPIGAEEMVINGQPLPVRASMGMLTQPISFLGLPVVTVP

LRTASGKPIGLQLIAAPFNEQACLRAARALEAMGITDARVAESAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002905421.1\_2905 [gene=hpxZ] [locus\_tag=BN49\_RS16115] [protein=oxalurate catabolism protein HpxZ] [protein\_id=WP\_002905421.1] [location=2972741..2973127] [gbkey=CDS]

MINLDNVDRPAILAEVTAAFYQYEEALVSNNIEALDALFWHDPRTVRLGAGENLYGIEAIRAFRAARPAA

GLARDLRHTTITTFGADMAVCSTEFTREGSARLGRQQQTWVRFPYGWRIVAAQVSLMD

>lcl|NZ\_FO834906.1\_prot\_WP\_004212128.1\_2906 [locus\_tag=BN49\_RS16120] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004212128.1] [location=2973213..2973635] [gbkey=CDS]

MVFIRAAEAEDIPSLQTLFLQLGYQTETAILAQRITAPQSMMSALVAETENAVCGVIVINFILPVHENRL

WALISALVIEESSRGSGIGQQLLQAAERLARDKQCAQIELSSSEKRIRAHQFYENNGYKEVRKRFVKHLS

>lcl|NZ\_FO834906.1\_prot\_WP\_016532138.1\_2907 [gene=asd] [locus\_tag=BN49\_RS16125] [protein=aspartate-semialdehyde dehydrogenase] [protein\_id=WP\_016532138.1] [location=complement(2973673..2974791)] [gbkey=CDS]

MKQVGIVGWRGMVGSVLLQRMIEENDFDDITAHFFSTSSAGAPGPVINGRSDRLKDANSLSALAEMDIII

TCQGGDYTKAIYPALINHGWQGYWIDAASALRMDEKACIILDPVNRENIDSAVKAGIKLFVGGNCSITLS

LMGLAGLIKADLIEWMSVMTYQSASGAGAKQVRELIAQSAYISQHLSADELTSSGSVLPLVNKVSELINS

AGMPVENFGVPLMGSIIPWIDSDLGDGNSREEWKGEAETNKILGLAPGTIPVNGLCIRVGVIRCHSAAIT

LKLKREVSEAEFAELVTHSHPWVNYVRNNKQESVSKLTPAAISGSLQVGIGRYKKMSLNNDPVYSVLTVG

DQLLWGAAEPLRRMLNILLGKI

>lcl|NZ\_FO834906.1\_prot\_WP\_032408689.1\_2908 [locus\_tag=BN49\_RS31075] [protein=hypothetical protein] [protein\_id=WP\_032408689.1] [location=2974993..2975115] [gbkey=CDS]

MKRRSETGAASSPGTMKSNLHFDSYYVNLLAKATWLLDSP

>lcl|NZ\_FO834906.1\_prot\_WP\_016532139.1\_2909 [locus\_tag=BN49\_RS16135] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_016532139.1] [location=2975112..2975669] [gbkey=CDS]

MKNEPLCHAPCPIARSLGRIGDSWSIMILRDAFAGFTRFDEFQKSSNVAPNILSRRLKELVDDGLLEKVC

YSSTPPRYEYHLTPRGRDFRMVLLALAEWGNRHFAPEGRQMQLVEIATQRRVEPVMVDKATGEEIIPGKY

AMVPSPAASPLMKYRHEYLLRKREGDSGQKFQPEPYRDASNESDQ

>lcl|NZ\_FO834906.1\_prot\_2910 [locus\_tag=BN49\_RS29155] [protein=EmrB/QacA family drug resistance transporter] [pseudo=true] [partial=5'] [location=<2975694..2975886] [gbkey=CDS]

HLNNARILFSAARQTSPRGDLTGCRAGAAGGANPGLFRCVLPHHDGFFTCRAAGSLDEKAAGTL

>lcl|NZ\_FO834906.1\_prot\_WP\_042942689.1\_2911 [gene=fabF] [locus\_tag=BN49\_RS16140] [protein=beta-ketoacyl-ACP synthase II] [protein\_id=WP\_042942689.1] [location=2975906..2977180] [gbkey=CDS]

MGVSVKRIVVTGMGIVSPLGCGVQHVWQSLLAGKSGITRLSEQLVADIPCKVAGQVPSIDSDPLHGFDPL

ATIPAKERKKMDRFIEFALVAAREALAQAGWSPASEAEQERTATVIATGIGGFSEIANAVHTTDERGPRR

LSPFTIPSFLANLAAGHVSIAHGFRGPIGAPVTACAAGAQAIGDAARMIRSGEADIALCGGAEAAIHRVS

LAGFAAARALSSASSDQPEAASRPFDRDRDGFVMGEGAGLIVIESLEHALARGATPLAELVGYGTSADAY

HLTAGPEDGNGARRAMEIAIRQAGVTVEEIDHINAHATSTQVGDKGELAAIKTLFGAHPVAITSTKSATG

HLLGAAGGIEAIFTIQALRDQMVPPTLNLHHPDEDAAGLNLVALQVRPQKMRYALSNGFGFGGVNASLLL

KRWQ

>lcl|NZ\_FO834906.1\_prot\_2912 [locus\_tag=BN49\_RS31465] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=complement(2977184..>2977375)] [gbkey=CDS]

SVLRSKLTLIDNFGWLDNASIPFSMSRIGAIVSTGIALYLIYSSSRAKAATVEIPRRPVPRGS

>lcl|NZ\_FO834906.1\_prot\_WP\_074075335.1\_2913 [locus\_tag=BN49\_RS16155] [protein=ASCH domain-containing protein] [protein\_id=WP\_074075335.1] [location=2977529..2977885] [gbkey=CDS]

MGDSPELANELADLIKKGIKTASCGSYASYQQEEFAPRVGSYNIILDGQNVPVCVIRLISMQLVRFCDVT

EAFARKEGEGDLSLEYWKKEHQRFFSSEGHFSEDMELIAEEFVVVEVL

>lcl|NZ\_FO834906.1\_prot\_WP\_071609167.1\_2914 [locus\_tag=BN49\_RS29160] [protein=hypothetical protein] [protein\_id=WP\_071609167.1] [location=2978088..2978987] [gbkey=CDS]

MLSYMLSQYARLPVSEVTLRSWLKQWLSEQESRCTDRNFSARFPWRETGLCQEYFLQRKLKIDGKQFLTG

PRYQGGNINKPFIDIVGMDSDLNHTALELISKEWSQLRAQYVRILVPGQSFPQGIPDQYIYATSFSEPPE

FNDKSLTLQVATYEDFDWCCQALGDAYKHTWQTVRELSASNLVAVDDEELCDHISEREVYIIYENDVRAG

LLICQKGNLAFLRGYRITDKVILPAFRGRSLSARAQRLLYRLLIHSDSELSLYMGTITPENIPSMKTAER

AGRTCILSYQFLPICRTHD

>lcl|NZ\_FO834906.1\_prot\_WP\_171819476.1\_2915 [locus\_tag=BN49\_RS16165] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_171819476.1] [location=complement(2979453..2980253)] [gbkey=CDS]

MIMAGAKSQMPGSIDKAPRHDEATGWSSTAISYQRGEADPPHHHVEGQLLFATRGVMLVQTESDRWVIPP

QRALWLPPLHIHSYHLLSQTDLRAIYFSSSLIAECTSFTKSQQVHVITATPLVKELIAGLFSEDYARPSQ

RKIALLLLDILSEAPPLTMALPMPNDERLFSAARSLLVNQRWEASLSELAFMSAMSERTFSRLFMKDTGF

SFRTWKQRARICASLDLLANGVPIKQVAYQLGFSCPAAFTAAFRCILGATPRDYVP

>lcl|NZ\_FO834906.1\_prot\_WP\_016532143.1\_2916 [locus\_tag=BN49\_RS16170] [protein=GMP synthase] [protein\_id=WP\_016532143.1] [location=2980346..2981071] [gbkey=CDS]

MRVHFIVHESFEAPGAYETRAINQGHDVTYSRVYAGDRLPADAVGIDFLIVMGGPQDPDTTLEACPHFNA

KAEQALIASAVKTGKAVIGICLGSQLIGEALGAPFSHSPEKEIGKFPITLTEDGRKDEMFSHFGKTLEVG

HWHNDMPGLTPEAKIIAYSEGCPRQIVAYSDRVFGFQCHMELTLDVVERLIAHSEKDLSRAAEYRFVDTP

EALRAHDYSEMNQVLFDFLHKLEARYKAAQA

>lcl|NZ\_FO834906.1\_prot\_WP\_000333416.1\_2917 [gene=hxsD] [locus\_tag=BN49\_RS16175] [protein=His-Xaa-Ser system protein HxsD] [protein\_id=WP\_000333416.1] [location=2981341..2981613] [gbkey=CDS]

MCERTFEKELYSEWVIRNSLYWMTPLTRWKLLEELSSWTISFENDSPECLYEFERLLNDYALREKLQHKT

GALRDSIVHKVLRSVDERLS

>lcl|NZ\_FO834906.1\_prot\_2918 [locus\_tag=BN49\_RS16180] [protein=(4Fe-4S)-binding protein] [pseudo=true] [partial=3'] [location=2981613..>2982041] [gbkey=CDS]

MELMPFNFDRLPNGRVFISNLAGFHHFINEQELLDLADEQISAEQSNALESKLFITNESSSAIAPYALSS

AFAKRLMNELAIRPIFMIVPTLRCDHTCKYCQVSRASVNASGYDLDPDLIPHIISTIKKLSIPPYKIEIQ

GGE

>lcl|NZ\_FO834906.1\_prot\_2919 [locus\_tag=BN49\_RS29165] [protein=IS3 family transposase] [pseudo=true] [location=complement(2982054..2983286)] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQPAISLA\*AIPGGKSYCCGCRRTGRS

CL\*TCCRHEAD\*RTPAPARQKNDGK\*TP\*RSR\*IWASKKVDSARALIARGWGVSFVSRCLRVSRAQLHVI

LRRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNAL

LLERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSET

VQDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIK

RDYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_2920 [gene=hxsB] [locus\_tag=BN49\_RS16190] [protein=His-Xaa-Ser system radical SAM maturase HxsB] [pseudo=true] [partial=5'] [location=<2983354..2984341] [gbkey=CDS]

LEIQGASLRATLAVRFNSVYL\*AMY\*NAGKLRF\*DGDSIKPVCLE\*GYA\*MVERQEHNVLCFA\*W\*GGCS

QQ\*SNSWSWACLQ\*NSIRSRGYQTVFRRWSRCNGYYSY\*RSYQAS\*IDCPSSLVSWPQGHVYPTC\*SLWV

CTKSIVHLFYGRILKFLCLVDR\*NP\*DQQ\*RDKDC\*TFGLHSSEKDLQSRF\*WLCGFEVAMWGRA\*QYSF

QL\*RSSIW\*\*\*EPYVAEGES\*NGVQCG\*G\*DAIIFQESLL\*RSIEFIVQFCFARL\*YMRLSTILRCRPMP

EHKCTR\*ACR\*\*ESFNVLSVSQGDVQISDELHLRRWSEG\*DAKRMDICL

>lcl|NZ\_FO834906.1\_prot\_WP\_032104306.1\_2921 [gene=hxsC] [locus\_tag=BN49\_RS16195] [protein=His-Xaa-Ser system radical SAM maturase HxsC] [protein\_id=WP\_032104306.1] [location=2984334..2985446] [gbkey=CDS]

MSEVIRNDIFHFASNKNVPTGFYRLCKRKPANPLFFLPNLLVVAEGNNDAIQPCFDCSVISTELFESIED

GDIGIINNGNMIRVILSRRANYNTVLVTERCNNLCMFCSQPPKKSNDDWLLTQSALAIASFGLDGVVGVS

GGEPLLYGDDFLHFIDFIIENSPDTALHVLTNGRKFADINFTQEVAKRGKKIKITFGIPLYSSRPLVHDH

LVGSDGAFNETVKGLINAGNSGINIELRVIPTLANYTELDDIVEFVGRVFSNINQISLMGLESIGWARKN

WSTIFIEHSSYSEKIMSAIDVAHKSGIPLTIFNYPLCHLPERAWELAAQSISDWKNYYPKECDECTQKSS

CTGYFSSSTGRFLQPPRPIL

>lcl|NZ\_FO834906.1\_prot\_WP\_071829955.1\_2922 [gene=hxsA] [locus\_tag=BN49\_RS29170] [protein=His-Xaa-Ser repeat protein HxsA] [protein\_id=WP\_071829955.1] [location=2985443..2986078] [gbkey=CDS]

MKKFNFAALLPGFLALNNSVWASDSSTGANDLPGMTLNEHDLVIAPLNTEVPFYVAGHRSHSSHRSHSSH

RSSSGGGYYGGSTPYYPKTYSSTSSSGSSSSGTSSSSSSSSVRSLRSNDNNNSTTTNSGGTTEANRASNG

LTSGTEKRKRLIMRVQFALLDRGYYNGNIDGIMGPSTRQSIKNYRIANGLPTPATETLDTQLLNSLNILA

R

>lcl|NZ\_FO834906.1\_prot\_WP\_046043347.1\_2923 [locus\_tag=BN49\_RS16205] [protein=hypothetical protein] [protein\_id=WP\_046043347.1] [location=complement(2986474..2987490)] [gbkey=CDS]

MKLKRMLQMNFIKEFQENLDNDFEEQLFIACLRNYCSHGNPLRFGNFAYALRELINHVLSRMAPDERVIT

APWFTANKNNVKVTRKQQAKYIAQKHIPDGLLDAAALKKLDDGIGWFNKNYQSLNYYTHITEESLKSQPK

DFFEKAKLLIELCNKIFDNFGDLERILTHSIIDKVSDHVNEVTRDNTPNEVDILSSQTIVETCIVESIEP

LSLTEDYVYLLVRGTLEITRQYGRGDDYLAQGDYYPFTFAVSVRASDFEDIRPLVRTAIVDTGSWYDDGN

GSAMADKIYSTRRFLEMIAQVHIKPARLRSLFPELSYVIPDDEPDEMVQGLNYTEIEF

>lcl|NZ\_FO834906.1\_prot\_WP\_016531540.1\_2924 [locus\_tag=BN49\_RS16210] [protein=hypothetical protein] [protein\_id=WP\_016531540.1] [location=complement(2987715..2987939)] [gbkey=CDS]

MNHLTVEKIIIIILLILWGFDTFRTRKRKRYDPAIEAADASERHQWRYLRWGFRIIQVLAGVYIVVQLIQ

VLLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531541.1\_2925 [locus\_tag=BN49\_RS16215] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_016531541.1] [location=complement(2988142..2988909)] [gbkey=CDS]

MRNVKIDEVDRLDRDVVALGNDYAQGFILPPHQHRRAQLLYGATGLMYVTTQDGEWGGPPQHAVWIPPET

VHAVRFAGVTTRSLYIEPDCVAAFIKHRRCEVISVSPLLRQLLLEAVDLPPLYDSPRDRTLIQLMLLELA

AMPVREFDIPLPQHPALLALCQAFLLNPSIHDPAARWARALFMSPSTFRRHFLKQLGLSFSAWRQRACVV

SALAWLIAGKPVNEVALSLGYDNASSFATMFRRVTGQPPSFYHPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004176099.1\_2926 [locus\_tag=BN49\_RS16220] [protein=sulfite exporter TauE/SafE family protein] [protein\_id=WP\_004176099.1] [location=2989019..2989810] [gbkey=CDS]

MNEIVIIALAGFTTGITTVLFGFGGGFVVVPFVYQLMLRQPAIAGNAMHVAVATSTAVMIFNAGWVSYRN

WRAGRLAAQTLFPLLWFIAIGAVVGSCLAGILSENIVRALFIFYMLATISDCLLRKGFFTGSARRRLSLP

VVTGGGVIIGTIAALLGVGGSVMTVPLLRRHGYAMQECVSASNPLSLPVALCGAVTYAVIGWHSIPLSGF

LGFISLKILGLLVLTGWAGIVFSRRAIPAVPDVWYARIYVLLLCLVLLAMLIQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004179983.1\_2927 [gene=puuE] [locus\_tag=BN49\_RS16225] [protein=allantoinase PuuE] [protein\_id=WP\_004179983.1] [location=complement(2989899..2990831)] [gbkey=CDS]

MGENQEHYPRDLRGYAGEPPHARWPGGARIAVQFVLNYEEGAENHVLHGDAGSEQFLSDIIGAASYPARH

MSMDSLYEYGSRAGFWRIHREFSQRGLPLTVFGVAMALARHPEIVAAIKAADYDVVSHGWRWIHYQHMDI

AEEREHLQKAVQVLTDLFGKPPTGWYTGRDSPNTRQLVVEHGGFDYDSDYYGDDLPFWSEVACSDGSQRP

HLIVPYTLDANDMRFATAQGFNTAEQFYTYLKDSFDVLYAEGETAPKMMSVGMHCRLLGRPGRFRALQRF

LDYIQQHDKVWVCTRQQIADHWRETHPYRG

>lcl|NZ\_FO834906.1\_prot\_2928 [gene=hpxA] [locus\_tag=BN49\_RS16230] [protein=allantoin racemase] [pseudo=true] [location=complement(2990716..2991587)] [gbkey=CDS]

MSSVRIQVINPNTSLAMTETIGAAARAVAAPGTEILAVCPRAGVPSIEGHFDEAIAAVGVLEQIRAGREQ

GVDGHVIACFGDPGLLAARELAQGPVIGIAEAAMHMATMVATRFSIVTTLPRTLIIARHLLHQYGFHQNC

AALHAIDLPVLALEDGSGLAQEKVRERCIRALKEDGSGAIVLGCGGMATLAQELTRELRVPVIDGVSAAV

KMVESLVALGLATSKHGDLAFPEKKALSGQFQSLNPF\*KGQEMGENQEHYPRDLRGYAGEPPHARWPGGA

RIAVQFVLNY

>lcl|NZ\_FO834906.1\_prot\_WP\_004179987.1\_2929 [locus\_tag=BN49\_RS16235] [protein=GntR family transcriptional regulator] [protein\_id=WP\_004179987.1] [location=complement(2991587..2992303)] [gbkey=CDS]

MNNEHRLQAAPALQDKDESIYQALMTAIVEHQLPPGSKLPEEALAEVFAVSRTGIRKVLQRLAAVQLVTL

TPKRGAHVTSPSVEESQAIFRTRALLEVANLPDVIARCQPPHLAALENIIQREQQAHAAHDGPAAIRHSA

DFHIQLQAISGNPVLTEMVTRLSQRSSLVIAAWGAPWRQGCRCDDHQQLVGLLRDKALQPLSEALMHHFD

HIVASLCFERDGVSLPDFSRLFAGHKES

>lcl|NZ\_FO834906.1\_prot\_WP\_016531546.1\_2930 [locus\_tag=BN49\_RS16240] [protein=NCS1 family nucleobase:cation symporter-1] [protein\_id=WP\_016531546.1] [location=2992448..2993944] [gbkey=CDS]

MPHSSHTQQTKTHEAAAGYSPRLCNDDLAPTRDQNWSWYNIFSFWMSDVHSMGGYVVAASFFTLGLASWQ

VLLCLLVGICIVQLCANLVAKPSQMAGVPYAVICRQAFGVFGANIPAVIRGLIAFAWYGIQTYLAANALM

LVLLKFWPSLASLTSSSFLGLSPLGWLCFATMWLLQAMVFWHGMNAIKRFIDIAGPAVYVVMLALAGWIV

YKTGLDGISFTLASKSLSAGEQTWQMITATALVVSYFSGPLLNFGDFSRYGKSMGEIRRGNRWGLPFNFL

LFSVVTVVIVSGTQSLFGKMITDPIETVSRVGNDLAVAIGLLTMITATIGINIVANFVSPAFDFSNCAPQ

KISFRTGGMIAAVGSILLTPWNLFNSPELIHYTLDVLGAFIGPLFGILIADFYLIKRGRVSVDDLFDDTP

QGKYWYRNGFNPKAIAALLPSVGLGLIISFIPALHEVANFSWFIGVCLGATTYRWLARDEREVQAKAAFR

SGAVAQKE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043351.1\_2931 [gene=guaD] [locus\_tag=BN49\_RS16245] [protein=guanine deaminase] [protein\_id=WP\_046043351.1] [location=2994046..2995356] [gbkey=CDS]

MMDYQTAVRGAFFDIAGVAETPDEVAAQARYLDDALLFLQEGKIIALLPWQQGEAFLHPLKGYVDLRGKL

LLPGFVDAHVHYPQTEMIGAFGEQLLEWLTTYTFPVESQFADAEYAQEIAQFFVTQLISHGTTTALVFCT

LHPASVEALFSEALRLNMRLIAGKVMMDRHVPDYLCETAGESYEQTRALIRRWHQRGRLGYAITPRFAPT

STPGLLEAAQRLRAEFPDTWLQTHLSENREEIAWVKQLWPEHARYLDVYHHYQLTGERSVFAHGIHLDDA

EWQCLHDTGSAVAFCPTSNLFLGSGLFRLPACWQHQVRMGIGSDVGAGTTFSMLRTLGEAYKVGQLQSYR

LRASEAFYHATLGGARALRLEEKIGNFQPGKEADFVVIDPAVTPLQRLRIGRCHDIYEQLFVLMTLGDER

NISETWVNGERVWCQD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530404.1\_2932 [locus\_tag=BN49\_RS16250] [protein=DUF2931 family protein] [protein\_id=WP\_016530404.1] [location=complement(2995451..2996110)] [gbkey=CDS]

MEIIREACLLPLLALAACQGKPLPNTAMHSDAPTEWSFNFFTPKALPAVVTFAAILDVDGNDYRFNTLNS

TPDLPGVSGEWNDKDRAPVGYWNHVKRPPRHIIFCWDSIIDKKVYETHLTIPKSVLEQMLMPSKYKDYRG

RIAWYDRMQIGLAPEGKVAVWLQGSGSESNYRVTPSVLKTVSGNKLDICKDITRSDFSYGYDKDIIDFIK

GKHYPYGNW

>lcl|NZ\_FO834906.1\_prot\_WP\_227504833.1\_2933 [locus\_tag=BN49\_RS16255] [protein=DUF2235 domain-containing protein] [protein\_id=WP\_227504833.1] [location=complement(2996101..2997477)] [gbkey=CDS]

MNDADAVTAYSQCVRLKHGYSGTAAGSYIGYYSNVHWLYILYRQDIRPDSGAGQHAIYVEGIGTEDGAGD

NTYGMGTGRGDTGVVRKTDKAVAALTVGIQEYLLQHASDGSCTIKEIQFDIFGFSRGAGAARHFANRVFS

QDRDIITAIRAGLNGIEFSGAPGGKTRFLGIFDTVAAIGTPVNGFNPHSADTGDVNLALRPGVAEKVFHI

TAQHECRFNFALNSVKPAWPELALPGAHSDIGGGYNPNENEAYFLTRPEFETVPFSIPDTETRIYRQTCA

KLKTMDGYPAIALLLNAVEVSVDTWHDDRMPADRYGTLQKRSGAALVINRPTFNDWSKVVLRVMIDAAQD

AGAVFEPIRDTNAHLKLRQELNGLCEKAIAMGRAIRSGKSAPGFTTPELRMLAEKYIHCSANWNSVIRDS

RAIISGAVKPAKLVTFTNRPDDRWQRTVYDMDGNKIWK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043353.1\_2934 [locus\_tag=BN49\_RS31470] [protein=PAAR domain-containing protein] [protein\_id=WP\_046043353.1] [location=complement(2997564..2997974)] [gbkey=CDS]

MAKGFFLYHLDKTTCGGRILSGAPDDTYHIGGIERQQVRVGDPVTCGKHEGRFRVCGGMGDTYDVGGSLK

EWAGSLDSYSSCPCRARFVPTVFSHSYDRDCNAGRVAERAETAKKKTNSLSLNSVRRTQRKNGKSH

>lcl|NZ\_FO834906.1\_prot\_WP\_227504849.1\_2935 [locus\_tag=BN49\_RS16265] [protein=hypothetical protein] [protein\_id=WP\_227504849.1] [location=complement(2998095..2998982)] [gbkey=CDS]

MAANGHAIKQRADAVLTLMSYTVVPDVTASDLNIGSGSNDKHNLAITHFGGGATLSESFPLYLEGTMGYS

RYDPRFVVSNGEQTRNVPTKWNSLTTTGGVGWDFSLHRDSLGGNLVLRPIVNVMLGTLASDARIGSWAIE

RKTNADLQFLDGGRFNAWGLGGALMLDYERFSATQDIDAELRYSYMHLQSFGSSAEVVQGEASAENLGLY

LRRRAPIADWTLLGNPLRYVLEGAHTEFLGEQRGALGFTGLTSLGVGLELDSSKYPVFITRTRLVARYMF

GNNTTGYGVGLAKSF

>lcl|NZ\_FO834906.1\_prot\_WP\_032104313.1\_2936 [locus\_tag=BN49\_RS16270] [protein=sensor domain-containing diguanylate cyclase] [protein\_id=WP\_032104313.1] [location=complement(2999161..3000417)] [gbkey=CDS]

MLLKELAVFEVLSTPIWVVHPFNERVVYANQASRTLSGEMSLNEMRNGIYSTCPETQLQHYLRYLDTMSE

IFEVWTLPTANGLQSVYCKTTLIDTEDCGCLLLFEAVKLLAQNQSIHTGSRRYQRRNNGFFARFFMTNTA

PMLLIDPHKDGRIVDANIAALRFYHYSDEEMRTKHTWQINTLGRDVIPIMNNIANLPGGHKPLNFTHILA

DGSLRHVQTYAGPVVLYNIRLMLCIIHDITEEVHLKKELEFSAAHDPLTGLLNRREFHRLVEAPTFIPRG

YCLLLIDIDHFKSINDIHGHQKGDEVLLVLSRILETSVDREDKIYRWGGEEFLLFLPHSPIGRALILAEG

IRQAVSEYQTLSVTVSIGVAEHHDGETVDQLFSRVDKALYAAKNDGRNRVTRMPFENVELLHSRGGAT

>lcl|NZ\_FO834906.1\_prot\_WP\_016531860.1\_2937 [locus\_tag=BN49\_RS16275] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_016531860.1] [location=3000816..3001856] [gbkey=CDS]

MNKIATKITLADIAREARVGVATVDRVLNKRAAVKESTARRVLEAARRLGFTLEQPHYRLAAGKAPVTIR

MGFILLQESHSFYLPLARALTREAAPWLPAGQAPVILHFAIDAVEAMAQAIHRLSDEVEVLGLVALDHPL

IRHAVARAAARGVRVFTLLSDLSVPQRSGYIGLDNHKAGRTAAWFIERLCRGNGEIGIIIGDNRFTCQES

CEISFRSCLREQGKGQQILEPVRSHERADIARTVTEQMLTQYPALQAIYAPCGGVEGIVDALRDSGRQQE

IALVCHGPLSDSELALIDGTIDIMLNHRLDEFAAVTLRAMADAASRPHSEVISLPQPFDIITKENM

>lcl|NZ\_FO834906.1\_prot\_WP\_016531859.1\_2938 [locus\_tag=BN49\_RS16280] [protein=sugar phosphate isomerase/epimerase] [protein\_id=WP\_016531859.1] [location=3002049..3002972] [gbkey=CDS]

MIHPIANAPCSWGVDDPKNPNLPAWATVLKEAAQAGYRSIELGPWGYLPTDPASLRAALEQHQLSLVAGT

IFDDLVSEAHFPTLVALTHQICRNLSQVAAAEPIPGRPFQPPYLVIIDFGNPERARFAGRGALAPRLNDK

DWQRMMEHIIALSTLAWQEYGVRAVIHPHAGGSIEFADEIERLANDIPHHVAGLCLDTGHLYYAGMDPLD

WLDRYYHRLDYLHFKDVDPQVYQRAIHEGIDFFTACAEGVMCPLGSGAIDYPAIKDFLARRGYQGWITIE

QERDPRHAAGSLQAVTESLRYLRDVGF

>lcl|NZ\_FO834906.1\_prot\_WP\_015958454.1\_2939 [locus\_tag=BN49\_RS16285] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_015958454.1] [location=3002986..3004158] [gbkey=CDS]

MINGLKPLDRTLRWGMVGGGGSSQIGYIHRSAALRDNTFTLLAGAFDIDAERGRQFGQQLGVDPDRCYAD

YQSLFRGEAARPDGIQAVSVATPNNTHYAICRAALEAGLHVVCEKPLCFSSEEADELVALSQRRRKIIGV

TYGYAGHQLILQARQMIADGLLGDIRIVNMQFAHGFHAQPVEQENASTRWRVDPRFVGPSYVLGDLATHP

LFLVETMAPQLKITRLMCARQSFVKSRAPLEDNAHVLMEYDNGAIGSLWSSAVNCGSMHGQKVRIIGEKA

SLEWWDEQPNQLRYEIQGEPVRILERGMDYLDPLARQDDRIGGGHPEGLFEAWSNLYRRFAIAMDAADRR

DEALLADFWYPDARAGAFGVRWVENCVRSADNGACWVDFR

>lcl|NZ\_FO834906.1\_prot\_WP\_002905531.1\_2940 [locus\_tag=BN49\_RS16290] [protein=DUF4056 domain-containing protein] [protein\_id=WP\_002905531.1] [location=complement(3004196..3005302)] [gbkey=CDS]

MRKAFWLLFALALPALAQDPVLPAVTAIHTAPTLGELPPPESLRPCCAFGYDLHVRAAGIPIPMYQIGNV

LTLGTLGKHHYNDSAFGAVKNLLGLSEEQNGLIYTRRGGFIDIAHVRDTADNTFYLFNRIAPTLGQAGRI

FYSEELGVRRVQLNAFTPPAGVRQRYQLAAWLAGHLAFEIAQWHEIAQWYGFQSVPGFSEEISAFSPEDL

YSNLLGARLAINVILSGHGGSLEDYNQAMDAALKQVLTRLLVATRGETEAMFQQIDGDWWNSHRRVPDKF

LVLKRNYDLQENRLPTPVPFETMPPYRLTMPEQVGGFRLRDLGELQIYPGHDMQALPVPAQYYGAGAFQG

LADRAHEADKTQLARTEK

>lcl|NZ\_FO834906.1\_prot\_WP\_015958456.1\_2941 [gene=tenA] [locus\_tag=BN49\_RS16295] [protein=thiaminase II] [protein\_id=WP\_015958456.1] [location=3005719..3006414] [gbkey=CDS]

MIVPAFSQGLYGRLRQLAAADWQRYVAHPFVQQLADGTLAENAFRRYLTQDYLFLIHFARSYALLVSKLR

ALPEMRAAAASMNAILNELPLHVGYCAQWGISEPEMAAQPEAPETLNYTRYVLDIGHSGDALDLLVALMP

CVAGYAEIGLGLLQHPATRLDDNPYASWIRNYGDEGYLQGVSAALALLETVWQQRGSEARITELSEIFTT

ATRLEAQFWQMGLNAAAETRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532548.1\_2942 [locus\_tag=BN49\_RS16300] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016532548.1] [location=3006411..3007139] [gbkey=CDS]

MTAPGIEVRGLSLHVGDRRLFDNLSFTVPGGQWVSLLGASGAGKTSLLRVMAGLAPATRGEVVASDGQPI

QGRLAWMGQKDLLYPWLSVRDNVALGARLRGEKVDRDRVAALLEQVELSSCADARPATLSGGMRQRAALA

RTLYEDRPIVLMDEPFSALDTLTRTRIQTLAATLLAGRTVVLITHDPQEACRLSHRLLVLSAADGDIDDS

HHLAGTPPRAPDAPALLIGQAALLQQLMRAQP

>lcl|NZ\_FO834906.1\_prot\_WP\_004180004.1\_2943 [locus\_tag=BN49\_RS16305] [protein=ABC transporter permease] [protein\_id=WP\_004180004.1] [location=3007136..3007876] [gbkey=CDS]

MTGRLWRGGMVFGGLMLLWGLASRSGIPHFLLPSPLAVAEALWVNRAYLGWHTLITLSEILSGLALGVTL

GVTLALGMILSPRLQRWLMPLVLTSQAIPVFALAPLLVLWLGFGMSAKVAMAVLVIFFPVTSAFFDGLRR

VNQEYLDLARSMNASFGAQLRHVRLMAALPALGSGLRMAAAVAPIGAIIGEWVGSAEGLGYVMLNANARL

QTDICFAALFILVLLTLLLWLAVDTLLHRLIDWSPE

>lcl|NZ\_FO834906.1\_prot\_WP\_004180008.1\_2944 [locus\_tag=BN49\_RS16310] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004180008.1] [location=3007901..3008836] [gbkey=CDS]

MKKSLFAGATLTALFSGHALANEPLTLVLDWYINPDHAPIMVAEQIGAFKAQGLDVRIVPPSDPALPPRM

VAARQADLAITYQPQVHFFADEGLPLVRVGTLINSPLNTVIALDKQIKTPADLQGKKVGYSVSGIEQATL

ATMAQHAGIDPASIKLVNVNFQLTSALLAGQVDAVIGGYRNIEAQELKLQGKTPVVMNVEDYGVPAYDEL

VIVAHRDAIHEAKIRKFLTALQAGVGYLRAHPQKSWEAFAAAHPELRTELNHQAWLQTVPLFATDPAALD

KARYETYEQFLYNNKLVKKVTPLTNYAVELH

>lcl|NZ\_FO834906.1\_prot\_WP\_002905540.1\_2945 [locus\_tag=BN49\_RS16315] [protein=diaminobutyrate--2-oxoglutarate transaminase] [protein\_id=WP\_002905540.1] [location=3009143..3010528] [gbkey=CDS]

MMTDKVRIDTLRADLLDANNETFLARQAEFESNVRSYPRKLPLAITKAEGVWLTDADNKQYLDCLAGAGT

LALGHNHPDVLQSIQSVITSGLPLHTLDLTTPLKDRFSEYLLSCLPGEGKEYCLQFTGPSGADAVEAALK

LAKKYTGRTAVISFSGGYHGMTHGALSVTGNLSPKAAVNGMMPEVQFMPYPHLYRCPLGIGGEAGVKALT

YYFENLINDVESGVRKPAAVILEAVQGEGGVNPAPVEWLQRIRKVTEEHGILLIVDEVQAGFARTGKFFA

FEHAGIQPDIIVMSKAVGGGLPLAVLGIKKQFDAWEPGHHTGTFRGNQLAMATGLTTLRHLRDNKIADKV

AAQGEWLKGKLAELQKRYPVIGHVRGLGLMIGIEIVKPNEAQDHMGCYPADGELSALLQKKCFEAGLILE

RGGRHGCVLRLLPSLLISDAELDVFLDKFEQALLAAGVKPV

>lcl|NZ\_FO834906.1\_prot\_WP\_075212563.1\_2946 [locus\_tag=BN49\_RS16320] [protein=aspartate aminotransferase family protein] [protein\_id=WP\_075212563.1] [location=3010538..3012019] [gbkey=CDS]

MTAMSTLNPILAGSAQSVEAYQQVIEQTSQAVVQWLKQPEMYQGKSVDELRERISLEFNEQGLGNQAAID

RAIEYFLKDSLSVHHPQCVAHLHCPSLVISQAAEVLINATNQSMDSWDQSPSATIIEMKLIEWLRARVGF

PAGDAGVFTSGGTQSNLMGLMLARDAFFARLGHSIQQDGLPGDIRKYKVLCSENAHFSVQKNMALMGLGY

RSVTLVKTDEFARMDVSDLQAKIAQAQANGEQIMAIVATAGTTDAGAIDPLRDIAGIAAEHQIWLHVDAA

WGGALLLSEQYRDYLDGLELVDSVTLDFHKQFFQTISCGAFLLKDARHYELMRYQAAYLNSEFDEENGVP

NLVSKSLQTTRRFDALKLWMGLEALGQKQYAAIIDHGVTMAKNVAEYVKSQPTLELVMQPQLASVLFRSR

PAQMAGSDAAAIALLNQRVGDALLASGRANVGVTEHNGVTCLKLTLLNPVVTLDDVKVLLNLVERTAQEL

LAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_042942915.1\_2947 [locus\_tag=BN49\_RS16325] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_042942915.1] [location=3012215..3013108] [gbkey=CDS]

MGIMMEKRLPGLDLDALRSFVTGMECGSFAQAALRLSRSTSAVSAQLKKLESQCGTALVTKQGRHLVLTA

EGEKLMSYARRLLALNDETLRALQGERLTGEIHLGMQEDFGESLMPGILGQFKRHHPQVRIVARVDRNGP

LRQALAEEALDLALLWQTEDQGPGLGLCPLAWIAHPDLDIRALLVSGEPLPLVMFDSPCLMRSRAIACLD

AAGIPWQVVFVSHSLSGIWAAVQAGLGLTIRTRIGMPGNLRPAGGLLPAPGSLAVSLRQTPREEHHSAAV

ALLGELMTEALQGWLDR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043355.1\_2948 [locus\_tag=BN49\_RS16330] [protein=cytochrome c biogenesis protein/redoxin] [protein\_id=WP\_046043355.1] [location=complement(3013541..3014731)] [gbkey=CDS]

MSILIAFLGGMLTLLSPCTLPVIPLLFASVRGRRGQLAIMLAGMALMFGAVSWLVTVASGWVVNLTLAGR

GLALAFFALVGLSLLSQRVAQRLTSPLVALGNQLNDASSRQRGWIGSLLAGLAVGLLWAPCAGPVLGAIL

SLGFVHPGQATTGGLLLAYGSGGALMLFLLGGCGAALITRLRRGQAFGERLRRLAGGAMLASVALIASGG

DRYLQSAGGLSQALEQRLAARLPQPEQKTSLQPIAAPQPSSAMPSLAGGSAWINSPALTPERLKGKVVLV

DFWTRECINCQHTLPYVRDWANKYRAAGLVVIGVHTPEYPWERSLPLLRQAVKDWRITYPVVADNEYAIW

NAFGNQYWPAHYIFDARGQLRYTAFGEGDYARQEQVIQQLLQESKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043357.1\_2949 [locus\_tag=BN49\_RS16335] [protein=ATP-binding protein] [protein\_id=WP\_046043357.1] [location=complement(3014834..3016177)] [gbkey=CDS]

MRFWPASLQSRLMALLFLALLLANTLTLSLLFYERMSSARSVMLGNLASDVATSVAILDRLPAAERPQWL

PKLARGNYRYLLDAGERGDYPDNWRARDAARSLQEALSAQYPVSIVAIPGPRQHIQAHITLHDGAPLTLD

LWPKLPAIARWLPVVLIAQFVLLLACAWYAVRQVLLPISRFTHAVNALEPASDTAGTMAEQGPEEVRRAA

RAFNSMQARIHDHLQERARILAAISHDLQTPITRMKLRVEMADQPELRDKLLQDLDNMTRLVREGIAFAR

TSQPLEEARQRLNLDAFLDTIVCDYADVGRSVQFCPEETAGVVWIPPQALRRVMTNLIDNALKFGTTATV

TLTRDAVGDITLHVLDEGPGIPEASLQAVLQPFYRLEDSRNRDTGGTGLGLAIAAQLVSQMDGALRLANR

PQGGLDASVRLAAAGLYPAVSPGKTDN

>lcl|NZ\_FO834906.1\_prot\_WP\_004176065.1\_2950 [locus\_tag=BN49\_RS16340] [protein=response regulator] [protein\_id=WP\_004176065.1] [location=complement(3016174..3016914)] [gbkey=CDS]

MERIDHILVVDDDRDIRELIVDYLEKSGYRASGAANGKAMWSVLKNHQIDLIVLDIMMPGEDGLTLCRQL

RANPQQDIPVLMLTARTDDSDRILGLEMGADDYLIKPFVARELLARIKAILRRTRALPPNLQITEAGRLI

VFGDWLLDTAARHLLDDSGAIVALSGAEYRLLRVFLDHPQRVLNRDQLLNLTQGRDAELFERSIDLLVSR

LRQRLREDAREPAYIKTVRSEGYVLSVPVSIRERHE

>lcl|NZ\_FO834906.1\_prot\_WP\_004180015.1\_2951 [locus\_tag=BN49\_RS16345] [protein=alpha/beta hydrolase] [protein\_id=WP\_004180015.1] [location=complement(3017001..3017993)] [gbkey=CDS]

MNRLSLIRYTSAVALGLSTLWSAAVCAAEDAGAFDKIQQIRAGDLNIGYVDIGPRDGQPVILLHGWPYDI

QSYAQVAPALAQKGYRVIVPYLRGYGTTRFLSASTPRNGQPSAMAADIVHLMDALNIRQADLAGFDWGAR

TADIVAALWPQRVKSLVSVSGYLISSQQIGEKPLPPQAELSWWYQFYFATPRGEAGYRQNTHDFAKFIWH

QASPQWQFSDATFAKTARALDNPDHVAITISNYRWRLGLEKGEAKYAGYEQRLAALPPITVPTITLEGAN

NGAPHPAPASYRAKFTGKYEHRDLPGAVGHNPPQEDPTAFVQAVVDADRL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043360.1\_2952 [locus\_tag=BN49\_RS16350] [protein=dipeptidase] [protein\_id=WP\_046043360.1] [location=3018237..3019256] [gbkey=CDS]

MAIFDGHNDLLLNLWLHHREDPVSAFFAGIENGHLDYPRMLQGGFAGGLFALFVPPQEYIARMTPQYASQ

RWDPIDILWQQLAILKQLIAHSAGRLRLCLSAADIERCREDKVLAMVAHIEGAGGFDGEGRDLQAFYAAG

VRSIGPFWNMANRFGSGVNGSFPGSPDTGPGLTAAGIVLIKQANALKMQMDVSHMNEKAFWDTAHHSTSP

LVATHSNAHALCPQPRNLTDQQLRAIRDSGGVVGVNFGNAFLRADGRRDSDTPLTTIVRHIDYLINIMGE

DHVALGSDFDGITLPDELGDVAGLPRLINTLRASGYDQLVLDKLLWRNWLRVLKNVWQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002905689.1\_2953 [gene=pqqA] [locus\_tag=BN49\_RS16355] [protein=pyrroloquinoline quinone precursor peptide PqqA] [protein\_id=WP\_002905689.1] [location=3019393..3019464] [gbkey=CDS]

MWKKPAFIDLRLGLEVTLYISNR

>lcl|NZ\_FO834906.1\_prot\_WP\_004148467.1\_2954 [gene=pqqB] [locus\_tag=BN49\_RS16360] [protein=pyrroloquinoline quinone biosynthesis protein PqqB] [protein\_id=WP\_004148467.1] [location=3019519..3020445] [gbkey=CDS]

MFIKVLGSAAGGGFPQWNCNCANCQGLRDGTIQAAPRTQSSIIVSDNGKEWVLCNASPDISQQIAHTPEL

NKAGVLRGTHIGGIILTDSQIDHTTGLLSLREGCPHQVWCTPEVHEDLSTGFPVFTMLRHWNGGLVHHPI

APQQPFTVDACPDLQFTAVPIASNAPPYSPYRDRPLPGHNVALFIENRRNGQTLFYAPGLGEPDETLLPW

LQKADCLLIDGTVWQDDELQAAGVGRNTGRDMGHLALGDEHGMMALLASLPAKRKILIHINNTNPILNEQ

SPQRQALTQQGIEVSWDGMAITLQDTAC

>lcl|NZ\_FO834906.1\_prot\_WP\_004143685.1\_2955 [gene=pqqC] [locus\_tag=BN49\_RS16365] [protein=pyrroloquinoline-quinone synthase PqqC] [protein\_id=WP\_004143685.1] [location=3020439..3021194] [gbkey=CDS]

MLITDTLSPQAFEEALRAKGAFYHIHHPYHIAMHNGDATREQIQGWVANRFYYQTTIPLKDAAIMANCPD

AQTRRKWVQRILDHDGSHGEDGGIEAWLRLGEAVGLSRDDLLSERHVLPGVRFAVDAYLNFARRACWQEA

ACSSLTELFAPQIHQSRLDSWPQHYPWIKEEGYFYFRSRLSQANRDVEHGLALAKAYCDSAEKQNRMLEI

LQFKLDILWSMLDAMTMAYALQRPPYHTVTDKAAWHTTRLV

>lcl|NZ\_FO834906.1\_prot\_WP\_004143686.1\_2956 [gene=pqqD] [locus\_tag=BN49\_RS16370] [protein=pyrroloquinoline quinone biosynthesis peptide chaperone PqqD] [protein\_id=WP\_004143686.1] [location=3021197..3021475] [gbkey=CDS]

MQKTSIVAFRRGYRLQWEAAQESHVILYPEGMAKLNETAAAILELVDGRRDVAAIIAMLNERFPEAGGVD

DDVIEFLQIACQQKWITCREPE

>lcl|NZ\_FO834906.1\_prot\_WP\_004212061.1\_2957 [gene=pqqE] [locus\_tag=BN49\_RS16375] [protein=pyrroloquinoline quinone biosynthesis protein PqqE] [protein\_id=WP\_004212061.1] [location=3021462..3022604] [gbkey=CDS]

MSQSKPTVNPPLWLLAELTYRCPLQCPYCSNPLDFARQDKELTTEQWIEVFRQARAMGSVQLGFSGGEPL

TRKDLPELIRAARDLGFYTNLITSGIGLTESKLDAFSEAGLDHIQISFQASDEVLNAALAGNKKAFQQKL

AMAKAVKARDYPMVLNFVLHRHNIDQLDKIIELCIELEADDVELATCQFYGWAFLNREGLLPTREQIARA

EQVVADYRQKMAASGNLTNLLFVTPDYYEERPKGCMGGWGSIFLSVTPEGTALPCHSARQLPVAFPSVLE

QSLESIWYDSFGFNRYRGYDWMPEPCRSCDEKEKDFGGCRCQAFMLTGSADNADPVCSKSPHHHKILEAR

REAACSDIKVSQLQFRNRTRSQLIFQTRDL

>lcl|NZ\_FO834906.1\_prot\_WP\_032104330.1\_2958 [gene=pqqF] [locus\_tag=BN49\_RS16380] [protein=pyrroloquinoline quinone biosynthesis protein PqqF] [protein\_id=WP\_032104330.1] [location=3022604..3024889] [gbkey=CDS]

MTLATRTVTLPGGLQATLVHQPQADRAAALARVAAGSHHEPSRFPGLAHLLEHLLFYGGERYQDDDRLMG

WVQRQGGSVNATTLARHSAFFFEVAADALADGVARLQEMLQAPLLLREDIQREVAVIDAEYRLIQQHEPS

RREAAVRHAASAPAAFRRFQVGSADALAGDLAALQAALGDFHRTHYVARRMQLWLQGPQSLEALGELAAR

FATGLAAGEAPPPAPPLRLGEFTALQLAVSSQPALWRCPLIALSDNVTLLREFLLDEAPGSLMAGLRQRR

LAGDVALNWLYQDRHLGWLALVFASDRPEEVDRQITHWLQALQQTTPEQQLHYYQLSRRRFQALSPLDQL

RQRAFGFAPGAPPAGFADFCSALQAAPSVSLACQTVSPGEPVATQGFSLPLSRWRRRPESDPALAFAFYP

QAAGDLVAKCPEKAAPLLHLPSPGEPPRLLLRPPFYCSPDQAEGLARGEQLRPLLAALRHAGGHGEWHLF

DGSWQLTLQLPEPGRRPEAILQAILRQLALPVASLTPPPESIAIRHLMAQLPERLGTSGHQKGWLAALAG

GSAEDAQWVARQLSLITAPVNPPMPAPAPCRRGVERLVYPGGDTALLVFIPLPDGASLAALRLLAQHCEP

LFFQRLRVEQQIGYVVSCRYQRVADRDGLLMALQSPDRRAGELLRCGKDFLRQLAPMDEATFRPLQQRLA

AQIRASRPPEARALSALRQEYGLPELTPQAVDALRVAEVADLAREMTRRRRRWQVLFTTGD

>lcl|NZ\_FO834906.1\_prot\_WP\_032104331.1\_2959 [locus\_tag=BN49\_RS16385] [protein=glutamine amidotransferase] [protein\_id=WP\_032104331.1] [location=complement(3024886..3025623)] [gbkey=CDS]

MTRNRLLLVQTGTPPTAIRQAHGDLPRWFRTLLAPWQTQLTTVRVFEDEPLPTPDNQTLAVLTGSWAMVT

DRLAWSERTADWIRQAVAIDMPLFGVCYGHQLMAHALGGEVAYHPGGRESGSQTITLSPWGVDDPLLSGL

PATFPAHLSHLQTVTRLPEGATVLAASAHDPHQIVRYGPHAVSTQFHPEFTAPIARSLIRHREAVLQAEG

IDAQRLHDEVQESPQGAAILTRFVSAFLTPDAPGH

>lcl|NZ\_FO834906.1\_prot\_WP\_002905759.1\_2960 [gene=mrdA] [locus\_tag=BN49\_RS16390] [protein=penicillin-binding protein 2] [protein\_id=WP\_002905759.1] [location=complement(3025736..3027646)] [gbkey=CDS]

MPLLRDEIRDHSAEEMLFIRRAAIAFLLVVVCFGVLIVNLYHLQVEQHDFYQTRSNQNDIKMLPIAPSRG

LIFDRNGIPLVQNITLYRLQVIPSKIPDMAALLQQLTPIVDLTPDDIASFRDDMHHTSRYKAVTLKSDLS

DVEVARFAVNEFRFPGVTVESYQQREYPYGAELAHVVGYVSKINDSDLQRLAKNGEEENYAADRNIGKQG

IEGYYEKALHGTTGYQEVEVDNHGRVVRLLKEVPPVAGKNLYLTLDLHLQQYIESVLKGQRAAVVVVDPR

DGGVLAMVSSPSYDPNPFVKGIGYQAYKSLLENPDRPLINRVTQGLYPPASTVKPYMALSALSAGVITPN

TTFFGAPTWTLPGTQRRYRDWLKTGHGMLNVTKAIEESADTFFYQVAFEMGIDRIHEWLSKFGYGQSTGI

DLNEEYAGVLPSREWKQRVHKKPWYQGDTISVGIGQGYWIATPIQMVKALTTLLNNGKVQDPHLLYSMKQ

GNHVERYQQPANLPQVGDPKSPYWGIVRNGMYGMANQPNGTGYKLFHTAPYQIAAKSGTSQVFSLKQNQT

YNAKMIPVRLRDHIFYTLFAPYQHPKVAMALILENGGGDGVVAGPTARAILDHIFVPQQASSAAADVPQR

DSADAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004143692.1\_2961 [locus\_tag=BN49\_RS16395] [protein=DMT family transporter] [protein\_id=WP\_004143692.1] [location=complement(3027845..3028321)] [gbkey=CDS]

MDTIVIILALCGGALLSVQAAINGRLGSQVGVLRSAFLTFATGALVTGLLILFFAPATSVNLLQVPKWQL

LGAFCGVPYIVIMVLAVQRIGTATATVAVIFGQLTMSLLIDNFGWLGNSTMAFSPARLAAVICLALALYL

IYTSGKSATSHEAARAEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004143693.1\_2962 [locus\_tag=BN49\_RS16400] [protein=DMT family transporter] [protein\_id=WP\_004143693.1] [location=complement(3028331..3028765)] [gbkey=CDS]

MALLFILLVIAGGMGLSVEAGLLGPLASQVGDLWATMSIFGIGAVLTFFLMLFFSPRSSPSFFSLPGWQL

TGGLLGAGYVVILTMATPVIGIAMTMIGILAGQVAKSLAIDHYGLFGSPRRKIDPRRAMALMLIMAALLL

VALG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530119.1\_2963 [locus\_tag=BN49\_RS16405] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530119.1] [location=3028865..3029797] [gbkey=CDS]

MADASSVDFRALQLFIAVYDNQSFSVVARREGVSPSLISRTIQQLEDALGQQLFYRNTRAVVPTEAGRFF

AASARELLGQYADAQRALQDRAQVPGGLVRINAPVYFGQRHIAPWLPELAARHPKLQFDLMLTDDFIDPH

RDATDILFRISSLPDAGYHARVFGSQRYYLTASPEYVSRYGSPTSPEALHQHRTLVYGGSQGANRWLFRQ

REEAWVHYPLTPLMTSNNADALLTSAIGGMGIVLFPDWMVSGALHNGTLVTLMDRYSAAISHTPSYIAAI

YPYTRHPSLNVRTVIDYFADVFGSPPYWQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180028.1\_2964 [gene=katG] [locus\_tag=BN49\_RS16410] [protein=catalase/peroxidase HPI] [protein\_id=WP\_004180028.1] [location=3030066..3032243] [gbkey=CDS]

MSTSNDPSNNASAGKCPFHAETPKQSAGSGTANRDWWPNQLRVDLLNQHSNRSNPLGENFNYREEFKKLD

YSALKADLRALLTDSQEWWPADWGSYIGLFIRMAWHGAGTYRTVDGRGGAGRGQQRFAPLNSWPDNVSLD

KARRLLWPVKQKYGQKISWADLYMLAGNVALENAGFRTFGFGAGREDVWEPDLDVDWGDEKEWLAHRHPE

SLAKQAIGATEMGLIYVNPEGPNASGEPLSAAAAIRATFGNMAMDDEEIVALIAGGHTLGKTHGAAETSH

VGAEPEAAPLEAQGLGWHSSYGSGAGADAITSGLEVVWTQTPTQWSNYFFENLFKYEWVQTRSPAGAIQF

EAKDAPEIIPDPFNPEKKRKPTMLVTDLTLRFDPEFEKISRRFLNDPQAFNEAFARAWFKLTHRDMGPKS

RYLGPEVPKEDLIWQDPLPAATHQPSAEDIASLKSAIAGAGLSVSELVSVAWASASTFRGGDKRGGANGA

RLALAPQKDWPVNAIASRVLPTLQAIQRASGKASLADIIVLAGVVGVEQAAAAAGVSVNVPFTPGRVDAL

PEQTDVESFDLLQPLADGFRNYRRIEGGVSTETLLIDKAQQLTLTAPEMTVLVGGLRVLGANYDGSKHGV

FTDRVGVLSNDFFVNLLDMATVWKAADDNAELFTGSDRKTGEAKYSATRVDLVFGSNSVLRALAEVYACA

DGQQKLVHDFVAAWTKVMNLDRFDL

>lcl|NZ\_FO834906.1\_prot\_WP\_023325230.1\_2965 [gene=zapE] [locus\_tag=BN49\_RS16415] [protein=cell division protein ZapE] [protein\_id=WP\_023325230.1] [location=complement(3032278..3033339)] [gbkey=CDS]

MLNNGCVPSESGPTEVTADFRFTRVMAEQAARARLTLDDDQLSLIARLDALGQQLVSTTGSPQGVYVWGR

TGRGKSFILDHFFASLPLAARRRVHFHHFFRELHQRLNAPGAPDLQTVMRQMTSGCRLLCFDEFHLHDPG

DAMLIKALLEHLFQHGIVLLATSNYPPEMLLPNPLYHDRFLPSIALIRAHLTVVALNGEEDYRERHLSQD

NAFCSGRMWVNPNAQQRQLYDLPSLPGEPVSLTVGYRTLLAAAASPALLHFTFTQLCQAATAVMDYLTLC

ESYAVWLLDEVPPLATVGPAAQQRFINVIDVLYEKQIRLLLVTRCDLETLVAGVELEDIQRTRSRLQQLP

RAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530950.1\_2966 [locus\_tag=BN49\_RS16420] [protein=MgtC family protein] [protein\_id=WP\_016530950.1] [location=complement(3033437..3034117)] [gbkey=CDS]

MVFPYMTHLLAAMLLGALIGAERQWRQRMAGLRTNALVATGAAVFILSAMSASPDSPGRIAAQIVSGIGF

LGAGVIMRDGMNVRGLNTAATLWCSAGIGVLCGLGQFWNATAATLIILCANILLREAAQRIHALPGAGDE

EKRYVLRVTCLREHENAVRQLLLNIAQQQRFTLQGLQSAAADTADHLEICAQLISHKQHQKTLAQIMAQM

CVQQNVTSVHWRVGEA

>lcl|NZ\_FO834906.1\_prot\_WP\_004180040.1\_2967 [locus\_tag=BN49\_RS16425] [protein=MFS transporter] [protein\_id=WP\_004180040.1] [location=3034705..3036111] [gbkey=CDS]

MSTTQVLGETPYASPGQPHASLTGRIDALPASFGLWSFITLLSLGGFFELYDLFQTGYISAGLLAEGIFH

TGQAGIFGIADQAAFASATFMGLFIGASLLAPLADKLGRRLTFMVALAWYGLFSLLMATQSSAEGVIFFR

FLVGIGLGIELVTIDTYLSEWVPTHLRNKAFAFAFFIQFLSVPAVALMSWMLVPTTLFGLSGWRWVIIFG

ALFSLAIWFIRKKLPESARWLESKGRHDDAHTVMCEMEARCGLTPSPKHAHAAQSVVKRGTFREIWAPQY

RQRTLMLMVMNFFQAIGFFGFGNWLPALLSGQGASITHSLLYAFFITLAYPLGCLFCTRFVHRFENKWQI

VLSALMTVIFGTLFALQNNPILLVICGFMITWSNAWLTISYHAYQAEVFPTHIRARAVGFCYSFSRLSTA

VTSILIGIILQYAGTPGVISFIVVSMLMVMLSVGIFGPRTRGIRLENI

>lcl|NZ\_FO834906.1\_prot\_WP\_004180041.1\_2968 [locus\_tag=BN49\_RS16430] [protein=PTS lactose/cellobiose transporter subunit IIA] [protein\_id=WP\_004180041.1] [location=complement(3036152..3036466)] [gbkey=CDS]

MDMEATVMELIINAGESRSLAMQALQAARKGVWQDVDRLMQDAADAAKRAHDVQTMLIGMDEGCGKVPVN

LILVHAQDHIMTSMLARELIAELIEVQRQLQHRN

>lcl|NZ\_FO834906.1\_prot\_WP\_002906016.1\_2969 [locus\_tag=BN49\_RS16435] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002906016.1] [location=complement(3036703..3037584)] [gbkey=CDS]

MDIKQLKYLIALDQTRHFGQAAAACHITQPTLSMRIRNLEEELNLTLIQRGQRFEGFTPEGERILAWARA

VLAAHDGLAAEAAICRGQMVGQLRVGMVPLASLNPMQLIKPLAEKYPALQFSLLSMTSEQIIDGVSRNQL

DLGICYLQHLDEGQFKIARLPQTRMGLLHDKRHFDFSAGTPGWETLATLPLGFLTKGMYYRESIEISFKA

KGLTPRYVFESDSTFQIIQAVQAGICCAIMPLNNGLEALSDNLEILPIAETHVDSQLALIMRQQEPVSTL

AEKCFAEAQGIFG

>lcl|NZ\_FO834906.1\_prot\_2970 [locus\_tag=BN49\_RS16440] [protein=FdhF/YdeP family oxidoreductase] [pseudo=true] [location=complement(3037734..3040033)] [gbkey=CDS]

MTNKRRAVPGVHPYDGPAGGWGALKATAIAVRTQMDAFEAPATLLRTNQPDGFDCPGCAWPDKEHKSTFQ

FCENGAKAVTWEATTKRVTPAFLAANTVSSLLAKSDFELEGYGRLTHPLVYDRDSDTLRPVAWEQAFARI

GEILRGLQPDEVEFYTSGRASNEAAWLFQLFAREYGTNNFPDCSNMCHESTSVGLPQSIGIGKGTVSLDD

FDQTELVISIGHNPGTNHPRMMGTLHELSRRGVPIIVFNPLRERALERFADPQNVMEMATRRSTPIASTY

YQVRAGGDAAALKGIAKALLQLEEEQGNVLDHAFIAQHTQGFTAFADDLHATRWQDIEQESGLTRESLTQ

VAAAYAKSRATIVTYGMGITQHNKGTSNVRLIADLLLMRGNIGKPGAGICPLRGHSNVQGNRTVGISEKP

SAAFLDSLQRVMGITPPRHHGHDAVKALEAMIAGDAKALICLGGNFAVAMPDHERAFPAMRALSSAFTSA

PSSTAHIS\*RRKRPLFCRVWDAPSLTCRPAAGSRSPSRIRCRWCMLRRASLSPPRRCCARSRRLSPVWRR

PPCPPAKWTGSTSWKTTIAFAI\*SNRPFQGSRIITSAFAILEASACRCRRPSASGLPPPVKPCSRYLKGC

MRTWWWRVRT\*CAW\*RCAVMTSTTPPSTRWMTATVASLAAATCCL\*TSRIWPPRVWSMAIGWISIPRCRE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004148478.1\_2971 [locus\_tag=BN49\_RS16445] [protein=hypothetical protein] [protein\_id=WP\_004148478.1] [location=complement(3040349..3041266)] [gbkey=CDS]

MIIRPEQHWFLRLFDWHGSVLSKIIFRLLLNVLMSIIAIISYQWYEQLGIHLTVAPFSLLGIAIAIFLGF

RNSASYSRFVEARNLWGTVLIAERTLVRQLRNILPAEHDAHRRIVSYLVAFSWSLKHQLRKTDPTADLRR

LLPEERVTEILASSMPTNRILLLAGNEIGQLREAGKLSDITYGLMDNKLDELAHVLGGCERLATTPVPFA

YTLILQRTVYLFCTLLPFALVGDLHYMTPFVSVFISYTFLSWDSLAEELEDPFGTAANDLPLNAMCNTIE

RNLLDMTGQHPLPETLRPDRYFNLT

>lcl|NZ\_FO834906.1\_prot\_2972 [locus\_tag=BN49\_RS16450] [protein=cation diffusion facilitator family transporter] [pseudo=true] [location=complement(3041516..3042440)] [gbkey=CDS]

MTQHNFENDNKYHERSVQARKSTLVSVVVNIFLSALQVVVGIFSGSQGLIADGMHSFSDLVADGVVLMAN

KKSRRPSDHDHHYGHWRYENGASLIIGAMLLLVGGGMLWSAAGHLAQPQTIPPVHSAALWMALVALAVKE

GLFRYMLAAARRLNSSLLIANAWHARSDAASSLVVALGIIGNLAGFAWFDPLAALAVGLLIARMGYRFAV

SALHDLMDRAVDEEMQQAIADTLRTTPGVAGLPRSENP\*GGGSGAGGCPSRGGWRDVGSRRASDCPSRAG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004143707.1\_2973 [locus\_tag=BN49\_RS16455] [protein=hypothetical protein] [protein\_id=WP\_004143707.1] [location=3042490..3042672] [gbkey=CDS]

MLNNIKAIALPFNDIAAVGNDYLLYVPLERCNLAPMNYLLKGGHRSGHFSLATTGVSDVT

>lcl|NZ\_FO834906.1\_prot\_WP\_004184165.1\_2974 [locus\_tag=BN49\_RS16460] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004184165.1] [location=3042662..3043348] [gbkey=CDS]

MSHNKPSRLRFAINLGNAVLAHLGETGKPAGITVELSHRLATRWGVSAEFVPYPAAGKVVADAGGEHWDI

AFLAIDPAREATLRFTSPYITIQGTALVSVDSPCQSVADMDRPATTINVGQNAAYDLWLTRHLQHASLHR

LPSSQEAIDAFLAGEGDMVAGIRQPLEATARQHAGVRVLADNFTEIQQAICVARADVDRFHAVNDALSEW

RADGSLQALIAGHLGQAN

>lcl|NZ\_FO834906.1\_prot\_WP\_016530230.1\_2975 [locus\_tag=BN49\_RS16465] [protein=oxygenase MpaB family protein] [protein\_id=WP\_016530230.1] [location=complement(3043350..3044219)] [gbkey=CDS]

MIGIRRMIEAQVLGLTGMALKEIDFERPKGEPGLFGPQSAIWQVHGDFTSMLCGGISALLLQMLHPLALA

GVWDHSRFREDILGRLRRTSQFISATTFATTPDAERLIAKVQGIHQRIAGVDKDGTPYQASDPALLTWVH

VAECSCFMASHLRYKRTVVSPERQEDYFRESAEIARRLGARDIPQTPQEVADYLEAMRPRLRCDERTREV

AEVLLSTRLPGRMNQPVGRVMMNAGIDLLPEWAQEMLGLSLTPLQRRTTRLMVHGVARVLRASVRNGAWH

CAMRRMTEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002906030.1\_2976 [locus\_tag=BN49\_RS16470] [protein=OsmC family protein] [protein\_id=WP\_002906030.1] [location=complement(3044324..3044755)] [gbkey=CDS]

MAIHKKGLAHWEGDLKHGKGTVSTESGALSQQPYGFNTRFEGVKGTNPEELIGAAHAACFSMALSLMLSE

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LNP

>lcl|NZ\_FO834906.1\_prot\_WP\_002906033.1\_2977 [locus\_tag=BN49\_RS31080] [protein=hypothetical protein] [protein\_id=WP\_002906033.1] [location=complement(3044869..3045015)] [gbkey=CDS]

MSTFSHSQDEERGKQPAREAPGEQGEVPRKRDDSKDDKSDPWHPQDGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002906035.1\_2978 [locus\_tag=BN49\_RS16480] [protein=YdeI family stress tolerance OB fold protein] [protein\_id=WP\_002906035.1] [location=complement(3045031..3045435)] [gbkey=CDS]

MKKLALAMACLFAVGVAQADDKGGFSQDAAPPPPHKLDDGYRGVEDGRIMTVEQAKTMHDGATVSLRGNL

LKRQGDDRYQFRDKSGTITVIIPVAAFNEQHVEPDDLVNINGSLDRKMTPPVVRIDRLLKQSPK

>lcl|NZ\_FO834906.1\_prot\_WP\_004180065.1\_2979 [locus\_tag=BN49\_RS16485] [protein=hypothetical protein] [protein\_id=WP\_004180065.1] [location=3045580..3046083] [gbkey=CDS]

MIKNQQPCPIVDENERSLRFEYRFRRYGIIVLSLIILTALSGLWSSGYFSEAHRETSGGELSVDYQRYAR

LMSETELNIQIKPDTASDTIISFAAPLLTRYQIGDIRPQPDKMYSADGKLHLVYQRSNPPSPISVWLAVT

PKTAGNISLQAVVNDRYSVTWQQFVYP

>lcl|NZ\_FO834906.1\_prot\_WP\_004148482.1\_2980 [locus\_tag=BN49\_RS16490] [protein=DUF421 domain-containing protein] [protein\_id=WP\_004148482.1] [location=3046092..3046538] [gbkey=CDS]

MEMVLRAAAIYLILLIIFKIAGRRTLMQLTNFDLILLLIISEATQQAMLSTDYSVTGSMLTIVTLVSIDI

LFGYIKKKFAQAENFLDGTPVIVVENGAVIDEKIKLVNISVDDILLAARQHHGIYELKAIKFAILERNGQ

ISIIPEQE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043365.1\_2981 [locus\_tag=BN49\_RS16495] [protein=SDR family oxidoreductase] [protein\_id=WP\_046043365.1] [location=3046857..3047852] [gbkey=CDS]

MSVMVITGGTAGAGKATALRFARAGYHVALIARDETGLQETRQACERFGIKTLAISADVVDAGALQRAAA

EVETTLGAIDVWINNAMTTVLAPFRQMSEEEFRRVTEVTYLGYVNGTRAALEVMIPRDRGVIIQAGSALA

WRSIPLQSAYCGAKAAIRGFTDAVRTELMHEKSHIQLTMVQLPGMNTAQFGWARNKMDQAMQPVPPVYQP

EVAAEAIYIVIQRPVNELWVGKSTIQSILGQVFFPRLLDRLMVKKAWEGQFTGQPKSSDQQDDLFTPVRG

NHPGHGPFNDGARRKAVTISADLPGKVAAGVGVAVATMALRALFRRSGKRR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043366.1\_2982 [locus\_tag=BN49\_RS16500] [protein=alpha-amylase family protein] [protein\_id=WP\_046043366.1] [location=complement(3047849..3049474)] [gbkey=CDS]

MQREEWFHRAVIYQVDSSLFYDANGDGFGDLAGIRQKLHYIRSLGATVLWLTPFYLTPLQDDGYDISDHL

QPDPRFGTIADVIELIARARELGLRVIIELVIQHTSAQHPWFQAARRDPRSPWRPYYLWADRPPENDDPP

MFPGVEESVWRWDEQAGQYYRHMFYHHEPDLNLAHPPVIAEIENIITFWLQAGVSGFRLDAASHLVKQAG

KGDETRGYPLLTHLRQVVQRLNPDAILLGEVDVAVEDYRHYFGQGDRLQMVLNFWLNKYLYLSLAQQRAA

PVVKALQAMVTPPDGCCFVNWLRNHDELDLEGIGERNKRQVIRTFAPDKSMSVYQRGVRRRLAPMLDGDT

RRIALAHAILLALPGVPVMRYGDEIGMGDDLSLPERYVVRTPMQWSAAANAGFSRAARDDLPVKPVASGR

FRYQRINVETALRHPRSLLHRVRNMVLARTEYTEPGSLPFTLLTLKPDAVLGLLYRSESREVLMLANCSQ

QAVEVLLPPLAEGYWSPILEDKLYQDGLHGGKDARLALSGYGYRWFSRSLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004891697.1\_2983 [locus\_tag=BN49\_RS16505] [protein=hypothetical protein] [protein\_id=WP\_004891697.1] [location=complement(3049514..3049696)] [gbkey=CDS]

MVKRQTIALLAAEEQVPLVLTARQQALVDAVANRMLPAERNPVSPVDKPRAKARAGSGSR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151243.1\_2984 [locus\_tag=BN49\_RS16510] [protein=ferritin-like domain-containing protein] [protein\_id=WP\_004151243.1] [location=complement(3049713..3050219)] [gbkey=CDS]

MTDIENYHNWLRDAHAMEKQAESLLVATIRRLDNEPQLRTRLEQHLYETRRQLSALQDIIARNHISRSAL

KDAMSRVAALGQTIGIMLPGDEVIKVIITAYVFAHFEVACYTALLTAAKRVGDHSAMHTLEGILAEERGM

ADWLLHYLPALTGQYLMDTDMPGVEAGH

>lcl|NZ\_FO834906.1\_prot\_WP\_004143717.1\_2985 [locus\_tag=BN49\_RS16515] [protein=hypothetical protein] [protein\_id=WP\_004143717.1] [location=complement(3050243..3050458)] [gbkey=CDS]

MKLTPVFIKRCHLVAAVMWVGLAIPSLIWWKDSVLWVILISIYANIVGHLSGYSAARADQAAEESEDSTS

K

>lcl|NZ\_FO834906.1\_prot\_WP\_004143718.1\_2986 [locus\_tag=BN49\_RS16520] [protein=general stress protein] [protein\_id=WP\_004143718.1] [location=complement(3050824..3051009)] [gbkey=CDS]

MAEHRGGSGNFAEDREKASEAGRKGGQHSGGNFKNDPERASEAGKKGGKNSHGGGRKSGDS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151242.1\_2987 [locus\_tag=BN49\_RS16525] [protein=SDR family oxidoreductase] [protein\_id=WP\_004151242.1] [location=3051666..3052580] [gbkey=CDS]

MQDEKPPMKKLPTSMLPEETAPRPEFPEQEQTPPGLDAEMEPSPDHGETSYTGSGRLAGKKALITGGDSG

IGRAVAIAFAREGADVAINYLPEEQKDADEVIALIKAEGRTAVALPGDIRSESFCQSLVADAVEQLGGLS

ILVNNAGRQQYCETLEELTTEDFDATFKTNVYAPFWITRAALPHLQAGSAIINTTSVQAYKPSPILLDYA

QTKACLAIFTKSLAKQVAKRGIRVNAVAPGPYWTVLQSSGGQPDEKVKQFGKDTPMGRPGQPVEIAPLYV

TLASDACSYTSGQVWCSDGGDGVV

>lcl|NZ\_FO834906.1\_prot\_WP\_004180069.1\_2988 [locus\_tag=BN49\_RS16530] [protein=YmjA family protein] [protein\_id=WP\_004180069.1] [location=3052777..3053022] [gbkey=CDS]

MSNDIPLKFYDIVDEYETEAAAPVKDEERDALARYFQLLIARLTNNEEIDEEAQREMAREAAINENRIDD

IANFLNQWGNE

>lcl|NZ\_FO834906.1\_prot\_WP\_004184171.1\_2989 [locus\_tag=BN49\_RS16535] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004184171.1] [location=complement(3053090..3053983)] [gbkey=CDS]

MDRVIAAQVYLRICELGSLSAAARALGMSRPMVSRYLEQMESWAGARLIHRSTRRLTLTPAGEKVLLKTR

GLTRIADEIAGERQRADPSGTLRVACAHFTAMQLISPLLPDFLARYPLLRLELDINNHPVSLIGERIDVA

IRITDNPEAGAIARRLGVCRSLLCAAPGWMRQHGPLTTPDDLQRHNCLLYSHFASQHWQFSDAQGREASV

AVNGNLSAGISSLLLEAAVAGCGIAMLPELEARGAIASGTLEVVLPEWTPKALSVYGIYLSRDYQPDGLP

LFLDALQRRLGEETGHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004189881.1\_2990 [locus\_tag=BN49\_RS16540] [protein=Vmh family MBL fold metallo-hydrolase] [protein\_id=WP\_004189881.1] [location=3054097..3054948] [gbkey=CDS]

MKLSALAVATALFSGAVFAAPLTLQTYNPQEKGLFAVNSTLVSGPHEAVLFDAQFSVKDGEKLVEMIKKN

GKPLSRIVITSGDPDFYFGLEPLVKAFPQAEVVATPEVVKHIAATKAAKLAYWGPQMKDGAPTQVYVPQA

LEANSFTIDGEKVTIMQPHDYAAFVWIRANKTILGGTGVAWGMHLWTADTQTPASRQQWRNTLDQMIALH

PQRVIPGHYLGTPPEGDSAVRFTKTYLQQFEQALKTHSDSAGVIKAMEAQWPGLAETSSLELSAKVNTGE

MKW

>lcl|NZ\_FO834906.1\_prot\_WP\_004143727.1\_2991 [gene=sra] [locus\_tag=BN49\_RS16545] [protein=stationary-phase-induced ribosome-associated protein] [protein\_id=WP\_004143727.1] [location=3055126..3055266] [gbkey=CDS]

MKSNHQARHLLGLNYKLSRQKKVVLEGDEETTINHIHATGRKRRGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002906122.1\_2992 [locus\_tag=BN49\_RS31085] [protein=hypothetical protein] [protein\_id=WP\_002906122.1] [location=complement(3055263..3055391)] [gbkey=CDS]

MESSGQSIEQKVFKRVNKQSIAIKKHHPGNRTVLFIITQAEN

>lcl|NZ\_FO834906.1\_prot\_WP\_002906125.1\_2993 [locus\_tag=BN49\_RS16555] [protein=NAD-dependent malic enzyme] [protein\_id=WP\_002906125.1] [location=3055448..3057145] [gbkey=CDS]

MQFTHKKNRSLYIPYAGPVLLEFPLLNKGSAFSMEERSNFNLLGLLPEVVETIEEQAERAWIQYQGFKTE

IDKHIYLRNIQDTNETLFYRLIGNHLEEMMPVIYTPTVGAACERFSEIYRRARGVFISYQNRHNLDDILQ

NVPNHNVKVIVVTDGERILGLGDQGIGGMGIPIGKLSLYTTCGGISPAYTLPIVLDVGTNNQQLLDDPLY

MGWRHPRITDDEYYQFVDDVIQAIKARWPDVLLQFEDFAQKNAMPLLNRYRNEICSFNDDIQGTAAVTVG

TLIAASRGAGSQLSEQKIVFLGAGSAGCGIAEQIIAQIVREGLSEEEARQRVFMVDRFGLLTDGMPNLLP

FQNKLVQKREQLQSWDTTSEALSLLDVVRNVKPNILIGVSGQPGLFTEEIIREMHKHCPRPIVMPLSNPT

SRVEATPQNILSWTDGEALVATGSPFSPVTVKGKQYPIAQCNNSYIFPGIGLGVIASGASRVTDEMLMAA

SETLAQHSPLVNNGEGPVLPELKDIQTVSRAIAFAVGKVAQEQGVAVKTSAEALLQAISDNFWLPEYRNY

RRTSI

>lcl|NZ\_FO834906.1\_prot\_WP\_004189877.1\_2994 [locus\_tag=BN49\_RS16560] [protein=hypothetical protein] [protein\_id=WP\_004189877.1] [location=3057329..3058024] [gbkey=CDS]

MLKLTPGANKANAILIRIVLFLIGGIAIITGMCLFSGDMWMLTPRAEQYQPATGDLVDVVIYEPSKFFFA

LLYVFIITLVWLLAVRKIPWRPIQHPILPLMVLIAAGIFIFLHPEVTPGRDASIQYGKHNTYYASIFWMK

TRSGSHSAKQSKYETFVEAKDPRWLIDRNNLRRAWRCEVQRHTQFYTLSFNEGWFPNGDPQVLANQCSQI

ADLDTVSEDELLVTKTIRSRK

>lcl|NZ\_FO834906.1\_prot\_2995 [locus\_tag=BN49\_RS16565] [protein=hypothetical protein] [pseudo=true] [partial=3'] [location=3058021..>3058551] [gbkey=CDS]

MSQQKMVLQPILRLWLGLFSGLLLVSAISAFHGEYWYFGDKQAFYAAKAGEVSVHELYTPAKILFAFIVS

TIPPLLWLLLVNRRAPRLLTHTLPSVLLLLAGLLFFFLRPDVIPGGETPVYRYGERERYYQTIRWQKPEP

GAWRGTRSEYNVYIEYRDPRGYRKVDNIKNAYTCETH

>lcl|NZ\_FO834906.1\_prot\_WP\_115217266.1\_2996 [locus\_tag=BN49\_RS29195] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_115217266.1] [location=complement(join(3058563..3059476,3059476..3059791))] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_2997 [locus\_tag=BN49\_RS31475] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=<3059882..3060043] [gbkey=CDS]

THRESRFFTLTTEEDWYPDSYPNILEAPCQAIKDPQAMTEYTRDHARWFPITF

>lcl|NZ\_FO834906.1\_prot\_WP\_004180073.1\_2998 [locus\_tag=BN49\_RS16575] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_004180073.1] [location=3060405..3062120] [gbkey=CDS]

MSTLLTAHALHVETAFGPLFNSLSFTLKKGDRIGLIGHNGCGKSTLLQVLDGTLAPTSGSVSLAGQCLMA

RVEQHLPEALHTQSLLQAVLAPLPADVREAQRWLAERLLAQMGFTPAVMEQQTATLSGGQHTRLLLARAL

IRQPDLLLLDEPGNHLDLPTLLWLESFLQTWQGSFVLVSHDNTLLDAVTNASWILRDQTLHCFALPCSAA

RQALQEQDESAALRHKAEQKEIDRVSASARRLATWGRVYDNEDLARKAKQMEKQVARLKDEQTELSVGPP

WRLVLQGDALPADRLLEMDTLPVSPAPGQPSLFTTGVARLRSGDRVAIMGRNGGGKSSLLRLLWQQMNNA

SPLPGLRLHPRLHPGYYDQTLAQLPDEASLLEALTPFAPSADTRKRALIAAGFGWARHSQKVSTLSGGER

SRLLFVGLSLARYSLLLLDEPTNHLDMEGKAALAQTLRDYPGGVLLVSHDRQLISESCNRFWLIDSAGLT

EWHSLEEVYARLQAVAPAPDSRLALQSTPAGADDDEEALLARLIDLEQWLADDMARKPKHQKPSLQAQWQ

EEIARLLNQLT

>lcl|NZ\_FO834906.1\_prot\_WP\_227504850.1\_2999 [locus\_tag=BN49\_RS31480] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_227504850.1] [location=complement(3062157..3062480)] [gbkey=CDS]

MALREGKIVGSLAIDGEDLGQQEAHLRWFILDDSCRGTGIGRRLLSEAMAFCDSRQFSAVQLWTFKGLDA

ARKLYESFGFTLIREWQGEQWGKLMTEQQFTRSESTG

>lcl|NZ\_FO834906.1\_prot\_3000 [locus\_tag=BN49\_RS31485] [protein=hypothetical protein] [pseudo=true] [partial=3'] [location=3062406..>3062558] [gbkey=CDS]

MRLLLAEVLAIDSQRADDFPFAERQPDLVGRGGEPGGKFRYAAGDLAFKKS

>lcl|NZ\_FO834906.1\_prot\_3001 [locus\_tag=BN49\_RS31490] [protein=MarR family transcriptional regulator] [pseudo=true] [partial=3'] [location=complement(<3062814..3063041)] [gbkey=CDS]

MSTTLAATHYSPSAVHTLLEVSMRGEMTAAQLVTLLGLEKSSVSRMVSRLLAAGELEERPCAEDARAKSL

ALTAKG

>lcl|NZ\_FO834906.1\_prot\_WP\_009307786.1\_3002 [locus\_tag=BN49\_RS16585] [protein=inorganic diphosphatase] [protein\_id=WP\_009307786.1] [location=complement(3063285..3063884)] [gbkey=CDS]

MHLVKTILTAGLLLSAAAQAHNVLEFPQPENNPEEFYAVTEIPTGGIVKYETDAKTGFIVADRFQSMPVA

YPANYGSLTQSLAGDGDPLDVVFYTRAPMAPGTLIKLRAIGVLKMVDGGEKDDKIIAVPASKIDPTYDDI

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>lcl|NZ\_FO834906.1\_prot\_WP\_002906221.1\_3003 [gene=adhP] [locus\_tag=BN49\_RS16595] [protein=alcohol dehydrogenase AdhP] [protein\_id=WP\_002906221.1] [location=3064137..3065147] [gbkey=CDS]

MKAAVVTHDHQVNVTEKTLRPLEYGEALLKMECCGVCHTDLHVKNGDFGDKTGVILGHEGIGVVQKVGPG

VTSLKPGDRASVAWFFEGCGHCDYCNSGNETLCRSVKNAGYTVDGGMAEECIVTANYAVKVPDGLDSAAA

SSITCAGVTTYKAVKVSHIKPGQWIAIYGLGGLGNLALQYAKNVFNAKVIAIDVNDGQLELAASMGADLT

INSRNEDAAKVIQEKTGGAHAAVVTAVAKAAFNSAVDAVRAGGRVVAVGLPPEAMSLDIPRLVLDGIEVV

GSLVGTRQDLVEAFQFAAEGKVVPKVTLRPLEDINAIFKEMEQGQIRGRMVIDLRS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043368.1\_3004 [locus\_tag=BN49\_RS16600] [protein=TIGR04028 family ABC transporter substrate-binding protein] [protein\_id=WP\_046043368.1] [location=3065317..3066939] [gbkey=CDS]

MHRHFRLPALAALFLTGAFSVWAADTPVKGGTLIYLEQQPHTNLYPPAGGFYPNGGILNQITDKLTWQNP

KTLEIEPWIAESWTSNADKTEYTFHLRKGVTFSDGTPLDAAAVAKNFDTYGLGDKAHRLPVSEVINNYQR

SEVIDPLTVKFYFNKPSPGFLQGTATIGSGLVSLSTLQRNFEELGDARHIIGSGPFVVQDEKPGRELTLV

ARKDYQWGPKNITQQGPANLDGITYIVTPEDSVRNGALLAGQAGFIRQVQAYDEKQATDQGFKIYAAPTR

GVNDSLSFRPDNPLVADLQVRQALLHATNARQVVETLFSANYPQATSVLASSAAGYVNLSDKLTFDQAKA

RQLLDDAGWKPAADGIRSKDGQRLALTVYESLPQPQNKEVLQLIAQQWRQVGVALTVKAGDAGSRTLDNL

DPQKTPLTVSEVGRADPDVVKSMFFPNNRDALLQKGGSSDKVQRFRDDKLNDLLTGISAAVEPQQRLQLT

GDAQRYLIDNAYVIPIFEEPQVFAGAPWVKGVSFEAVGRPSFYGAWLDKH

>lcl|NZ\_FO834906.1\_prot\_WP\_002906228.1\_3005 [locus\_tag=BN49\_RS16605] [protein=ABC transporter permease] [protein\_id=WP\_002906228.1] [location=3066950..3067894] [gbkey=CDS]

MSAYLLRRFGQGLLVLWAAFTLTFFLLQVLPGDAVLIKFQNPDLGLSPAQIAEMRLAYGADSPLWRQYLH

TLLAMLHGDFGYSLQAGLAVSSLIASNLPDTLSLALPAFLLAVALAFALAFASRLPGLRWLSNFLQSLPV

LFISLPTFWLGIALIQLFSFQLRWIPVINPGPLEGLILPVIAVALPISAPLAQILMRSMDQVAVQPFVAV

ARAKGMSETGVLWRHVMGNALLPALNIAGLLLGELIAGALITETVFGRSGLGQLTQQAVNNQDIAVLQAV

VMISALGFVLINLLVDLVMPRLDPRLHLQTGGAK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532407.1\_3006 [locus\_tag=BN49\_RS16610] [protein=ABC transporter permease] [protein\_id=WP\_016532407.1] [location=3067891..3068739] [gbkey=CDS]

MSLVDYTIAVRRRPEWRRVRLQPGLWLAWAVMIAALLMAIAPQWFTSANPLEGIPGAQRLAPQAHYWLGT

DQLGRDLWTRVVYGAVHSLSAALIAVAIGLVVGTALGTLAGALAGRVESTIMRLVDVLLAIPSLLLQLTV

IILLGIGTVNAAVAVGVAAIASFARLARAEVVRVRHSDYVEAARGSGGTFFAVFWRHILPNSLTAVLAFA

TLQFGQAMLALATLSFLGYGTPPPVPEWGLLIAEGRNYLSTAWWLTTFPGLAVVAVVLAANRLSRQWSGA

RP

>lcl|NZ\_FO834906.1\_prot\_WP\_016532406.1\_3007 [locus\_tag=BN49\_RS16615] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016532406.1] [location=3068736..3070352] [gbkey=CDS]

MTVLSVEDLRISYRSRGEWREVVHNISFSIQRGEMLAFVGESGSGKTTTAQAIIGLLADNARRDAGRIVL

NGEVISDWSDKRLNRLRGVSISLVPQDPGNSLNPVKTIGQQVEEILRLHQSLSAAERRQQVLNLLAKVGL

SHPEQRFDQYPHQLSGGMKQRVLIAIAIALQPDLIIADEPTSALDVTVQKRILDLLDILRRESGTAVLFV

THDLALAAERADRIMVFRQGEIQEQGATETIVQRPQHPYTRQLLHDLQDAPLGLTAARHRPLATPAIRVE

GISKRFSLGKQALQALDSVSFEVRRGSTHALVGESGSGKTTLARILLGFERADAGQVTIDGIDAGHLSRE

AQRQLRRKIQFVYQNPFASLDPRQTLFAIIEEPLKNFERLSAATRRQRVESVAARVALAPELLSRTPREL

SGGQRQRVAIARALILEPAILVLDEATSALDVTVQAQILALLQQLQQQLGLSYLFITHDLATVRRIADSV

TVLRAGQVVEHGDVNRLFAAPQQAYTRELIAAIPQVSSRLAQAHTENA

>lcl|NZ\_FO834906.1\_prot\_WP\_004200040.1\_3008 [locus\_tag=BN49\_RS16620] [protein=putative FMN-dependent luciferase-like monooxygenase] [protein\_id=WP\_004200040.1] [location=3070352..3071338] [gbkey=CDS]

MPKRLGFFTRLLDQGSAQTRYRLAAEQIRHAERLGFDSAWIAQHHFHEQEGGLPSPLVFLAHVAAQTDRI

RLGTAIITLPMENPLRVAEDAAVLDLLTDGRLEVGFGSGGTPTSFLPFGLTSEQRGAAFADHLHLIHSAW

RGDTLSHPDNRLYPPAPQLAERIWIATFSAEGAIRAGQAGHGLMLSRTQPRPPGEPRLPLDAIQNPIIDA

YLSALPDGVAPRILASRTAFVADSHAHALQVAEPGLRKQATQHRAAGHTIEGDSVTDYLQQLDAHVGDPE

HVIASLAQDSVLARATDISFQVHSVEPSHRDTLRSIELIAQHIAPHIR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532405.1\_3009 [locus\_tag=BN49\_RS16625] [protein=alkylhydroperoxidase domain protein] [protein\_id=WP\_016532405.1] [location=3071348..3072439] [gbkey=CDS]

MTLSQDILAELAEIAPGSPLYQARAVRDAATRHAQGSYEVLFRQQDADFPLDERFAVAAKVAKLHQADAL

AAHYAGFGLADPTTDRLVPALAFARLLTFTPVEATPGALHTLTSAGWSLRGIVTLAQLVAFVSFQSRLLL

GLRALNHKPIVSADTPLVAGYWHTTPYAQSGKAAPVRFTRDELRWEPWLADKPLAEFNAEEQAILAKYGH

SDSPYFRLLARNQPVLEQRTLTDRGIFYTAGGLPRAERELAATVASKINGCIYCASVHARKAAQLAKDET

AVDTLLAVTPGEDLRDGQSPRWQAEIDAAAALSVTPPALNANHLAALDEQGLDTLAQLDLLQSAAFFAWA

NRLMLTLGEPWRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002906449.1\_3010 [gene=araJ] [locus\_tag=BN49\_RS16630] [protein=MFS transporter AraJ] [protein\_id=WP\_002906449.1] [location=complement(3072446..3073600)] [gbkey=CDS]

MKKTIFSLALGTFGLGMAEFGIMGVLPDMAHDVGISIPAAGNMIAWYAFGVVIGAPIMALLSSRFSLKSV

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LVGVPGGTWLGHHFSWRYTFALIAVFNVAVFLAIFCWVPTLYDRASTRLREQFRFLASPAPWLIFAATMF

GNAGVFAWFSYIKPFMLNVSGFAESKMMLIMMLAGLGMVVGNLFSGKISGRYSPLRIAAMTDGVIAVTLL

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043372.1\_3011 [locus\_tag=BN49\_RS16635] [protein=VOC family protein] [protein\_id=WP\_046043372.1] [location=3073865..3074305] [gbkey=CDS]

MQSVDVGFTHIAFTVRCLASSIDFYTRYTAMTVIHQREPDLPSARKVAWLSDRTRPFALVLVQSDDPADT

PLGPFGHLGVACATQAEIDEKVALARREGVLRREPEQLGDPVGYFAFFADPDGNTLELSWGQRVGLEVIL

AGKPGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004180084.1\_3012 [gene=ppk2] [locus\_tag=BN49\_RS16640] [protein=polyphosphate kinase 2] [protein\_id=WP\_004180084.1] [location=3074373..3075191] [gbkey=CDS]

MGNKKSGNPVDTAAKIAPLDNKAYEKALRKLHVELVKLQRWVVHKGLKVCIVFEGRDGAGKGGTIKAITE

RVSPRIFRVVALPSPTEREKSQLYFQRYIKHLPAAGEIVIFDRSWYNRAGVERVMGFCTPEEVQKFLDGA

PMVERGMVESGIILLKYWLEVSPQEQERRLRDRIDDGRKIWKLSPMDIKSFNRWDEYTAARDAMFAATDT

AWAPWFVARSEDKKRVRLNIITHLLSQIPYEALPVEPVTLPKRKIGKMKQTNFPFRFIPEKF

>lcl|NZ\_FO834906.1\_prot\_WP\_004175994.1\_3013 [locus\_tag=BN49\_RS16645] [protein=hypothetical protein] [protein\_id=WP\_004175994.1] [location=3075370..3075555] [gbkey=CDS]

MKSNTLRKRPTDVPVQKASEQPGKDLREADKQRQHKEFIAAMNEFIAKGGTLTDDEFFRVL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530833.1\_3014 [locus\_tag=BN49\_RS29205] [protein=CcdB family protein] [protein\_id=WP\_016530833.1] [location=3075552..3075878] [gbkey=CDS]

MMLEQFNVYRNCSAQTNKTLPYYMIVQNDYYADLATRVIIPLIRPQQLPRWHQHVVPRINIEFDSFLLCT

PMISNLNNKRIPPQDFVCNLSHARQGVIDSIDTLITNC

>lcl|NZ\_FO834906.1\_prot\_WP\_016530834.1\_3015 [gene=fdnI] [locus\_tag=BN49\_RS16650] [protein=formate dehydrogenase-N subunit gamma] [protein\_id=WP\_016530834.1] [location=complement(3075931..3076587)] [gbkey=CDS]

MSKSKMIVRTTFIDRACHWTVVICFFLVALSGISFFFPTLQWLTETFGTPQMGRILHPFFGVLIFVALMF

MFVRFVHHNIPDKQDIPWLKGIVEVLKGNEHKVARVGKYNAGQKMMFWTIMSMIFVLLVTGVIIWRPYFA

EYFPMQVIRYSLLIHATSAIILIHAILIHMYMAFWVKGSIKGMIEGKVSRRWAKKHHPRWYRDVERREAM

KESREGMK

>lcl|NZ\_FO834906.1\_prot\_WP\_004143747.1\_3016 [gene=fdxH] [locus\_tag=BN49\_RS16655] [protein=formate dehydrogenase subunit beta] [protein\_id=WP\_004143747.1] [location=complement(3076580..3077464)] [gbkey=CDS]

MAMETQDIIKRSATNPITPAPRARDYKAEVAKLIDVSSCVGCKACQVACSEWNDIRDDVGHCVGVYDNPA

DLSAKSWTVMRFSETEQNGKLEWLIRKDGCMHCAEPGCLKACPSAGAIIQYANGIVDFQQENCIGCGYCI

AGCPFNVPRLNKEDNRVYKCTLCVDRVSVGQEPACVKTCPTGAIHFGTKKEMLEVAEERVAKLKKRGYAN

AGIYNPPGVGGTHVMYVLHHADQPELYHKLPKEPQIDTSISLWKGALKPLAAAGFIATFAGLIYHYIGIG

PNKEVDDDEEKHDE

>lcl|NZ\_FO834906.1\_prot\_WP\_086618330.1\_3017 [gene=fdnG] [locus\_tag=BN49\_RS16660] [protein=formate dehydrogenase-N subunit alpha] [transl\_except=(pos:586..588,aa:Sec)] [protein\_id=WP\_086618330.1] [location=complement(3077476..3080523)] [gbkey=CDS]

MDVSRRKFFKICAGGMAGTTAAALGFAPKMALAQARNFKLLRAKEIRNTCTYCSVGCGLLMYSLGDGAKN

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RDANFIEKNEQGVTVNRWLSTGMLCASAASNETGMLTQKFVRSLGMLAVDNQARVUHGPTVASLAPTFGR

GAMTNHWVDIKNANVVVVMGGNAAEAHPVGFRWAMEAKNNNDATLIVVDPRFTRTASVADIYAPIRSGTD

ITFLSGVLLYLIENNKINAEYVKHYTNASLLVRDDFAFEEGLFSGYDAEKRQYDKSSWNYQFDENGYAKR

DETLTHPRCVWNLLKQHVSRYTPEVVENICGTPKADFLKVCDVLASTSAADRTTTFLYALGWTQHTVGAQ

NIRTMAMIQLLLGNMGMAGGGVNALRGHSNIQGLTDLGLLSTSLPGYLTLPSDKQTDLHSYLSANTPKAT

LPEQVNYWSNYPKFFVSLMKSFYGEAAQKENDWGFEWLPKWDQAYDVIKYFNMMDNGNVTGYICQGFNPV

ASFPDKNKVVRSLSKLKYMVVIDPLVTETSTFWQNHGESNDVDPSAIQTEVFRLPSTCFAEEDGSIANSG

RWLQWHWKGQDAPGEARNDGEILAGIYHRLRELYRTEGGKGAEPLLKMSWRYKQPDHPESEEVAKENNGY

ALADLYDQNGTLLAKKGQLLNSFALLRDDGSTASSCWIYTGSWTEQGNQMANRDNADPSGLGNTLGWAWA

WPLNRRVLYNRASADINGKPWDAKRMLIQWNGSKWVGNDIPDFNTAPPGSNTGPFIMQQEGLGRLFALDK

LAEGPFPEHYEPMETPLGTNPLHPKVVSSPVVRLYEEDAIRLGKKDKFPYVGTTYRLTEHFHTWTKHALL

NSIAQPEQFVEISEGLAKSKGIANGDWVKVSSKRGFIRAVAVVTRRLRTLNVNGQQVETVGIPLHWGFEG

VARKGYIANTLTPNVGDSNSQTPEYKAFLVNIEKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530837.1\_3018 [gene=yddG] [locus\_tag=BN49\_RS16670] [protein=aromatic amino acid DMT transporter YddG] [protein\_id=WP\_016530837.1] [location=3080749..3081627] [gbkey=CDS]

MEKKRATTIGFAAIILWSTMVGLIRGVSEGLGAVGGAAMIYSLIGLLLIFTVGFPNLRQIPRRYLLAGSV

LFVSYEICLALSLGYAASRQQAIEVGMVNYLWPSLTILFAILFNGQKSSWLVIPGLILALLGVGWVLGGE

HGLQPDEIISNVISSPLSYLLAFVGAFIWAAYCTVTAKYARGKNAITLFVLLTALTLWLKFLASDQPPML

FSWPVVIKLMTVSVALGLAYAAWNVGILHGNVSLLAAASYFTPVLSSALAAILLSATLSWSFWQGAGMVC

LGSLLCWYATRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180092.1\_3019 [locus\_tag=BN49\_RS16675] [protein=benzoate diol dehydrogenase BenD] [protein\_id=WP\_004180092.1] [location=complement(3081624..3082397)] [gbkey=CDS]

MRFTDKVVVITGAAQGIGRQTAEQAAAEGAALLLIDRSSYVHELAATLAQSGCLVLALEADLEAWESTEQ

AFAAGVAHFGRIDVLINNVGGTIWARPFAEYQPDQIEKEIRRSLFPTLWGCRAALPWMLKQGKGSIVNIS

SVATAGVNRVPYSAAKGGVNALTRSIAMEYSGSGIRINAVAPGGTEAPPRLTPRNEEQPSEQEKAWYQQV

VDQTVASSLLHRYGTLAEQANAILFLASDEASYITGVTLPVAGGDLG

>lcl|NZ\_FO834906.1\_prot\_WP\_021313424.1\_3020 [locus\_tag=BN49\_RS16680] [protein=benzoate 1,2-dioxygenase electron transfer component BenC] [protein\_id=WP\_021313424.1] [location=complement(3082407..3083423)] [gbkey=CDS]

MTFNIALNFEDGVTRFIQCNAGEKVLDAAYRQKVNLPMDCSDGVCGTCKCHCASGEYDLGEDYLDEALSD

DEAQARQVLTCQMVPTSDCVIDVPVAAAQCKTALTNTGAQVRQVNLLSDTAIELVVALDEPLAFLPGQYV

NIQVPGTPHVRAYSFSSQPGSLEGRFLIRNVPGGMMSQWLTQRARPGDRLTLSGPMGSFYLRHGERPLLM

LAGGTGLAPLLSMLHTLQTQGSQRPVMLLYGVTRDCDLVKTDALDTFTQQLTGYRWLPVVADENSTCPQR

GFVTDHLDDAMLNNGDVDIYLCGPPPMVNAVATALRDRGITPAGFWYEKFIASQSAAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529237.1\_3021 [gene=benB] [locus\_tag=BN49\_RS16685] [protein=benzoate 1,2-dioxygenase small subunit] [protein\_id=WP\_016529237.1] [location=complement(3083433..3083918)] [gbkey=CDS]

MLNLEQVRQFLYYEARLLDDRQWDEWLSCYSPQVVYWMPAWGDDDQLTRDPQKEISLIYYPNREGLEDRV

YRVKTERSGASTPEPRTTHIISNVELMGESDEGLEVRYSWVTWSHRYQHTDAYFGSTCCTLVEQDGRPQI

VRKTVRLNNDYIRQVIDVYHI

>lcl|NZ\_FO834906.1\_prot\_WP\_046043377.1\_3022 [locus\_tag=BN49\_RS16690] [protein=Rieske 2Fe-2S domain-containing protein] [protein\_id=WP\_046043377.1] [location=complement(3083918..3085300)] [gbkey=CDS]

MQKTLSTLKDKINNALVVDRENHIYRCHRSIFTDQQLFDFEMKHIFEGNWVFLAHESQIAEPGDYYTLTL

GRQPVIITRDKKNELHALINSCAHRGAMLCRRKTGNKNSFTCPFHGWTFSSNGKLLKAKDESTGGYPPSF

KQDGSHDLQKLPRFQSYRGFLFGSLKADVQPLEAYLGETCKIIDLIVDQAPEGLEVLKGSSSYVYEGNWK

LGAENGADGYHVSVVHWNYASTMSRRNYEAEGTHAVDANGWSKSLGGGYGFDNGHMLLWTRALNPEVRPV

YAHRERLQAEFGERRADQMVNETRNLCLYPNVYLMDQFSTQIRVIRPIAVDKTEVTIWCFAPKGESDQAR

ALRIRQYEDFFNVSGMGTPDDLEEFSACQRGYLGENLPWSDLSRGALRWVDGADEHAQHAGFSPRLSGVK

SEDEALYIAHHHHWQTLMLAAIEQEQQRYDQSITQRVEVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004175986.1\_3023 [gene=catA] [locus\_tag=BN49\_RS16695] [protein=catechol 1,2-dioxygenase] [protein\_id=WP\_004175986.1] [location=complement(3085410..3086336)] [gbkey=CDS]

MSNVFVQQPAIQKLLRDSAGLDVAGGDERFKAIIHRLLENICTLIDDYNVTEEEFWHAVNYLHELGGRQE

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DTEGRPVANAIVDIWHANTLGNYSFFDPGQSEYNLRRRIRTGADGRYSVRSIMPSGYGCPPDGPTQKLLD

RLGRHGNRPAHIHFFVSAPGHKHLTSQINLNGDKYLWDDFAFATRDGLIADPVKVTDREIIAQRNLEGEH

TEVCFDFTLCKALSADEEQRGIRVRAKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002906471.1\_3024 [gene=catC] [locus\_tag=BN49\_RS16700] [protein=muconolactone Delta-isomerase] [protein\_id=WP\_002906471.1] [location=complement(3086403..3086693)] [gbkey=CDS]

MLFKVEMTVNIPPGFPANEAEEIKQREKAYSQQLQREGKWRHIWRVAGLYANVSIFDVQDAEELHQILMG

LPLYPFMAIKVEALCRHPSSIRDDDR

>lcl|NZ\_FO834906.1\_prot\_WP\_072143290.1\_3025 [locus\_tag=BN49\_RS16705] [protein=muconate cycloisomerase family protein] [protein\_id=WP\_072143290.1] [location=complement(3086713..3087876)] [gbkey=CDS]

MDVGTKSYISHQEQKMTATVEQIESWIVDVPTIRPHKLSMTTMGCQSLVIVRLTRSDGICGIGEATTIGG

LSYGVESPEAISSAITHYLTPLLKGQPADNLNALTARMNGAIKGNTFAKSAIETALLDAQGKALGLPVSA

LLGGALQTALPVLWTLASGDTAKDIAEGEKLLAEGRHRAFKLKIGARELATDLRHTRAIVEALGDRASIR

VDVNQAWDAATGAKGCRELAAMGVDLIEQPVSAHDNAALVRLSQQIETAILADEAVATAYDGYQLAQQGF

TGAYALKIAKAGGPNSVLALARVAQAAGIGLYGGTMLEGTVGTVASLHAWSTLPLQWGTEMFGPLLLKDD

IVSVPLTFADGQVALPQTPGLGVELDEDKLHFYTRQP

>lcl|NZ\_FO834906.1\_prot\_WP\_009485870.1\_3026 [locus\_tag=BN49\_RS16710] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_009485870.1] [location=3087992..3088882] [gbkey=CDS]

MVVKPAQFSAPHFAQGIVICRELYAATEKDAMSDNIPNTLSARQAEHDPNFMLSLARGLEVLNAFTPQRQ

RLTISQLSQKTQISRAAVRRCLYTLAALGMVHSPDGRSYELLPRVLAVGHAYLAGTPLAKVAQTALDNLG

KALGESCSAATLDGDNVLYIARAAVNNLLSIDLGRGSRLPAWATSMGRVLLSALPEEQLEVTLSRVTLIR

YTPHTLCDLSGLRAEIARVRMQGYALADRQIEVGLCSLAVPVLSRHGQVVAALNVGVPAATVSAAALKEK

ALAPLRRAAMDLSLQL

>lcl|NZ\_FO834906.1\_prot\_WP\_004175980.1\_3027 [gene=kmrA] [locus\_tag=BN49\_RS16715] [protein=efflux MFS transporter KmrA] [protein\_id=WP\_004175980.1] [location=complement(3088877..3090376)] [gbkey=CDS]

MSRQWMTLMAILLVYIPVAIDATVLHVAAPTLSVALGSSGNELLWIIDIYSLVMAGMVLPMGALGDKIGF

KRLLLLGSAIFGIASLCAALSPTAMTLIASRALLAVGAAMIVPATLAGIRSTFAEASQRNMALGLWAAVG

SGGAAFGPLVGGILLEHFYWGSVFLINVPIVLVVIAINAKVVPRQPARREQPLNLLQALVLIAAILMLVF

SAKSALKGQLALWLTALVALGGAAMLTWFIRKQLSAARPMVDMRLFTHRIILSGVMMAMTALITLVGFEL

LMAQELQFVHQKTPFEAGIFMLPVMVASGFSGPIAGLLVSRLGLREVATGGMLLSAFSFLGLALTDFSTQ

QWLAWGLMTLLGFSVASALLASSSAIMAAAPKEKAAAAGAIETMAYELGAGLGIALFGLILTRSYSASIA

LPSGLSGAMAQQAASSIGEAVSLSQALPAGVAQALMAAAKTAFIQAHSLVLATAGVLLLLLAAGIWRSLA

TVAKPQSAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004888643.1\_3028 [locus\_tag=BN49\_RS16720] [protein=TetR family transcriptional regulator] [protein\_id=WP\_004888643.1] [location=3090500..3091075] [gbkey=CDS]

MHYLQRDARREGIMQAAMRLALRGGFAAMTVRQIAREAQVAAGQLHHHFTSIGELKAQVFIRLIREMLDM

PLVAEDASWRERLFSMIGSEDGRLEPYIRLWREGQVLADSDPDIKAAYLLTMNMWHAETVAIIEQGLASG

EFRSAEPAADIAWRFIALVCGLDGIYALDAQALDEAAFSRYVNKMITLELF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151231.1\_3029 [locus\_tag=BN49\_RS16725] [protein=NarK family nitrate/nitrite MFS transporter] [protein\_id=WP\_004151231.1] [location=3091250..3092632] [gbkey=CDS]

MSVQNDKDNHYLLNNWRPENKAFWENKGQAIARRNLWISVACLLLAFCVWMLFSAVAVNLNKVGFHFTTD

QLFLLTALPSLSGAILRVPYSFMVPLFGGRYWTVLSTVILIVPCIWLGVAIQNITTPFWVFIIIALLCGF

AGANFASSMGNISFFFPKAKQGSALGVNGGLGNLGVSVMQMVAPAVIFLPLFTFLGVHGVTQPDGSTITL

SNAALVWVPLLLLATVAAWFGMNDIAGSKASIRDQLPVLKRPHMWLLSLLYLATFGSFIGFSAGFAMLAK

TQFPAVDILKLAFFGPFIGALARSFGGIISDRLGGVRVTLVNFVLMALFTGLLFLTLPGSGSGSFLAFYV

VFMGLFLTAGLGSGSTFQMIAVIFRQLTIDSVKQRGGSDEEAQHEAVTDTAAALGFISAIGAIGGFFIPK

AFGTSLAMTGSPVGAMKVFFVFYVVCVLVTWLVYGRRKPA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043381.1\_3030 [locus\_tag=BN49\_RS16730] [protein=nitrate reductase subunit alpha] [protein\_id=WP\_046043381.1] [location=3092747..3096487] [gbkey=CDS]

MSKLLDRFRYFKQKGETFANGHGQVYNNNRDWEDSYRQRWQFDKIVRSTHGVNCTGSCSWKIYVKNGLVT

WETQQTDYPRTRPDLPNHEPRGCPRGASYSWYLYSANRLKYPLARKRLIELWREALAQHPDPVLAWDSIM

QDPAKTRSYKAARGKGGFVRSSWKELNQLIAAANVWTIKHYGPDRVAGFSPIPAMSMVSYAAGTRYLSLI

GGTCLSFYDWYCDLPPASPMTWGEQTDVPESADWYNSSYIIAWGSNVPQTRTPDAHFFTEVRYKGTKTIA

ITPDYSEIAKLCDQWLAPKQGTDSALAMAMGHVILKAFHLDNPSDYFLNYCRTYTDMPMLVILEPRDDGS

YTPGRMLRASDLLDGLGESNNPEWKTVAYNSDGELVAPNGSIGFRWGEKGKWNLEQRADGKDVELKLSLL

DIRDSVVSVGFPYFGGNENPHFRSVSQSPVTLHPLPAKQLTLASGESGLVVSVYDLILANYGLDRGLDDV

NAAKDFAEVKAYTPAWAEQITGVPRQHIEQIAREFADTAHKTHGRSMIILGAGVNHWYHMDMNYRGMINL

LVFCGCVGQSGGGWSHYVGQEKLRPQTGWLPLAFALDWSRPPRQMNSTSYFYNHASQWRYEKLTAQELLS

PLADASKFSGSLIDFNVRAERMGWLPSAPQLNINPLTIKQQAEAAGLSPAEFTVQSLKSGDIRFAAEQPD

SGKNHPRNLFIWRSNLLGSSGKGHEYMLKYLLGTDSGIQGDELGASDEVKPEEVEWQTAAIEGKLDLLVT

LDFRMSSTCLFSDIVLPTATWYEKDDMNTSDMHPFIHPLSAAVDPAWEAKSDWEIYKDIAKSFSQVCVGH

LGKETDVVLVPLQHDSPGELSQPFEVLDWRKGECDLIPGKTAPSIALVERDYPATWERFTSLGPLLDKLG

NGGKGISWNTQSEVDFLGKLNYVKPDGPAKGRPRIDSAIDASEVILSLAPETNGQVAVKAWQTLGEFTGR

DHTHLALNKEDEKIRFRDIQAQPRKIISSPTWSGLESEHVSYNAGYTNVHELIPWRTLSGRQQLYQDHPW

MRAFGESLVAYRPPIDTRSVSQMKAVPPNGFPEKALNFLTPHQKWGIHSTYSENLLMLTLSRGGPIVWLS

ETDAKELGIEDNDWIEAFNANGALTARAVVSQRVPPGMTMMYHAQERIMNIPGSEVTGRRGGIHNSVTRV

CPKPTHMIGGYAQLAYGFNYYGTVGSNRDEFIMIRKMKNIAWLDDEGRDQVQEAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004148517.1\_3031 [gene=narH] [locus\_tag=BN49\_RS16735] [protein=nitrate reductase subunit beta] [protein\_id=WP\_004148517.1] [location=3096484..3098028] [gbkey=CDS]

MKIRSQVGMVLNLDKCIGCHTCSVTCKNVWSSREGMEYAWFNNVETKPGIGYPKNWEDQDQWQGGWIRGI

SGKLTPRLGNRVSVLSKIFANPVLPAIDDYYEPFTYDYQHLHNAPEGKYLPTARPRSLISGERMDKINWG

PNWEELLGGEFEKRARDRNFEAMQKEMYGQFENTFMMYLPRLCEHCLNPSCVATCPSGAIYKREEDGIVL

IDQDKCRGWRMCISGCPYKKIYFNWKSGKSEKCIFCYPRIESGQPTVCSETCVGRIRYLGVLLYDADRIE

EAASTEHETDLYERQCEVFLNPNDPAVIEEALKQGIPHNVIEAAQKSPVYKLAMDWKLALPLHPEYRTLP

MVWYVPPLSPIQSVADAGGLPSNGNILPAVESLRIPVQYLANLLSAGDTGPVLRALKRMMAMRHYKRSQT

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FNLFNSRRIDAIDVSGVRKHGEGE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530848.1\_3032 [gene=narW] [locus\_tag=BN49\_RS16740] [protein=nitrate reductase molybdenum cofactor assembly chaperone] [protein\_id=WP\_016530848.1] [location=3098028..3098723] [gbkey=CDS]

MRILKVIGLLLEYPDELLWENRDDALALIRADVPSLTPFVGELLTAPLLDRQAEWCEVFERGRATSLLLF

EHVHAESRDRGQAMVDLMNQYQQAGLQIDCRELPDHLPLYLEYLSILPPAEAREGLQNIAPILALIGGRL

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QRRFSQDVAPQYVDIRAGGPK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530849.1\_3033 [gene=narI] [locus\_tag=BN49\_RS16745] [protein=respiratory nitrate reductase subunit gamma] [protein\_id=WP\_016530849.1] [location=3098720..3099400] [gbkey=CDS]

MIQYLNVFFYDIYPYLCGTVFLVGSWLRYDYGQYTWRASSSQMLDKRGMVLWSNLFHIGILGIFFGHLFG

MLTPHWVYSWFLPMSQKQLMAMILGGICGVLTLVGGIGLLMRRLTNPRIRATSTTADILILCILLIQCAL

GLTTIPFSAQHPDGSEMLKLVDWAQAVVTFHGGASAHLDDVAWIYRVHLVLGMTIFLIFPFTRLVHVWSA

PVEYFTRRYQVVRSRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002906551.1\_3034 [gene=nhoA] [locus\_tag=BN49\_RS16750] [protein=N-hydroxyarylamine O-acetyltransferase] [protein\_id=WP\_002906551.1] [location=complement(3099598..3100443)] [gbkey=CDS]

MSPFLRAYFSRLSWTGEPDVSIDTLRELHLQHNSAIPFENLDVLLPREIHLDDGALEEKLIAARRGGYCF

EQNGLLERALREIGFNVRSLLGRVVLANPPQMPPRTHRLLLVEVAGERWIADVGFGGQTLTAPIKLLADI

PQQTPHGSYRLVHEGDEWTLQFNHHEHWQSMYHFDLGRQYASDYVMGNFWSAHWPQSHFRHHLLMCRHLP

DGGKMTLTNFHFTHWENNHVVEKVDFADVSALYEALQTRFGLGVDDPKHGFSEAALAAVMAAFDTHPEAG

K

>lcl|NZ\_FO834906.1\_prot\_WP\_046043384.1\_3035 [locus\_tag=BN49\_RS16755] [protein=iron ABC transporter permease] [protein\_id=WP\_046043384.1] [location=complement(3100520..3102175)] [gbkey=CDS]

MKQTFLSGATLAALVMLVALPLVFILLQAIFPHFSAGSLGDAFGGIPALLADPQLAAMLGGTLWIAAGVA

LVSVMIGLPLGILRGMFSLPLPRLWDLLFLIPFLTPPYISALSWMLALQSQGYLQQLTGWQLNDLLFSRS

GIVLVMTFNIFPVVYFAVSRSLLASGTRLAVVARVHGASAWRAFWHVTLPMLSPALAAGMLLAFTLAIEE

FGVPAALGSRAGVVMLTVGIEKKLADWPVDLPGAALLSLLLMAVALFAWWLQRRLVGEKEVTSVTGKPGE

NHGTLLGWMTLPAVLAMAAVGGLAVGVPAVSMMLTSVMGTLSGGVSVENVTLRHFAALFDQQGDALSALG

TSLSLALGSALIVGALGLLAAWLVMVQKIKGRGMVDALSLMPAALPGVVVGVGLILLWNQPFWPRSPYNT

LWMLLLSYCCLLMPWPVRYVGSALRQLGPNLEPAARVHGASPLQALRLIVLPLVFPALLAAMLMVFAVAS

RELVTSLLLSPAGTQTVGVFIWRQFEQGSVGQGMAMASLTLLTGLVLMLTALALMQRRTRG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530099.1\_3036 [locus\_tag=BN49\_RS16760] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016530099.1] [location=complement(3102233..3103201)] [gbkey=CDS]

MNTVMTVKKGVVLAMALSAMMLSSAHALTVYTAGPGSLAKSLASGFEQQTGVKVTVFQATTGKVMARLEA

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WRDLTQPAFKDKVTTPDPALSGASLDLLIGLQNSMGDQAWQLFDDLKKNGMVVSGPNAQAVTPVMQGAKA

AVFGAVDYVSYGNIQQGESLKVIFPASGTVIAPRPMMILKTSQHPGEAKAFIDYVLSPEGQAKVADAWLM

PARRDVAAKRPLLDALKVLPTTSEGSSERGAVLARFSQLYAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_171819477.1\_3037 [locus\_tag=BN49\_RS16765] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_171819477.1] [location=complement(3103198..3103902)] [gbkey=CDS]

MMRTLTPIPLQEVSFAFAETPIHDRFTLHIEPGRIVALLGPSGCGKSTLLRLLAGLSVPASGEIRFGDRL

VARAGWGLPPEQRDIGMVFQDYALWPHMSVAQNVAFPLRMRGVSRSERERRVSEALARVGLNGFAERKPS

GLSGGQQQRVALARAIVAAPRVLLFDEPLSNLDSELRESLCGEMSRLLRQLGITALYVTHDRREAELLAD

QIVYLSAGRVAAVRAVTPTSGEVA

>lcl|NZ\_FO834906.1\_prot\_3038 [locus\_tag=BN49\_RS16770] [protein=flavin reductase family protein] [pseudo=true] [partial=3'] [location=3104114..>3104575] [gbkey=CDS]

MSRFRHVELQYASRLLNHGPTILITSYDAPSDRRNVMAAAWSMPVEFAPPRVAIVVDKSTWTREIIERNG

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TLFGEVVSAAADER

>lcl|NZ\_FO834906.1\_prot\_3039 [locus\_tag=BN49\_RS31495] [protein=porin] [pseudo=true] [partial=5'] [location=<3104681..3104779] [gbkey=CDS]

SLDE\*TVLDDFGSKGFTAGGIWNFGVQTEIWF

>lcl|NZ\_FO834906.1\_prot\_WP\_016532004.1\_3040 [gene=pptA] [locus\_tag=BN49\_RS16775] [protein=tautomerase PptA] [protein\_id=WP\_016532004.1] [location=complement(3104819..3105046)] [gbkey=CDS]

MPHVDIKCFPRELTDEQKTALAADITEVLIRHLNSKEGAVSVALTQIEPDAWQAVWDSEIAPQMAQLIKQ

PGYSM

>lcl|NZ\_FO834906.1\_prot\_WP\_020804703.1\_3041 [locus\_tag=BN49\_RS16780] [protein=glutathione S-transferase family protein] [protein\_id=WP\_020804703.1] [location=complement(3105117..3105734)] [gbkey=CDS]

MITVYGVPGWGSTISELMLSLADIPYEVVDVEGFDQPGPARERLRQINPLCQVPTLRLADGSIMTETAAI

ALMILDQRPDLAPAPGTPQRPQFQRLLVWLVANVYPTFTYADYPERWAPAAAEQLVENCRQYRKNLYLWF

EQQLAAGPWALGASVTLLDCYIAAMYRWGPRQAWFDDHAPKFAAIARAFCQRPELAAALRRNKLI

>lcl|NZ\_FO834906.1\_prot\_WP\_171819494.1\_3042 [locus\_tag=BN49\_RS16785] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_171819494.1] [location=complement(3105812..3106663)] [gbkey=CDS]

MSAYAALDLRANEQPLPVTRDPQAIAKIPPGYRSVEPGTLTVAISALNSPPLALLASDNRTRIGSDPDIA

RLLAGSLGLKLRLVPTAWEDWPLGIASGRYDVALINIAVTEKRKEKFDFATYRVDSLAFSVKSTSDIAAV

NGPADLAGRKVIVGSGTNQERILLGWNEDNRAAGRPQAQPVYLTDDASGNLYIQSGRADIFFGPQSVAAY

KAALNGQTRVVGLGPKKAWVATTTKKGNGLVYALQAALDGAIARGEYQQVLARWGEQGEAVAQSVVNPPG

ITY

>lcl|NZ\_FO834906.1\_prot\_WP\_002906697.1\_3043 [locus\_tag=BN49\_RS16790] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_002906697.1] [location=complement(3106702..3107481)] [gbkey=CDS]

MPSSHNGHISITGVSKYYGRHKALDDVSLEIPPGTVTVILGPSGSGKSTLLRTINHLERVDEGFIQIDGD

YIGYRRKGDKLYEMKEKEILRQRINVGYVFQNFNLFPHLTVLENLIEAPIAHQQVTRKEAIARAYELLDV

VGLRNKADAWSRHLSGGQQQRIAIARALALNPRVILFDEPTSALDPELVGEVLDVIKKLARSGTTLVVVT

HEIGFAREVADQVVFMVDGRIVEQGSSDEVLNHPQHPRTRQFLSRVLPS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529453.1\_3044 [locus\_tag=BN49\_RS16795] [protein=amino acid ABC transporter permease] [protein\_id=WP\_016529453.1] [location=complement(3107465..3108391)] [gbkey=CDS]

MHSSETIKVVPARYPLRVVGALVALLVLAVVIQSVAFNPRWEWGVFARWFFDPVSLEGLGQTLLLTLLGT

VLSVIFGGLLALARLSSSWLLSSLAWGYIWLFRSLPLIVVLIILYNFSYLYDTLSLGIPFTGVTWASYQT

INVLGQFSTAVVGLTLVQSAYTAEIIRGGFLGVDHGQYEAAAALGLPAWRRTLRIILPQALRTILPSGFN

EIISLAKGTAMVYVLAMPELFYTIQMIYNRTQEVIPLLMVGAAWYLAITSVLSAIQYLVERGLARSERRS

AVNSARSSRTTQSARQAQPQEAVHAQLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004180127.1\_3045 [locus\_tag=BN49\_RS16800] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004180127.1] [location=complement(3108401..3108910)] [gbkey=CDS]

MSEAFRDISPEAPELQPIISGLFAEYAARYGDYFSRDAEVELSEWYLPPQGLFIVLEREGEIIATGAYKP

KDRHTAEIKRIWTHRRLRQQGLAAKVVQELERRAVLAGYSHIYLTTGFRQPEAVKLYLSQGYEAQFDLTR

DPEEYSQPPYDGRLRFTKALAVSAYSHSA

>lcl|NZ\_FO834906.1\_prot\_3046 [locus\_tag=BN49\_RS31500] [protein=NtaA/DmoA family FMN-dependent monooxygenase] [pseudo=true] [location=complement(3108922..3111185)] [gbkey=CDS]

MSENRQLRLGTILHGASGNMSAWRHPAAQADASINFDFVTQTALKAEAGKLDFIFVADGLYINEKSIPHF

LNRFEPLTVLSALAAITRRLGLVGTLSTSYSEPFTTARQFASLDHLSQGRAGWNVVTSPLEGSAKNFSRA

QHPDHALRYRIADEYLQVVKGLWDSWEEDAFVRNKETGQFFDKNKLHTLDHHGDFFKVAGPLNIARTPQG

RPIIFQAGASDDGKKLAARHADAIFTHQDSLAEAQAFYRDVKSQLAAYQRSPDQLHIFQGVSVIVGDDAE

DAERQYQTTAALVSIEDALNYLGRYFEHHDFSQYPLDEPFPDIGDLGQNSFRSTTDEIKRHARERGLTLR

QVALEAASPRPRFTGTASDVADGLQLWFEQHAADGFIIQGGTPETFPRFVDEVVPLLQARGLFRRDYPGT

TLRESLGLALPANQFQK\*\*KRITLCRKQHSCWPSRWHLAPHRGVRTSRSMAPE\*AWRPTKRRFIQRKIRR

PLPCCRKICIWRCRGNSPSRWRP\*TLRR\*RSLPMTTKPCSAARRISPGWWRRASGWK\*TWFPLHGKTGRW

ASPPANMMPRSAILPSPKSGKRSSISPPTAKTRWASTSKAPVR\*ARLTKRKISPG\*RLLSAPAPTRRRSC

WRGTRRTSRRG\*SRLSRSTPRMMPPRRWPCRPDEPTPSSAPT\*LARGRRR\*PAKPNSWAASMAAGRKRRI

SR\*R\*KKTAGW\*MPSRRR\*TGLSPAGTTPKCLTAGAKGWKAFRNRKSIRPDWAT

>lcl|NZ\_FO834906.1\_prot\_WP\_004200077.1\_3047 [locus\_tag=BN49\_RS16815] [protein=M20 peptidase aminoacylase family protein] [protein\_id=WP\_004200077.1] [location=complement(3111210..3112331)] [gbkey=CDS]

MSFEQQLISWRRELHQNPELSLQEVATTARIRDWLQSGGLTLLPYDLKTGLVAEVGSGDKVIALRADIDA

LPIEEATGLPYRSQNQGVMHACGHDIHTSVMLGAALLLKEREAELPGRVRILFQPAEENFGGAKTLIRAG

ALEEVSAIFGMHNEPGLPVGEFATRGGAFYANVDRFVFKVTGKGAHAARPHEGKDAILLASQLVTVLQSV

ASREVNTLDSVVLSVTRIQGGNTWNVLPESVELEGTLRTHSSEVQQRVKARVSEIAAGFASAFGAQIDVF

WYAGPTALVNDARWADFASEVAARAGYRTHHADLHLGGEDFAVYLQHIPGAFVSIGSASEYGLHHPAFNP

DERLIAPAAHYFARLAEEALQHI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151219.1\_3048 [locus\_tag=BN49\_RS16820] [protein=MsnO8 family LLM class oxidoreductase] [protein\_id=WP\_004151219.1] [location=complement(3112321..3113328)] [gbkey=CDS]

MSYRISILDKSPLAAGETAAQALARTLTLAQHAEAWGYHRFWVAEHHNTDQLASPSPELVIAWLLGHTRR

IRLGSGGVMLQHYSPYKVAENFNLLAALAPGRIDLGVGKAPGGLPLSTRALQQGLHQEEKGTFADQLAQL

DNWLSLTEPGGEESLRATPIPPRRADGFLLGASLESAELAARLDWNFVFAAHLNGDSALRRAVFNRWREL

SPREAMVAVQVVVADDPATAAALAQQVEVWGVELENGQRVTVGSEAQAVAFARQAGSRPTRIARRESSLI

SGTPEQVKARLDALQAEEQLDELIIDTPISDGPARLHSLRLLAQAHYGKEVLNVL

>lcl|NZ\_FO834906.1\_prot\_WP\_004180132.1\_3049 [locus\_tag=BN49\_RS16825] [protein=adenylate kinase] [protein\_id=WP\_004180132.1] [location=complement(3113420..3113971)] [gbkey=CDS]

MNINVVGTSGSGKSTLARRLAHRLELPWIELDRLYWRPNWQGAPDEAFFAAIAAATATPGWVLDGNYNRS

RSVKWRAVDLVIWVDYGFWRTLRQAVWRAASRAWRHQELWPGTGNCESFRRSFCSRESIILWTLKTWRQH

RRRYLADMQDPQYRHIRFVRVRNPRQAEALLRELEAQRSAGHI

>lcl|NZ\_FO834906.1\_prot\_WP\_032104973.1\_3050 [locus\_tag=BN49\_RS16830] [protein=LysR family transcriptional regulator] [protein\_id=WP\_032104973.1] [location=3114245..3115132] [gbkey=CDS]

MLKENVNDLLSFMVVARERSFTRAAAQLGVSQSALSHAMRHLETRLDVRLLTRTTRSVVPTEAGERLIQR

LGQHLEEIEQALAALRDTRERPAGNLRITAGEHAASAVLWPALKPFMLQYPDINIEITVDNGLTDIVGDR

FDAGVRLGEQVAKDMIAVRIAPDMRMAVVGSPAYLQRAGTPQTPWDLAQHRCINLRLPTRGGLYAWEFAR

DGREIQVRVEGQLILNSLPQRIDAAEAGLGLAYVPDDCVAEALASGRLVRVLAEWTPVFPGYHLYYPSRR

QHTSAFTLLLETLRR

>lcl|NZ\_FO834906.1\_prot\_WP\_014907513.1\_3051 [gene=ansP] [locus\_tag=BN49\_RS16835] [protein=L-asparagine permease] [protein\_id=WP\_014907513.1] [location=3115321..3116775] [gbkey=CDS]

MNTKHESAAEHHAAKRHWLNSHEAGYHKAMGNRQVQMIAIGGAIGTGLFLGAGARLQMAGPALALVYLVC

GIFSFFILRALGELVLHRPSSGSFVSYAREFLGEKAAYVAGWMYFVNWAMTGIVDITAVALYMHYWGAFG

DVPQWVFALGALAIVGTMNMIGVKWFAEMEFWFALVKVLAIVAFLVVGTIFLGSGKPLDGNATGFHLITD

NGGFFPHGLLPALVLVQGVVFAFASIELVGTAAGECKDPETMVPKAINSVIWRIGLFYVGSVVLLVLLLP

WNAYQAGQSPFVTFFSKLGVPYIGSVMNIVVLTAALSSLNSGLYSTGRILRSMSMGGSAPKFMSKMSRHH

VPYAGILATLGVYVVGVFLNYLVPSQVFEIVLNVASLGIIASWGFIVVCQMRLRKAIKEGKAAKVSFRMP

GAPFTSWLTLLFLFSVLVLMAFDYPNGTYTIGSIPLLAVLLVAGWFGVRKRVHEIHSTAPTLRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002906779.1\_3052 [locus\_tag=BN49\_RS16840] [protein=YgdI/YgdR family lipoprotein] [protein\_id=WP\_002906779.1] [location=complement(3116826..3117047)] [gbkey=CDS]

MKKPFMVICAGAMLALLAGCSSNYVMTTKSGQTIVTHGKPQLDKETGMTSYIDESGNKREINSSDVSQLV

EDN

>lcl|NZ\_FO834906.1\_prot\_WP\_016531109.1\_3053 [locus\_tag=BN49\_RS16845] [protein=YncE family protein] [protein\_id=WP\_016531109.1] [location=complement(3117216..3118277)] [gbkey=CDS]

MSLRHFAAPRLRHSLLVTSLLLAGSFSAHAAEEMLRKAVGKGAYEMAYSQQENALWVATSQSRSLDKGGV

VYRLDPTTLDVTQIIHNDLKPFGAAINHATGTLWFGNTVDSTVTAIDAKTGAVKGRLVLDERQRSETVRP

LQPRELAVNEQTNTVYITGLGKESVIWVVDGATLKLKTTITGTGAMATGLAIDPQAKRLYTTNADGELLT

IDSESNTIASRKKLQDDGKAHFYLNLSLDTAGHRAFITDSKQPEVLVVDTRDGKVLEKIAAPESLAVLFN

PARNEAYVTHRKAGEVSVIDGKSYKVVKTFKTPTHPNSLAFSEDGKTLYVSVKQASSREKEATAPDDVIR

IAL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043386.1\_3054 [locus\_tag=BN49\_RS16850] [protein=TonB-dependent receptor] [protein\_id=WP\_046043386.1] [location=3118536..3120641] [gbkey=CDS]

MKILSVRHAALPALLLPLIAAAQAADEQTMVVTAAPTTVSELDTPAAVSVVNGDEMRQAAPRVNLSESLG

AVPGLQVQNRQNYAQDLQLSIRGFGSRSTYGVRGLRIYVDGIPATMPDGQGQTSNIDIGSVDTIEVLRGP

FSALYGNSSGGVINVTSQTGTQPPTVEASSYYGSFGTWHYGMKATGAVGDGSHAGDVDYTVSTNRFTTHG

YRDHSGARKNLANARLGVRINDVSKLTLLLNSVDIKANDAGGLTADEWRNNPRQSPRGDQYNTRKNTRQT

QAGLRYERQLSAQDDLSVMMYAGERETTQFQSIPRAPQLKPSHAGGVIDLTRHYQGIDTRLTHRGELLVP

VTLTAGLDYENMSERRKGYENFVMVNGAPQYGEQGALRRNERNLMWNVDPYLQTQWQLTDKLSLDAGVRY

SSVWFDSNDYYITPGNGDDSGNASYHKWLPAGSLKYALTDAWNVYLSAGRGFETPTINELSYRSDNQSGL

NFGLKPSTNDTVEIGSKTRIGNGLFTAALFQTNTDNEIVVDSSSGGRTSYKNAGKTRRQGMELGLDQQFG

ESWRLKAAWTWLDATYRTNVCDDASCNGNRIPGIARNMGYASFGYQPEQGWYAGSDIRYMSDIMANDENT

AKAPSWTVVGLTTGYKWSYGRMDMDLFGRIDNLFDREYVGSVIVNESNGRYYEPAPGRNYGIGLNLAWRF

E

>lcl|NZ\_FO834906.1\_prot\_WP\_016530448.1\_3055 [locus\_tag=BN49\_RS16855] [protein=amidohydrolase] [protein\_id=WP\_016530448.1] [location=3120839..3122545] [gbkey=CDS]

MDNVVYADCVLINGKVATVDAHFSFKRAIAVKQGWIINVGEDQEIQQHIGPQTQVIDLGGKLILPAAHDS

HIHIGWLADSWHCLNCQDVRSLAVLRERLRDQAARTPAGAWIRVCGLDPNAIKECAAEQRSLTRWDIDDV

TADHPTLLALWDGHSCIVNSRALALSGLDASTPDPLGGHLGRTASGELDGNFIDLPALHLASGTMPRLTV

AALKENLLAAQRLMNSEGYASYTEGAMGPGENTREVGAAGDRAIAAYRELQDEGKLTARVSIAFYSAERG

VQSCATLKRDLDSFDFSQFTDRDWLDCRTIKLFCDGVPTSHTAWMNQDYADRPGYRGRSVFGGPEATEEA

QVEALQQMILLAHQRGFQVAVHAVGDKAVKVTINSFVQAIQRYPGESRRHYVLHGSMGDRQDFVTAAKYG

ILLSEQPSPGGPAYDYEQRARYCGIKGEICKGLRDIIDLGVIVAGGSDGIMALVNWRKMVQAAVTRKSSS

SGNVIRPELAISVADGVRMYTINAAYQEGKEAVRGSIEVGKVADFQVLDRDIFAVAHEEIGASRVVMTMV

GGNVVFQD

>lcl|NZ\_FO834906.1\_prot\_WP\_015958496.1\_3056 [locus\_tag=BN49\_RS16860] [protein=DUF406 domain-containing protein] [protein\_id=WP\_015958496.1] [location=complement(3122643..3122942)] [gbkey=CDS]

MKDVVDKCSTKGCAIDVGTIIDNEDCVYRAEKVFPNREEAESTVAAVRERAAAAAPASEPPQVDYTIVAA

GDAVKLDLSIAFSCQAEKIIFELSLRNLL

>lcl|NZ\_FO834906.1\_prot\_3057 [locus\_tag=BN49\_RS16865] [protein=hypothetical protein] [pseudo=true] [location=complement(3123032..3123261)] [gbkey=CDS]

MSRIAINHNRQCHSSSLLAMFCDQTNAASRGRRDGVQNSVMETTIAARQRVSLRDRP\*TWCHVLRWRKMA

PGATRY

>lcl|NZ\_FO834906.1\_prot\_WP\_046043387.1\_3058 [gene=rihA] [locus\_tag=BN49\_RS16870] [protein=pyrimidine-specific ribonucleoside hydrolase RihA] [protein\_id=WP\_046043387.1] [location=3123223..3124158] [gbkey=CDS]

MALPIMIDCDPGHYDAIALVLALASPELEVKAVTASAGNQTPEKTLRNVLRMLTLLNRPDIPVAGGAWKP

LMRDLIIADNVHGESGLDGPSLPEPAFAPQNCTAVELMASVLRESQEPVTLVATGPQTNVALLLASHPEL

HAKIARIVIMGGAMGLGNWQPAAEFNIYVDPQAAEMVFQSGIPVVMAGLDVTPKAQILPADIERFRQIGN

PVSTIVAELLDFFMAYHKDEKWGFDGAPLHDPCTIAWLLKPEIFTTIERWVGVETEGKYTQGMTVVDYYH

LTGNRPNTTLMLDVDREAFVDLLAQRLAFYA

>lcl|NZ\_FO834906.1\_prot\_WP\_002906792.1\_3059 [locus\_tag=BN49\_RS16875] [protein=NADP-dependent oxidoreductase] [protein\_id=WP\_002906792.1] [location=complement(3124221..3125258)] [gbkey=CDS]

MTDQPQRHRRWVLASRPHGEPTAENFRLEESEVPTPGPGQVLLRTVYLSLDPYMRGRMSDAPSYSPPVAI

GAVMVGGTVSRVVSSNHADYQPGDWVLGYSGWQDYELSDGSGLVKLGDNPQHPSWSLGVLGMPGFTAYMG

LLDIGQPKAGETLVVAAATGPVGATVGQIGKIKGCRTVGIAGGAEKCRYAVETLGFDLCLDHRADDFAEQ

LAQACPQGIDVYYENVGGKVFDAVLPLLNTAARVPVCGLVSGYNATGLPDGPDRLPLLMATILKKRIRMQ

GFIIGQDYGHRIAEFQQQMGRWVQEGKIKYREQLIDGLDQAPQALIGLLKGENFGKVVIRVAADD

>lcl|NZ\_FO834906.1\_prot\_WP\_002906794.1\_3060 [locus\_tag=BN49\_RS16880] [protein=XRE family transcriptional regulator] [protein\_id=WP\_002906794.1] [location=complement(3125324..3125905)] [gbkey=CDS]

MNTIEDNLNQRISARIRIERESRGWSLNDLAERAGASRAMIHKIERGESSPTASMLGRLSGAFGISMSTL

IARAEMQEGKLLRFASQPVWRDPQSHYLRRHVSPRSDLPIDLVQIELPPGSDVPMPAASYALARQLIWLQ

QGELVFVEGNTRHEMQAGDCLELGPPNDCRFINESAETCVYLVVRLNQSPSGS

>lcl|NZ\_FO834906.1\_prot\_WP\_002906796.1\_3061 [locus\_tag=BN49\_RS16885] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002906796.1] [location=3126068..3126586] [gbkey=CDS]

MSIRPAIKDDCAAIAEIYNHAVVHTAAIWNDKTVDTDNRIAWFEARQLAGFPVLVSEEDGVITGYSSFGD

WRAFDGFRHTVEHSVYVHPEHQGKGLGRKLLVALIAEARRLNKHVMVAGIESQNHASLHLHETLGFITTG

QMPQVGTKFGRWLDLTFMQLQLDARQDPDGKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530444.1\_3062 [locus\_tag=BN49\_RS16890] [protein=DMT family transporter] [protein\_id=WP\_016530444.1] [location=3126583..3127032] [gbkey=CDS]

MNASLTLACLIAAGVGLVVQNTLMVRITQSASTILIAMLLNSLVGIVIFVTMLLLRQGVAGFQELALSVK

WWTLIPGLLGSFFVFASISGYQNVGAATTIAVLVASQLVGGLIMDLVRAHGVPVRALIGPLCGAVMLVVG

AWLEARRQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002906801.1\_3063 [locus\_tag=BN49\_RS16895] [protein=YdcY family protein] [protein\_id=WP\_002906801.1] [location=complement(3127041..3127274)] [gbkey=CDS]

MAHLDEVIVKVDDTLAEGVIAHMNELLIALSDDAQLSREERYIQQQRLRTAIAHHGRQHQEEQDARREQL

TKGGAIL

>lcl|NZ\_FO834906.1\_prot\_3064 [locus\_tag=BN49\_RS16900] [protein=ABC transporter substrate-binding protein] [pseudo=true] [partial=5'] [location=complement(3127291..>3128616)] [gbkey=CDS]

TLRQGVKFNSNKFFKPTRDFNADDVLFSVLRQMDPQHPYHKVSQGNYEYFHDVGLDKLIKSVKKVDDYHV

QFELNEPNAAFLADWGMDFASILSAEYGEAMLKKGTPENVDNWPVGTGPYALQQYKVDSQIRYIANPHYW

EGEVPTKHLIFSITPNVETRLAKLQTNECQIIPAPSPVQFPVIKGNKDLALHAIEALNVGYLAFNTEKKP

FDNVLVRQALNYATDKQAIVKAVFLDSGSVAKSPIPSTMLGYKKDLPDYDYDPQKAKALLKQAGLEQGAE

VTLWSMPVQRPYNPNSKRIAEMIQNDWAKVGVKAKIVSYEWGEYLAGMRKGEHDSALYGWMSDNGDPDNF

AGTLLSCDNIQTGSNAARWCDKSYDALVKKALLVSDPQARAKLYEQAQEIFYQQAPWITLATGKTFYATR

SNVSGYTVSMMGSDFSKAKLN

>lcl|NZ\_FO834906.1\_prot\_3065 [locus\_tag=BN49\_RS31505] [protein=hypothetical protein] [pseudo=true] [location=complement(3128598..3128889)] [gbkey=CDS]

MSTGKTTLALLLSALLPAGAAWAAGNDTLVYCSEASPESFNPQIASSGPSFVASSQVLYNRLVSFDPVKN

TPIPSLATEWHVSEDGKTWTFTLRQGV

>lcl|NZ\_FO834906.1\_prot\_WP\_004200088.1\_3066 [locus\_tag=BN49\_RS16910] [protein=aldehyde dehydrogenase] [protein\_id=WP\_004200088.1] [location=3129159..3130592] [gbkey=CDS]

MTITCNLYINGQWHDAEGRRTFTRRHPAHDEAASVAAAASLADGKRCVEAAACAFPLWRDTAPAERRRLL

LEAAEQMLLREAKFIAAMAAETGATAHWAGFNVHLAADILREAAALTTQIEGQIIPSNVPGNLAMGVRQG

AGVVLGMAPWNAPLILATRALATPLACGNTVILKGAELSPATQGLIIDALDAAGFPPGVVNYLTCAPEDA

PALVESLIAHPAVRRVNFTGSTPVGRIIARTCGQYLKPAVLELGGKAPLLVLDDADIEQAAAGAVFGAFA

NAGQICMSTERIIVDNAVAEAFIPLLARRAAALPAALTGPVVDMNTIARCNALIDDALAKGARLLTGGKA

NDTHMSPTLLDGVTREMRLWREESFGPVKAIIRVHSEEEALAVANDSEYGLSAAVYSRDSARAWNVAQRL

HTGICHINGPTVHDEAQMPFGGCKASGYGRFGGRAGIAEFTELRWITIQTQPRELPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004891556.1\_3067 [locus\_tag=BN49\_RS16915] [protein=alpha/beta hydrolase] [protein\_id=WP\_004891556.1] [location=complement(3130606..3131355)] [gbkey=CDS]

MNGFYSSVAGATLRWHDFPGDGLPVVFIHGLGCASSYDYPRIASDPALRERRKILIDLPGFGYSDKPRVF

SYNIHEQALVLEQFLSHLRLQRFALFGHSMGGSIAIEAAGLLGERVTTLLVSEPNLFAGGGEYSRRIAAQ

SESAFVADGYARLLAEERSPWAGCLQNSAPWAVWRAASSLICGSDTPWFTQLCQLRCQKMLIVGERSLPY

ADSDLVQAQGIPVGIVPHAGHSMAWENPQGLAQLIASHS

>lcl|NZ\_FO834906.1\_prot\_WP\_002906888.1\_3068 [locus\_tag=BN49\_RS16920] [protein=GhoT/OrtT family toxin] [protein\_id=WP\_002906888.1] [location=complement(3131444..3131617)] [gbkey=CDS]

MTLYQKMLVFYAIMGVICAVISWFLTKESRMIRLLAALLIGATWPFSFPMALLVSLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002906891.1\_3069 [gene=yncL] [locus\_tag=BN49\_RS29210] [protein=stress response membrane protein YncL] [protein\_id=WP\_002906891.1] [location=3131813..3131905] [gbkey=CDS]

MDVSSKTVVMINVCAAFALISLLSVRFGWF

>lcl|NZ\_FO834906.1\_prot\_WP\_002906893.1\_3070 [locus\_tag=BN49\_RS16925] [protein=hypothetical protein] [protein\_id=WP\_002906893.1] [location=complement(3131957..3132208)] [gbkey=CDS]

MKIFAFILLAIGAVALSYGNAPAKRIQSCEKMGVGQAVCAAAEWDSEKVNVLPRYNPSLNKVIAAAQLAP

AARQQDNNSVVRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531599.1\_3071 [locus\_tag=BN49\_RS16930] [protein=hypothetical protein] [protein\_id=WP\_016531599.1] [location=complement(3132346..3132543)] [gbkey=CDS]

MLQRLAIAIYLLTMTARAIYCACGEGGDPFPLADGEIFSSLAKLTPLNRKYFTARDKLLIFTVIA

>lcl|NZ\_FO834906.1\_prot\_WP\_021313832.1\_3072 [locus\_tag=BN49\_RS30725] [protein=small membrane protein] [protein\_id=WP\_021313832.1] [location=3132692..3132814] [gbkey=CDS]

MSGIITLVISLILLVAAVYNLISYIRDRRSASLPSKKTKR

>lcl|NZ\_FO834906.1\_prot\_WP\_032104223.1\_3073 [gene=patD] [locus\_tag=BN49\_RS16940] [protein=aminobutyraldehyde dehydrogenase] [protein\_id=WP\_032104223.1] [location=complement(3133155..3134582)] [gbkey=CDS]

MQHNLLINGKLVAGEGEKVPVYNPATGEVILDIAEATAAQVDAAVEAADRAFDAWSQTTPKTRAECLLKL

ADAISAQAETLAQLESLNCGKPLHCVINDEMPAIADVFRFFAGAARCLPGMAAGEYLEGHTSMIRRDPVG

VVASIAPWNYPLMMAAWKLAPALAAGNCVVIKPSEITPLTALKLAELAKDIFPEGVINVLFGRGKTVGDP

LTAHVKVRMVSLTGSIATGAHIIGHTASSIKRTHMELGGKAPVIVFDDADIDAVVDGVRTFGFYNAGQDC

TAACRIYAQQGIYDQLVEKLGAAVASLKMGAPEDAATELGPLSSLAHLERVSAAVEAARALPHIKVVTGG

SRADGAGYYFQPTLLAGARQEDAIVQREVFGPVVSVTPFSDEAQALSWANDSQYGLASSVWTKDVGRAHR

LSARLQYGCTWVNTHFMLVSEMPHGGQKLSGYGKDMSMYGLEDYTVVRHVMVKHS

>lcl|NZ\_FO834906.1\_prot\_WP\_004143773.1\_3074 [locus\_tag=BN49\_RS16945] [protein=ABC transporter permease] [protein\_id=WP\_004143773.1] [location=complement(3134605..3135411)] [gbkey=CDS]

MHSERAPWYLRLATWGGVIFLHFPLLIIAIYAFNTEDAAFSFPPQGLTLRWFSEAAGRSDILQAVTLSLK

IAALSTAIALVLGTLAAGALWRSAFFGKNAVSLLLLLPIALPGIITGLALLTAFKAVGLEPGLLTIVVGH

ATFCVVVVFNNVIARFRRTSWSMVEASMDLGATGWQTFRYVVLPNLGSALLAGGMLAFALSFDEIIVTTF

TAGHERTLPLWLLNQLGRPRDVPVTNVVALLVMLVTTIPILGAWWLTRDGDNDAGNGK

>lcl|NZ\_FO834906.1\_prot\_WP\_004189770.1\_3075 [locus\_tag=BN49\_RS16950] [protein=ABC transporter permease] [protein\_id=WP\_004189770.1] [location=complement(3135401..3136330)] [gbkey=CDS]

MTMAIIPAQTGRISGIFWRRPALGLFLLLLGPLMWFGIVYLGSLLTLLWQSIYTFDDFTMSVTSDFTLAN

LRALFNPANYDIIVRTLVMALCVTLASALLALPMAWYMARYTSGKMKAFFYIAVMLPMWASYIVKAYAWV

LLLAKDGVAQWFLGHLGLEGALNALLSVPAVGGNTLSTSGLGRFLVFVYIWLPFMILPVQAALERIPGSL

LQASADLGAAPRQTFRYVVLPLAIPGIAAGSIFTFSLTLGDFIVPQLVGPPGYFIGNMVYSQQGAIGNMP

MAAAFTLVPIVLIALYLAFVKRLGAFDAL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043393.1\_3076 [locus\_tag=BN49\_RS16955] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_046043393.1] [location=complement(3136332..3137345)] [gbkey=CDS]

MTYAVEFQNVSRLYGDVRAVDGVSIGIRDGEFFSMLGPSGSGKTTCLRLIAGFEQLSGGTIHIFGQPASE

LPPWQRDVNTVFQDYALFPHMSILDNVAYGLMVKGMAKKARHARAQEALEKVALGFAHHRKPSQLSGGQR

QRVAIARALVNQPRVLLLDEPLGALDLKLREQMQVELKKLQQSLGITFIFVTHDQSEALSMSDRVAVFNN

GRIEQVDAPQDLYLHPRTAFVAGFVGTANVFAAEAARRLCGMAGSWSLRPEHVRLQGGGEVQVQGVVQAV

QYQGAATRIELRLADGDKLMVSQANIDGAAAASVPRTGQIVQASWSRSAMTPLESGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002907384.1\_3077 [locus\_tag=BN49\_RS16960] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_002907384.1] [location=complement(3137362..3138507)] [gbkey=CDS]

MSKKIARCSLYVLGMACLTVQAAEPLTSLDKPEGRLDIIAWPGYIERGQTDKQYDWVSQFEKDTGCQVNV

KTAATSDEMVSLMAKGGYDLVTASGDASLRLIMGKRVQPINTALIAGWGSLDPRIAKGAWFNVGGKVYGT

PYQWGPNLLMYNTRVFPTPPDSWRVVFVKQDLPDGKTNQGRVQAYDGPIYIADAALFVKATQPQLGIEDP

YQLTETQYNAVLKVLRDQQPLIHRYWHDATVQMNDFKNEGVAASSSWPYQANGLKAEGQPVATVFPKEGV

TGWADTTMLHSEAKHPVCAYKWMNWSLTPKVQGDVAAWFGSLPVVPEGCKASALLGDKGCETNGYEQFNR

IHFWKTPVAEGGKYVPYSRWTQDYIAIMGGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180141.1\_3078 [locus\_tag=BN49\_RS16965] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_004180141.1] [location=complement(3138812..3140224)] [gbkey=CDS]

MKKYQQLAQQLTEQIALGVWLPGDRLPSLREQVISSGMSFMTVSHAYQLLESQGRIVARPQSGYYVAPQP

VKLRQPAPPAQVTRDEAVDINTYIFEVLQASRQASMLPFASAFPDPRLFPLQQLNRSLAQVSKTATAMSV

IENLPPGNAELRHAIARRYALQGMNVSPDEIVITAGALEALNLSLQAVTEPGDWVVVENPCFYGALQALE

RLRLKALSVATDVREGIDLTALEAALQNYPVKACWLMTNGQNPLGFTLSAEKKAALVALLARYNVMLIED

DVYSELYFGREKPLPAKFWDRQEMTLHCSSFSKCLVPGFRIGWVAAGKQARRIQQLQLMSTLSTSSPMQL

ALVDYLSTKRYDAHLRRLRRQLAERKQQAWQALLRHLPPEVIVHHSDSGYFLWIELPEGADASALSARAL

ASHISIAPGKMFSTSDSWTSFFRFNTAWGWGEREEQGVKRLGELIREQLA

>lcl|NZ\_FO834906.1\_prot\_3079 [locus\_tag=BN49\_RS16970] [protein=cytochrome ubiquinol oxidase subunit I] [pseudo=true] [location=3140912..3142305] [gbkey=CDS]

MFGLDAFHLARVQFAFTVSFHIIFPAITIGLASYLAVLEGLWLKTKYPVWRSLYHFWSKIFAVNFGMGVV

SGLVMAYQFGTNWSGFSQFAGSITGPLLTYEVLTAFFLEAGFLGVMLFGWNRVGPGLHFFATCMVALGTI

ISTFWILSSNSWMQTPQGFEIVDGQVVPVDWLAVIFNPSFPYRLLHMTVAAFLSSALFVGASAAWHLLRG

NQSPAIRKMFSMALWMTLLVAPVQALIGDMHGLNTLKHQPAKIAAIEGHWENPPGEPTPLLLFGWPDMDQ

QRTRYGLEIPALGSLILTHSLDKQVPALKEFAPEERPNSTVVFWSFRLMAGLGMLMLLLGVLALWLRRGD

RLYHSRPFLRFALWMGPSGLIAILAGWVTTEVGRQPWVVYGVQRTADAVSAHGDLHMSVSLLTFIVVYSA

VFGVGYSYMLRLIRKGPQEMLPATTGTPARCPPPLKVICRRSPT

>lcl|NZ\_FO834906.1\_prot\_WP\_016531444.1\_3080 [gene=cydB] [locus\_tag=BN49\_RS16975] [protein=cytochrome d ubiquinol oxidase subunit II] [protein\_id=WP\_016531444.1] [location=3142305..3143315] [gbkey=CDS]

MGIELSVIWFVIIVFATLMYIVMDGFDLGIGLLFSTVRGGGDRDVMVNSVAPVWDGNETWLVLGGAGLFG

AFPLAYAVIIDALSIPLTLMLIGLIFRGVAFEFRFQATPSHRPFWDRAFFGGSLLATFSQGVVVGAVING

FTVSGRAFSGGMFDWLTPFSLFCGFGLCVAYALLGATWLVMKSEGALQQRMRSVSRQLLGALLAVFAVIS

LWTPLAHPAIAARWFSLPNLYFLLPVPLLVILVSGWLWRTLHQRDRHVSPFTLTLGLVFLGFSGLGISIW

PHIIPPAITLWQAAAPPQSQGFMLVGALLIIPVILGYTCWSYYVFRGKVQPGEGYH

>lcl|NZ\_FO834906.1\_prot\_WP\_004180143.1\_3081 [locus\_tag=BN49\_RS16980] [protein=DUF2474 domain-containing protein] [protein\_id=WP\_004180143.1] [location=3143315..3143440] [gbkey=CDS]

MRTAWPKRLLWLIALWGGSVLTLAAISLLFRLLMTAAGLKV

>lcl|NZ\_FO834906.1\_prot\_WP\_016531445.1\_3082 [locus\_tag=BN49\_RS16985] [protein=hypothetical protein] [protein\_id=WP\_016531445.1] [location=3143537..3143821] [gbkey=CDS]

MKKLALLYAIMTLGMSSWAFAADNPPPPPEKGAQHQGKPPVKNVQHEGKQAQYNSKQPQRDGKQPQHNGK

QPQHNGKQPPKGSEHSGKPLPPKA

>lcl|NZ\_FO834906.1\_prot\_WP\_042941993.1\_3083 [locus\_tag=BN49\_RS30475] [protein=DUF2554 family protein] [protein\_id=WP\_042941993.1] [location=3143970..3144200] [gbkey=CDS]

MLKRSISALLLLCALFSGHLLAHRQGHEYFPVQSLEQQLQHEADSDELRSQHEEAAADLREHHRWQDDRK

PRASCQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002907469.1\_3084 [locus\_tag=BN49\_RS16995] [protein=U32 family peptidase] [protein\_id=WP\_002907469.1] [location=complement(3144213..3146174)] [gbkey=CDS]

MRLHNHRLELLSPARDAGIAREAILHGADAVYIGGPGFGARHNASNSLSDIAGLVPFAHRFGAKVFVTLN

TILHDDELEPAQRLITDLYDAGVDALIVQDMGIMELDLPPIELHASTQCDIRSVEKAKFLSDAGFSQIVL

ARELNLSQIKAIYDHTDATIEFFIHGALCVAYSGQCYISHAQTGRSANRGDCSQACRLPYTLKDDQGRVV

AYEKHLLSMKDNDQTANLAALIDAGVRSFKIEGRYKDMSYVKNITAHYRQMLDAIIEDRGDLARASAGRT

EHFFIPSTDKTFHRGSTDYFVNARKGDIGAFDSPKFIGLPVGEVLKVGKDHLDVEVSEPLTNGDGLNVMI

KREVVGFRANTVEKTGENRYRVWPNEMPADLHKVRPHQPLNRNLDHNWQQALLKTSSERRIAVDVTLSGW

QEQLVLTMTCEDGVSVTHTLDGEFAEANQAEKALANLRDGVTKLGQTIYYAREVQVNLPPLFVPNSLLNQ

LRRETAEMLDEARLNAWQRGTRKPVSVPPPVYPETHLSFLANVYNHKARAFYQRYGVQLIDAAYEAHEEK

GDVPVMITKHCLRFAFNLCPKQAKGSIKSWKATPMQLIHGDEVLTLKFDCRPCEMHVVGKIKNHILKMPH

PGSIVASVSPDDLMKTLPKRKGA

>lcl|NZ\_FO834906.1\_prot\_WP\_020806151.1\_3085 [locus\_tag=BN49\_RS17000] [protein=hypothetical protein] [protein\_id=WP\_020806151.1] [location=3146208..3146375] [gbkey=CDS]

MAAIVVRTGRRRKPFPPSLDDEFSLFNKVLTEKIFPSNHGEEYCHHVFRIFLVTL

>lcl|NZ\_FO834906.1\_prot\_WP\_002907473.1\_3086 [locus\_tag=BN49\_RS17005] [protein=XRE family transcriptional regulator] [protein\_id=WP\_002907473.1] [location=complement(3146386..3146955)] [gbkey=CDS]

MNIAQHLAATLKTLRQQRGWSLSRLAEETGVSKAMLGQIERNESSPTVATLWKIATGLNVPFSAFIVPDA

SAAPSAFDPQQQAMVVTPVFPWDPELRFDHFSITLAPGALSESTPHEKGVIEHVVVISGTLDLCLQGEWH

SLQAGEGRRFAGDATHAYRNRGAQAAHFHSLIHYPKEKTASEPAARQDD

>lcl|NZ\_FO834906.1\_prot\_WP\_009307732.1\_3087 [locus\_tag=BN49\_RS17010] [protein=benzoate/H(+) symporter BenE family transporter] [protein\_id=WP\_009307732.1] [location=3147141..3148307] [gbkey=CDS]

MRSFSLPLPTLFAGFVAVLVGYASSAAIIWQAAAAAGATPGQIAGWMTALGLAMGISTLALSAWRKVPVL

TAWSTPGAALLVSGLQGVTLAEAVGIFIFANALIVICGATGLFARLMKIIPHSLAAAMLAGILLRFGLQA

FAGLQDHLPLCGGMLAAWLLCKALWPRFAVVAALVIGALIAAASGDVASAAVPLAFVTPEWVAPQFTPAL

LLSVGLPFFLVTMASQNAPGFATLQASGYTVPVSALIVVCGGLALLLAPFGVYSICIAAITAAICQSPEA

HPDPNQRWLAAIAAGGFYLLAGLFGGSITALMSALPPAWIQMLAGLALLGTIGGSLFQAVHQASERDAAV

LTFLVTASGVTLAGIGSAFWGVVLGGVSYGVLSALRRP

>lcl|NZ\_FO834906.1\_prot\_WP\_004151213.1\_3088 [locus\_tag=BN49\_RS17015] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004151213.1] [location=complement(3148284..3149153)] [gbkey=CDS]

MGYGTFETLRRQNAVLKGTVELNSGIQLAAWYNNCDTVTVRSDHHTLSLYVADGYESYQKTPHGWKNGGG

PDRFCLMPKGDESVWDIRGDLSFVHLYCTDAHLRRVGEEVWDRSPANFTLQEKTFASDDKITAVYRQFLL

ANDWRQPANQLTLSAASSLLLTHLIQHYSTVQWRLPTVTGGLAPGVKRHVLAWIDAHLDQPLTLADLAQQ

AGLSEFHFARMFRQSLNMAPHQYVMQQRMAKAQNLICHSALPLTEIALACGFSSPSHFSHRVKAATGLTP

SQLRAAQRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151212.1\_3089 [locus\_tag=BN49\_RS17020] [protein=DMT family transporter] [protein\_id=WP\_004151212.1] [location=3149334..3150230] [gbkey=CDS]

MNALLYALVVVIWGTTWIAIFLQQGPVAAPVSIFWRFAVASVTMLAILLVTRRLRPLGAKDHLCCLLQGC

CVFCFNFWCFYTAAAWINTGLESVIFSMAVLFNAINSFLFFRQQPPGRFWAAAALGLAGIVILFWDDLLA

NGLNASLLWGIGLSALGTYGFSLGNMFSIRHQRRGLETLTTNSWAMLYGTLVMGAIALLRGDNFMPEWTV

SYLGALLYLALFGSVIAFGAYFTLVGRIGASKAAYSTLLFPLVALSISTVYEGYVWHSSAVIGLALILLG

NMVMFAKPEQLLLRRRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002907480.1\_3090 [locus\_tag=BN49\_RS17025] [protein=DUF3313 domain-containing protein] [protein\_id=WP\_002907480.1] [location=complement(3150277..3150945)] [gbkey=CDS]

MRTRVLLKVAALAGILALTGCAAKVAQPDQYSGFLKDYSSLKETTSASGKPELRWIDPNFNPANYDNIVY

HPVTYYPVPKPTTQVGEKALQDILNYTNKELKQAISERKPLATTAGKRSLIFRGAITGVDSSKEGLQFYE

VIPVAMIVAGTQAATGHRTMDTNLYFEAEVIDASTNKPVIKVVRKGEGKTLANENTPLTVDTLKQVIDDM

AVDAVKFDPSQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002907481.1\_3091 [gene=tehB] [locus\_tag=BN49\_RS17030] [protein=tellurite resistance methyltransferase TehB] [protein\_id=WP\_002907481.1] [location=complement(3151207..3151803)] [gbkey=CDS]

MTKRDADYFSQKYSLTRTHSEVLHAATIVPPGRALDLGCGNGRNSLYLAANGFAVTAWDKNPMSVNNLES

IRAAERLDNLQTAVKDLNSLSFDGEYDLILSTVVMMFLEPDTIPGLIANMQRCTAAGGYNLIVAAMDTED

YPCTVGFPFAFKPDELRDYYQGWELLKYNEDVGELHRTDANGNRIKLRFATLLARKPA

>lcl|NZ\_FO834906.1\_prot\_WP\_002907483.1\_3092 [gene=tehA] [locus\_tag=BN49\_RS17035] [protein=dicarboxylate transporter/tellurite-resistance protein TehA] [protein\_id=WP\_002907483.1] [location=complement(3151800..3152804)] [gbkey=CDS]

MNKTQTPRQVLNLPAGYFGMVLGTIGMGFAWRYASTLWPVSRSIGDGLVTLAMAMWVLLSMAFISRAIRF

PASVLREMRHPVSSSFVSLFPATTLLVAIGLAPWCRPLAIGLFVPGVALQLAYAAWQSGGLWRGNHPREA

TTPGLYLPTVANNFISAMACGALGFSDAGLVFLGAGVFSWLSLEPAILQRLRSAGELPTPLRTSLGIQLA

PALVACSAWLSVNGGEADTFAKLLFGYGLLQLLFMLRLMPWYLRQPFNASFWSFSFGISALATTGLHLGQ

ARGDGFFHHLAMPLFIFSNLVVGLLLLRTALLLVSGKLLLQVDRETLLNKKEGS

>lcl|NZ\_FO834906.1\_prot\_WP\_002907485.1\_3093 [gene=ydcK] [locus\_tag=BN49\_RS17040] [protein=YdcK family protein] [protein\_id=WP\_002907485.1] [location=3152916..3153896] [gbkey=CDS]

MRKYRLSEQTRQYCYEEEHGKQSVTLRQIVALIDFADVKAGSEGGWVDEECALSQQGECWIYDVNSVVFA

GARIRDDARLTGFCVVSHEATIGGQACIHAAQISHHAQISDNVTVTQSQVRGYCRLADEARLLPHCQVIA

ARGLTADRDKVLQIYQRATVSASRILHQAQIYGDAFVEHAFVEHRAEVFDQARLEGNEENDVWVCDNARV

YGHARLIAGRGEDAIPTVRYSSQVAENAVIEGNCLLKHRAMVGGEAQLRGGPILLDDDVLIQGRTVITGD

VIVEHQVSINDEVQIAAQEGEAIHLRGPKTLDGQQHITRTPLLGAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531655.1\_3094 [gene=rimL] [locus\_tag=BN49\_RS17045] [protein=50S ribosomal protein L7/L12-serine acetyltransferase] [protein\_id=WP\_016531655.1] [location=complement(3153882..3154460)] [gbkey=CDS]

MTADIPAVPESIPVTDALTLIAIDERYVSDLHQLVVKNQRWLQQSLSWPAEVRNEDETRRHVQGNVMLHQ

RDYAKMFLLFLDKQLVGVLSFNQIEPQNKTAYIGYWIDEEHQGQGLLSRSLQAFIRHYAASGLVRRFVIK

CRVANTRSNQVALRNGFVLEGCLRQAEYLNGSYDDQNIYARIIDRDEALKRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002907489.1\_3095 [locus\_tag=BN49\_RS17050] [protein=glucan biosynthesis protein] [protein\_id=WP\_002907489.1] [location=complement(3154514..3156169)] [gbkey=CDS]

MNRRRFLKSSMAVAAVCGTSGVASLFSQAAFAEDAGIADGQTRRFDYAVLQAMAHDLARQPWGGAPRDLP

PTLANLTPQAYNSIQYDANHSLWNNIEERKLDIQFFHVGMGFRRRVRMFSLDASTQQAREIHFRPELFKY

NDAGVDTRQLEGQSDLGFAGFRVFKAPELARRDIVAFLGASYFRAVDSTYQYGLSARGLAVDTFTDTPEE

FPDFTSFWFETVKGDATVFTVYALLDSPSITGAYKFTIHCQDTQVIMDVENHLYARKDIKQLGIAPMTSM

FSCGNNERRMCDTIHPQIHDSDRLSMWLGNGEWVCRPLNNPQKLQFNAFQDKNPRGFGLLQLDRDFSHYQ

DVMGWYNKRPSLWVEPRNQWGKGAVSLMEIPTTGETLDNIVCFWQPEKAVKAGDELDFRYRLYWSAQPPV

STPLARVLATRTGMGGFPEGWAPGEHYPDKWARRFAIDFVGGDLKAAAPRGIEPVITLSSGEAKQIEILY

VEPFDGYRILFDWYPTTDSTDPVEMRLFLRCQGEAISETWLYQYFPPAADKRNYVDDRIMK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043398.1\_3096 [locus\_tag=BN49\_RS17055] [protein=NAD(P)-dependent alcohol dehydrogenase] [protein\_id=WP\_046043398.1] [location=3156607..3157695] [gbkey=CDS]

MQVKAAVTLGYQQPFVIKDVEVAPPGKDEILVKIVATGVCHTDAVMRDNPGVVPMPAILGHEGAGIVASV

GEAVSGIRVGDHVVLSYAACHHCENCLSNHPSACEDFNTLNFGGRREDGTTPYRLGDQDLSLFFGQSSFS

QYVVTRASNAVVVDPEVDLTLLGPLGCGIQTGSGTVLNRLKPVVGESLVVFGCGAVGLSAIMAAKLTGCS

QIIAVDIHASRLALARELGATHQINGKEQDAVAVIKQITGKGAHYAVETTGVSAIVLQAVHAVKPLGTVA

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ASGKVIKPVVVM

>lcl|NZ\_FO834906.1\_prot\_WP\_023278953.1\_3097 [locus\_tag=BN49\_RS17060] [protein=carboxylesterase/lipase family protein] [protein\_id=WP\_023278953.1] [location=complement(3157742..3159247)] [gbkey=CDS]

MQHPSKPLAKTRQGTLAGSAEQGIHIWRGIPYAAPPVGPLRWRAPQPAARWQGVRPAETFSAASWQDIDY

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LGHLGFFAHPALEQEAGERLYNFALLDQIAALQWVQENIHAFGGDAANVTLFGESAGARSVLSLMASPKA

KGLFHKAIIQSGYTLPDLPREKALEKGRLLAEHFALPQASAEELRAIPAEAFWSLTAPLNTGPAPIAGDA

VLPQPMLETFFAGRQHPIPVMIGSNSDEASVMAVFGVDIAGQIQKLRRERRLGLGLIKLLYPGVKGDEAL

GREVCRDMAFTTLGYVVMQAQQRVGQPCWRYWFDYVAEAEHDAYPHGAWHGNEVPYVFDNLRLTDPVRQY

ASEADLAFAAQVADYWAQFARLASGEQTLSGAVRWPACLRGRDRLLRIGLHKRAGFKVENRFMRARLALF

RRVMKHHVTLE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531132.1\_3098 [locus\_tag=BN49\_RS17065] [protein=VOC family protein] [protein\_id=WP\_016531132.1] [location=complement(3159289..3160632)] [gbkey=CDS]

MANTITADEIREHFSQAMSAMYQQEVPQYGTLLELVADVNLAVLENNPQLHEQLANADELARLNVERHGA

IRVGTAEELATLRRMFAIMGMYPVSYYDLSQAGVPVHSTAFRPIDDAALARNPFRIFTSLLRLELIENHA

LRERAEAILARRKIFTPRCLALIAQYEAEGEFTSADAREFVQEALETFRWHRQATVDEETYHALHREHRL

IADVVCFPGCHINHLTPRTLDIDRVQSLMPECGIEPKALIEGPPRREVPILLRQTSFKALEEPVMFAGEH

RGTHCARFGEIEQRGVALTPKGRALYDRLLQAAGTGKDNLSHQQHLQEVFSEFPDSEFLLRQQGLAWFRY

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ALGCPVQDEFELYRQAEERSKRRCGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002907552.1\_3099 [gene=pcaH] [locus\_tag=BN49\_RS17070] [protein=protocatechuate 3,4-dioxygenase subunit beta] [protein\_id=WP\_002907552.1] [location=3160872..3161612] [gbkey=CDS]

MNDKWSPREVVHRDYSSHPPAYAPGYKTSVLRSPKNALISLQNSLSEITGPVFSRDDLGPLDNDLILNYA

KEGLPIGERIIVHGYVRDGFGRPMKNTLVEVWQANAGGRYRHKKDQYLAPIDPNFGGCGRVLTDENGYYC

FRTIKPGPYPWRNQASDWRPAHIHFSLSGDAWAQRLITQMYFEGDPLIKQCPIVRTINNDDAVRTLIAEL

DMHAAVPLDCLAYRFDLVLRGHRATLFENRTQGAAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004184258.1\_3100 [gene=pcaG] [locus\_tag=BN49\_RS17075] [protein=protocatechuate 3,4-dioxygenase subunit alpha] [protein\_id=WP\_004184258.1] [location=3161609..3162229] [gbkey=CDS]

MKEYLPETASQTAGPYVHIGLAPDAAGFHIFEKNFGPVLTTADTAGERITIEGRVIDGSGTPVRDVLLEI

WQANAAGRYNHPDDRQQQKAVDPAFRGWGRTCSDFTSGIWRFETIKPGPVVGRDGRLMAPHVNLWVVARG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004143800.1\_3101 [locus\_tag=BN49\_RS17080] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_004143800.1] [location=3162407..3163330] [gbkey=CDS]

MEKNGLFSQRIRLRHLHTFVAVAQQGTLGRAAETLNLSQPALSKTLNELEQLTGTRLFERGRLGAQLTLV

GEQFLTHAVKVLDALNSAGQALNRKEGLNNDIVRIGALPTAALGILPTVIGQFHKQQKDITLQVATMNNT

MLLAGLKSGEIDIGIGRMSDPELMSGLHYELLFLESLKLVVRPGHPLLQETVTLSRVMEWPVVVSPKGTV

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GILTRVDATLTPGTQTLLSAIRKSMPA

>lcl|NZ\_FO834906.1\_prot\_WP\_020324764.1\_3102 [locus\_tag=BN49\_RS17085] [protein=membrane-bound PQQ-dependent dehydrogenase, glucose/quinate/shikimate family] [protein\_id=WP\_020324764.1] [location=3163630..3166002] [gbkey=CDS]

MATGNAPRGFPRILQWLLAGLMLIIGLAVGILGAKLALVGGTLYFALMGVVMVIAAVLIFRNRRGGILLY

AVAFIASVIWAISDAGWNYWPLFSRLFALGVLAFLAALVWPFLASPPAKKGPAYGVAAVLAVALAVSFGW

MFKSAPLVSATEAVPVKPVAPGEQQKNWAHWGNTTHGDRFAALDQINKQNVNQLQVAWVAHTGDIPQSNG

SGAEDQNTPLQIGDTLYVCTPYSKVLALDVDSGKEKWRYDSKSSSPNWQRCRGLGYYEDSQAQTAPAAGT

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NATPDFFGGERTALDDKYSSSIVAVDATTGQVRWHFQTTHHDLWDFDLPSQPLLYDLPDGKGGTTPVLVQ

TSKQGMIFMLNRETGEPVAKVEERPVPAGNVKGERYSPTQPYSVGMPMIGNQTLTESDMWGATPIDLLLC

RIQFKEMRHQGVFTPPGEDRSLQFPGSLGGMNWGSVSLDPNNSLMFVNDMRLGLANYMVPRAKVAKDASG

IEMGIVPMEGTPFGAMRERFLSPLGIPCQKPPFGTMSAVDLKTGKLVWQVPVGTVEDTGPLGIRMHMPIP

IGMPTLGASLATQSGLLFFAGTQDFYLRAFDTANGKEIWKSRLPVGSQSGPMTYVSPKTGKQYIIINAGG

ARQSPDRGDYIIAYALPDHH

>lcl|NZ\_FO834906.1\_prot\_WP\_004189749.1\_3103 [locus\_tag=BN49\_RS17090] [protein=S-(hydroxymethyl)glutathione dehydrogenase/class III alcohol dehydrogenase] [protein\_id=WP\_004189749.1] [location=complement(3166072..3167190)] [gbkey=CDS]

MKSRAAVAFGPGQPLKIVEIDVAPPKKGEVLVKITHTGVCHTDAFTLSGDDPEGVFPAVLGHEGGGIVVE

VGEGVTSLKPGDHVIPLYTAECGECKFCKSGKTNLCQAVRATQGKGLMPDGTTRFSYNGEPIYHYMGTST

FSEYTVCAEISLAKVNPQAPLDKVCLLGCGVTTGIGAVHNTAKVKAGDTVAVFGLGGIGLAVIQGAVQAQ

AGRILAVDTNPDKFTLAKEMGATDFINPNDYDKPIQDVIVELTDGGVDFSFECIGNVNVMRAALECCHKG

WGESVIIGVAGAGQEIKTRPFQLVTGRVWRGSAFGGVKGRSQLPGMVEDAMAGKIRLDPFITHRLPLEQI

NEAFDLMHEGKSIRTVIHFGDQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002907563.1\_3104 [locus\_tag=BN49\_RS17095] [protein=metal/formaldehyde-sensitive transcriptional repressor] [protein\_id=WP\_002907563.1] [location=complement(3167215..3167490)] [gbkey=CDS]

MPHSPEDKKRALSRVRRIRGQVEALERALESGEPCMTILQQIASIRGAANGLMGEMVEIHLQDELVSGDT

TPEQRAARMAEVGHLLRSYLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002907640.1\_3105 [gene=cybB] [locus\_tag=BN49\_RS17100] [protein=cytochrome b561] [protein\_id=WP\_002907640.1] [location=complement(3167595..3168122)] [gbkey=CDS]

MRDKYSGLQIGIHWLVFLLVVVAYAAMELRGFFPRSERPLINMVHVSCGITIFVLMVARLLVRLKSPAPP

IVPKPSPMMTGFAHLGHLAIYLLFIALPLIGMVMMYWRGNPWYAFGLTMPYAPQSDFERVDTLKAIHEWL

ANAGYFVIGLHALAALLHHYWWKDNTLLRMMPRKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004143806.1\_3106 [locus\_tag=BN49\_RS17105] [protein=hypothetical protein] [protein\_id=WP\_004143806.1] [location=3168382..3168744] [gbkey=CDS]

MKEIGLPLLLLTALASPAFAADCQPNGIGGSFCINDDGTTTDTVPNEVNGMDTYSNNGGYTSSLPDRSGA

DEALEGSSLSTQQGVGSGQSDSALAGRDWHSPANLNDGAATSSMSLLDKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002907644.1\_3107 [locus\_tag=BN49\_RS17110] [protein=hypothetical protein] [protein\_id=WP\_002907644.1] [location=complement(3168754..3168939)] [gbkey=CDS]

MESVIHNNIEGFLLLLLSMWPILLVVFIGVAISFYTMLLRKTALACLLFALAIGAAGWSLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004180158.1\_3108 [locus\_tag=BN49\_RS17115] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004180158.1] [location=complement(3169183..3169647)] [gbkey=CDS]

MAKQESLRTSECPVARTLESIGERWCLMIIREAFDDVRRFSEFQKNLGLAKNILASRLKHLVDIGIFEIL

PASDGSAYKEYVLTEKGRSVFPIVVALRQWGERYMFEQGETYSVLLDNAHGQPLQYLDVRSAQGDKLQPG

DCHRRRIVSDTRAE

>lcl|NZ\_FO834906.1\_prot\_WP\_032104210.1\_3109 [locus\_tag=BN49\_RS17120] [protein=MFS transporter] [protein\_id=WP\_032104210.1] [location=3169841..3170995] [gbkey=CDS]

MLTTGITALFSLTCALAVANVYSAQPLLDSMAVSLKVSPGMIGSVITATQAGYAIGLLFLVPLGDWLNRK

YVVMSQLLLSVAALVAAGLSPNIATLLGAMLIVGLMAVVVQVLVAWVAVLATPQKRGQAVGTLTSGIVSG

ILLSRFISGAIADIAGWRAVYLTAACLMLVIAGVVWKIMPSPPQQPQPQKPTYLSLLKSVFQLYLTEPQL

RKRGILALFIFAAFSMLWTTMVMPLTALSLSHTQTGMFGLAGFAGMLAAARAGKWADQGWAQRTTGLALA

LLTISWLPIGYAETSLLWLIAGVIALDFAVQAVHVSSQSLIIAARPAAASRLVGAYMCFYSLGSATGAIV

ATQLYSHWGWQAVCLAGAAVSACAFLIWSGSRQS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151209.1\_3110 [gene=add] [locus\_tag=BN49\_RS17125] [protein=adenosine deaminase] [protein\_id=WP\_004151209.1] [location=3171153..3172154] [gbkey=CDS]

MIDSSLPLTDIHRHLDGNIRAQTILDLGREFNIALPATTLDTLRPHVQVTSLEPDLVSFLAKLDWGVKVL

ASLEACRRVAYENVEDAARNGLHYVELRFSPRYMAMTHRLPVDGVVEAVIAGVQEGCRDFQVDARLIGIL

SRTFGEAACQEELAALLAHREGITALDLAGDELGFPGTLFRNHFNQARDAGWHITVHAGEAAGPESIWQA

IRELGAERIGHGVKAVEDPALMDYLAEHRIGIESCLTSNVQTSTVASLAQHPLKQFLEHGVLASLNTDDP

AVQGVDIIHEYTVAAPAAGLSREQIRQAQINGLTLAFLGEQEKAALIQRVAKG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043408.1\_3111 [locus\_tag=BN49\_RS17130] [protein=oxidoreductase] [protein\_id=WP\_046043408.1] [location=complement(3172190..3173230)] [gbkey=CDS]

MSDAIRVGLVGFGYASKTFHAPLIGGTPGMALKAVASSDADKVHADCPGVKVMSAPGDLLDDPDIDLVVI

ATPNDTHFPLAKAALEAGKHVVVDKPFTVTLSQARELESLAKHCGRILSVFHNRRWDSDFLTVSALINEG

QLGEVCYFESHFDRFRPQVRRRWREQAGPGSGIWYDLAPHLLDQVVVLFGLPVSITVDLAQLRPGAQSTD

YFHAVLAYPQRRVVLHGTLLAAAESARFIVHGSRASYIKYGLDPQEERLKNGERLPQEDWGYDMRDGTLT

RAEGDERSQEKWLTLPGNYPAYYAAIRDALNGVGENPVPASEAIQIMTLIELGIESARHRATLSLV

>lcl|NZ\_FO834906.1\_prot\_WP\_004227851.1\_3112 [gene=blr] [locus\_tag=BN49\_RS29215] [protein=division septum protein Blr] [protein\_id=WP\_004227851.1] [location=3173421..3173558] [gbkey=CDS]

MTTVFTRIVELIGWIVFGISALLLVIAHHIDNYQSPPPADVVHTK

>lcl|NZ\_FO834906.1\_prot\_WP\_004180160.1\_3113 [locus\_tag=BN49\_RS17135] [protein=GH1 family beta-glucosidase] [protein\_id=WP\_004180160.1] [location=3173674..3175044] [gbkey=CDS]

MAAFPHNFLWGAATAAYQVEGGHDADGKGPSIWDIYSHLPGTTFEGTTGDIAVDHYHRFREDVALMAEMG

LQSYRFSISWPRLLPAGRGKVNEAGVQFYSDLIDELLAHNIEPMITLYHWDLPQALQDEGGWEARTTAEA

FAEYARLCYARFGSRVKLWATFNETIVFIGHGYINGLHPPAVRDPARAIQACHHVFIAHALAVKAFREMA

VAGEIGFVNVLQPHTPLTDSEADIKATELADAIHTHWLYDPVLKGTYPADLLAQTQALWGVPRFAPGDDA

LLRDNRCDFIGLNYYRRETVSAQPPEIATGGEPGVEGLFYFVRNPQSTYTEWGWEIWPQGLTDGIMMIKA

RYGDIPIYITENGLGAKDPIIDGEVVDDPRIDYLSSHIGALEKALALGADVRGYYPWSFIDLLSWLNGYQ

KQYGFVYVDHQQNLARKRKKSFYWYKSVIASHGEQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002907652.1\_3114 [gene=ydgT] [locus\_tag=BN49\_RS17140] [protein=transcription modulator YdgT] [protein\_id=WP\_002907652.1] [location=3175261..3175476] [gbkey=CDS]

MTVLDYLLKFRKISSLESLEKLFDHLNYSLTDTQEIVNMYRAADHRRAELVSGGKLFDVGQVPKSVWRFV

Q

>lcl|NZ\_FO834906.1\_prot\_WP\_002907654.1\_3115 [locus\_tag=BN49\_RS17145] [protein=DUF2569 domain-containing protein] [protein\_id=WP\_002907654.1] [location=3175552..3175992] [gbkey=CDS]

MTSQSAERIGGWLLAPLAWLLVALLSASLSLLFFANALMSPQTYTLLRAMSAGHMALWVASLLFALAMWY

YTLWLTIAFFKRRSVVPKHYIIWLLITLLLAIKAFAFSPVSDVLALRQLLFPLLAAALLAPYFRRSQRVK

RTFVNP

>lcl|NZ\_FO834906.1\_prot\_WP\_002907658.1\_3116 [gene=rsxA] [locus\_tag=BN49\_RS17150] [protein=electron transport complex subunit RsxA] [protein\_id=WP\_002907658.1] [location=3176071..3176652] [gbkey=CDS]

MADYLLLFIGTVLVNNFVLVKFLGLCPFMGVSKKLETAMGMGLATTFVMTLASICAWLIDTWILIPLNLV

YLRTLAFILVIAVVVQFTEMVVRKTSPALYRLLGIFLPLITTNCAVLGVALLNINLGHNFLQSALYGFAA

AVGFSLVMVLFAAIRERLVVADVPAPFRGNAIALITAGLMSLAFMGFSGLVKL

>lcl|NZ\_FO834906.1\_prot\_WP\_004143816.1\_3117 [gene=rsxB] [locus\_tag=BN49\_RS17155] [protein=electron transport complex subunit RsxB] [protein\_id=WP\_004143816.1] [location=3176652..3177230] [gbkey=CDS]

MSAVWIAVIAISLLGLIFGLILGYASRRFAVQDDPVVEKIDELLPQSQCGQCGYPGCRPYAEAVGVQGEK

INRCAPGGEAVMLKIAALLNVDPQPVDGDAQEAEPARMLAVIDEPNCIGCTKCIQACPVDAIVGATRAMH

TVMSDLCTGCNLCVAPCPTQCISLVPVATTPETWKWDLHTIPVRNIPVEQHV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043411.1\_3118 [gene=rsxC] [locus\_tag=BN49\_RS17160] [protein=electron transport complex subunit RsxC] [protein\_id=WP\_046043411.1] [location=3177223..3179382] [gbkey=CDS]

MFKLFSAFRKDKVWDFNGGIHPPEMKTQSNGTPLRQVSLPQRFVIPLKQHIGAEGELCVKVGDRVLRGQP

LTRGWGRMLPVHAPTSGTIAAIAPHTTAHPSALAEMSVIIDADGEDRWIERDGWSDYQTRTREALIERIH

QFGVAGLGGAGFPTGSKLRGGGDKIKTLIINAAECEPYITADDRLMQDCAAQIVEGIRILAHILQPEEVL

IGIEDNKPQAISMLRAVLCDAHGISLRVIPTKYPSGGAKQLTQILTGKQVPHGGRSSDIGVLMQNVGTAY

AVKRAVIDGEPLTERVVTLTGEAVTRPGNVWARLGTPVRHLLNDAGFCPSAEPMVIMGGPLMGFTLPWLD

VPVVKITNCLLAPSASEMGEPQEEKGCIRCSACADACPAELLPQQLYWFSKGQQHDKATAHNLADCIECG

ACAWVCPSNIPLVQYFRQEKAEIAAIRQEEQRAAEAKARFEARQARLEHEKAARAERHKKAAVQPAAKDQ

EAISAALARVRDKQRDAAQPIVIQAGAKPDNSEAIAAREARKAEARARKAQQQAAPMAAPAAEPVDPRKA

AVEAAIARAKARKAEQQAAPVDAPAAEPVDPRKAAVEAAIARAKARKAEQQAAPVEAPAVEPVDPRKAAV

EAAIARAKARKAEQQAAPVDAPAAEPVDPRKAAVEAAIARAKARKAEQQAAQQDLASAAANDDPRKAAVA

AAIARVQARKATQQAVNEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002907730.1\_3119 [gene=rsxD] [locus\_tag=BN49\_RS17165] [protein=electron transport complex subunit RsxD] [protein\_id=WP\_002907730.1] [location=3179383..3180435] [gbkey=CDS]

MVFRIASSPYTHNQRQTSRIMLLVLLAAVPGIVVQTWFFGWGTVLQIVLAALTAWATEAAILKLRKQPVA

ATLKDNSALLTGLLLAVSIPPLAPWWMVVLGTAFAVVIAKQLYGGLGHNPFNPAMIGYVVLLISFPVQMT

SWLPSYEIAAHIPAFSDALQMIFTGHTAAGGDMASLRLGIDGVSQATPLDTFKTSLHAGHSVQQVLQLPV

YGGVLAGLGWQWVNIAWLAGGLFLLWQKAIRWHIPVSFLVSLGLCATLGWIFSPQSLASPQMHLLSGATM

LGAFFILTDPVTASTTNRGRLIFGALAGLLVWLIRSFGGYPDGVAFAVLLANITVPLIDYYTRPRVYGHR

>lcl|NZ\_FO834906.1\_prot\_WP\_002907731.1\_3120 [gene=rsxG] [locus\_tag=BN49\_RS17170] [protein=electron transport complex subunit RsxG] [protein\_id=WP\_002907731.1] [location=3180446..3181066] [gbkey=CDS]

MLKTMRKHGVTLALFAAGSTGLTAAINELTKSTIDQQAALQQKALFDQVLPADRYNNDLLKSCYLVSAPA

LGKGQHKVWIAKNNDRPIGAVMEATAPDGYSGAIQLLVAADFSGTVLGTRVTEHHETPGLGDKIELRLSD

WITHFAGKVIHGQGDSHWAVKKDGGDFDQFTGATITPRAVVNAVKRAGLYAQTLPAQLPEFTACGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002907733.1\_3121 [locus\_tag=BN49\_RS17175] [protein=electron transport complex subunit E] [protein\_id=WP\_002907733.1] [location=3181069..3181767] [gbkey=CDS]

MSEVKDVIVQGLWKNNSALVQLLGMCPLLAVTSTATNALGLGLATTLVLTLTNLTISSLRRWTPAEIRIP

IYVMIIASVVSVVQMLINAYAFGLYQSLGIFIPLIVTNCIVVGRAEAFAAKKGPALSALDGFSIGMGATC

AMFVLGSLREILGNGTLFDGADSLLGSWAKVLRIEVFHTDTPFLLAMLPPGAFIGLGMMLAIKYLIDERS

KQRKAQAARAVSVAPSDVTGKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002907734.1\_3122 [gene=nth] [locus\_tag=BN49\_RS17180] [protein=endonuclease III] [protein\_id=WP\_002907734.1] [location=3181769..3182404] [gbkey=CDS]

MNKAKRLAILTRLRENDPHPTTELHFSSPFELLIAVLLSAQATDVSVNKATAKLYPVANTPAAMLALGVD

GVKSYIKTIGLFNSKAENVIKTCRILLEQHNGEVPEDRAALEALPGVGRKTANVVLNTAFGWPTIAVDTH

IFRVCNRTQFAPGKNVEQVEEKLLKVVPAEFKVDCHHWLILHGRYTCIARKPRCGSCLIEDLCEYKDKVY

A

>lcl|NZ\_FO834906.1\_prot\_WP\_004151206.1\_3123 [gene=dtpA] [locus\_tag=BN49\_RS17190] [protein=dipeptide/tripeptide permease DtpA] [protein\_id=WP\_004151206.1] [location=3183012..3184517] [gbkey=CDS]

MSTANNKPAESVSLNAFKQPRAFYLIFSIELWERFGYYGLQGIMAVYLVKQLGMSEADSITLFSSFSALV

YGLVAIGGWLGDKVLGTKRVIMLGAIVLAIGYALVAWSGHDAAIVYMGMATIAVGNGLFKANPSSLLSTC

YDKNDPRLDGAFTMYYMSINIGSFFSMLATPWLAARFGWSVAFALSVVGMVITIINFAFCQKWVKQYGSK

PDFAPVHMGKLLATIAGVVVLVAIATWLLHNQGIARMVLGVVALGIVVIFAKETIGLKGAPRRKMIVAFL

LMVEAIVFFVLYSQMPTSLNFFAIRNVEHSILGLAFEPEQYQALNPFWIMIGSPILAAIYNKMGDRLPMP

HKFAIGMVLCSGAFLVLPLGAKFASDAGIVSVNWLILSYALQSIGELMISGLGLAMVAQLVPQRLMGFIM

GSWFLTTAGAAIIAGKIANLMAVPENVTDPLVSLEVYGHVFLQIGIVTAVIAALMLLTAPKLNRMTQDDS

ADIKARETAAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529794.1\_3124 [gene=gstA] [locus\_tag=BN49\_RS17195] [protein=glutathione transferase GstA] [protein\_id=WP\_016529794.1] [location=3184628..3185233] [gbkey=CDS]

MKLFYKPGACSLASHIALRESGLDFTLQSVDLAQKRLENGEDYLLINPKGQVPALLLDDDILLTEGVAIM

QYIADQVPDRHLLAPVGSIARYQTLEWLNYVATELHKSFTPLFRPDTPEDYKPVARGLLEKKLQYVDAAL

ADKQWLTGHRFTIADGYLFTVLRWAYAIKLDMAAYGHIGSWMTQVAARPVVAAALAAEGLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002907739.1\_3125 [gene=pdxY] [locus\_tag=BN49\_RS17200] [protein=pyridoxal kinase PdxY] [protein\_id=WP\_002907739.1] [location=complement(3185276..3186136)] [gbkey=CDS]

MKNILAIQSHVVFGHAGNSAAEFPMRRLGANVWPLNTVQFSNHTQYGKWTGCVMPPSHLTEIVQGIADID

KLQTCDAVLSGYLGSAEQGEHILGIVRQVKAANPAAKYFCDPVMGHPEKGCIVAPGVAEFHVRYALPASD

IIAPNLVELEILCGHPVASVSEAVAAARELIAQGPEVVLVKHLARAGLSMDRFEMLLVTAEEAWHISRPL

VDFGLRQPVGVGDVTSGLLLVKLLQGASLRDALEHVTAAVYEIMLATKNMQEYELQVVAAQDRIAVPEHC

FSATRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002907740.1\_3126 [gene=tyrS] [locus\_tag=BN49\_RS17205] [protein=tyrosine--tRNA ligase] [protein\_id=WP\_002907740.1] [location=complement(3186198..3187472)] [gbkey=CDS]

MASSNLIKQLQERGLVAQVTDEEALAERLAQGPIALYCGFDPTADSLHLGHLVPLLCLKRFQQAGHKPVA

LVGGATGLIGDPSFKAAERKLNTEDTVQEWVDKIRKQVAPFLDFDCGDNSAIAANNYDWFGSMNVLTFLR

DIGKHFSVNQMINKEAVKQRLNRDDQGISFTEFSYNLLQGYDFACLNKLHGVALQIGGSDQWGNITSGID

LTRRLHQNQVFGLTVPLITKADGTKFGKTEGGAVWLDPKKTSPYKFYQFWINTADADVYRFLKFFTFMDI

AEINALEEEDKNSGKAPRAQYVLAEQVTRLVHGEEGLEAAKRITESLFNGNLSDLSEADFEQLAQDGVPM

IEMEKGADLLQALVDSELQPSRGQARKTVASNAVTINGEKQADPEYVFSDSDRLFGRYTLLRRGKKNYCL

VCWK

>lcl|NZ\_FO834906.1\_prot\_WP\_002907742.1\_3127 [gene=pdxH] [locus\_tag=BN49\_RS17210] [protein=pyridoxamine 5'-phosphate oxidase] [protein\_id=WP\_002907742.1] [location=complement(3187597..3188253)] [gbkey=CDS]

MSDNDELQQIAHLRREYTRGGLRRHDLPAEPLPLFERWLRQACDAKLADPTAMVVATVDERGQPYQRIVL

LKHYDEKGLVFYTNLGSRKAHQIENNPQVSLLFPWHMLERQVMVIGKAERLSTLEVVKYFHSRPRDSQIG

AWVSKQSSRISARGILESKFLELKQKFQQGEVPLPSFWGGFRVSIEQMEFWQGGEHRLHDRFLYQRDSGA

WKIDRLAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002907744.1\_3128 [gene=mliC] [locus\_tag=BN49\_RS17215] [protein=C-type lysozyme inhibitor] [protein\_id=WP\_002907744.1] [location=complement(3188311..3188634)] [gbkey=CDS]

MKKILIAVVPFMLAGCSYYNQFVERMQTDTLEYQCDQKPLTVHRNNARQQVSFIYDNQQLNLSEGLSASG

ARYTDGVYVFWSKGDTATVYKRDRIVLDNCQLQTAKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004143831.1\_3129 [gene=anmK] [locus\_tag=BN49\_RS17220] [protein=anhydro-N-acetylmuramic acid kinase] [protein\_id=WP\_004143831.1] [location=complement(3188727..3189851)] [gbkey=CDS]

MRSGRFIGVMSGTSLDGIDVVLATITENMVAQQASLTWPIPHAIKEEILAICQGQSLTLSQLGRLDTRLG

RLFADAVLALMRQESLKPTDVIAIGCHGQTVWHEPQGEAPHTLQIGDNNQIAAHTGITVVGDFRRRDMAL

GGQGAPLVPAFHHALLAHPVERRMVLNIGGIANVSLLAPGQPVRGYDTGPGNMLLDAWIWRQKGKPYDKD

AQWASEGKVLLPLLQDMLSDPWFALPAPKSTGREYFNYGWLEQHMARYPGLRGEDVQATLAELTAVTISE

QVLLSGGCERLLVCGGGARNPLLMARLAALLPGTEVSTTDEAGISGDDMEALAFAWLAWRTLAGLPGNLP

SVTGASEASVLGAIFPANPPQNRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002907749.1\_3130 [gene=slyB] [locus\_tag=BN49\_RS17225] [protein=outer membrane lipoprotein SlyB] [protein\_id=WP\_002907749.1] [location=3190119..3190586] [gbkey=CDS]

MILRVLAVSMIGFTLAGCVSSSGLSGDVYSASEAKQVQSVTYGTIVHTRAVQIQSGDDSNAIGAIGGAVL

GGFLGNTIGGGTGRSLATAAGAVAGGVAGQGVQGAMNKTQGVELEIRKDDGNTIMVVQKQGSTPFSVGQR

VAIAGSGSQVTVSPR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151205.1\_3131 [locus\_tag=BN49\_RS17230] [protein=GGDEF domain-containing protein] [protein\_id=WP\_004151205.1] [location=3190809..3192170] [gbkey=CDS]

MPEHVHHIVKRLILYICICLLAGIGISGMTAFFHTSFSSTSSILFPLLTSFLMVFHITIACFMGMKYWSS

KRRLYLTPVSFGFACSALLMLGTLSSYPDWLTCNPAPVVNQNDAVIYYFFRNIMMAVLFMSSIILYYFRQ

RIMHSWKAHVLTFTACILFTLTIIVLSWLYSSHSPWLSVNFIDDLSHTFTPLWQSIIGWLLMAVWFITLI

LLISLSKLRNIFWFSGAFFCSAYLFTLFQLLSTAGELDQTWYQARFFETLCTLFLILVLLVDVFILYRES

NHKYVHSYQNSIRDPLTRLYNRSFFYDTLNQQLAKVNAQHPLSVLISDLDHFKRINDSYGHVAGDKVIQF

AASVLESHSRVDDAAARIGGEEFALLLVNTGEKEAQAIAERIRLAVSAGESHLPERMTISMGVYTTYDNS

VTAEACVQRADEAMYEAKNNGRNQVIVWHQQGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004143833.1\_3132 [gene=slyA] [locus\_tag=BN49\_RS17235] [protein=transcriptional regulator SlyA] [protein\_id=WP\_004143833.1] [location=complement(3192204..3192644)] [gbkey=CDS]

MKLESPLGSDLARLVRVWRALIDHRLKPLELTQTHWVTLHNIHQLPPEQSQIQLAKAIGIEQPSLVRTLD

QLEEKGLISRQTCASDRRAKRIKLTEKAEPLINEMEEVIGKTRDEILSGVSKQEVETLLHLIRKLEQNIL

DLQAKD

>lcl|NZ\_FO834906.1\_prot\_WP\_002907752.1\_3133 [locus\_tag=BN49\_RS17240] [protein=DUF1656 domain-containing protein] [protein\_id=WP\_002907752.1] [location=3192817..3193053] [gbkey=CDS]

MKLSLNTSGLPLQDLVFGASVYFPPLFKAVLLGFFIWLFLHRQLRDWMYAGDIWHPLLMDLSLFALAVCL

ALVLLIAW

>lcl|NZ\_FO834906.1\_prot\_WP\_016529792.1\_3134 [locus\_tag=BN49\_RS17245] [protein=HlyD family secretion protein] [protein\_id=WP\_016529792.1] [location=3193064..3193960] [gbkey=CDS]

MKTLKYLSTLLVAAVALIAAWLLWNFYTQSPWTRDGKVRAEQVGITPQVSGSILQLNVTDNQRVKAGEVL

FTIDDTPYRIAVLNAQAQLAKAQAEVAKAQAEQSKAASEARRRRSLSQNAISAEDLENVNTALNTATTTL

AAARAGVGVTEAALKHAQWQLSQTVVKAPVDGWVTNLSTRVGDYATTGHPVFALVDSHSFYVLGYFEETK

LRHIRIGDPAQIILYSNQQTLKGHVASIGRAIVDQSVEQGTGLVANIKPNIPWVRLAQRVPVRIAFDTLP

ADVTLVSGTTCTVSIGGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529791.1\_3135 [locus\_tag=BN49\_RS17250] [protein=FUSC family protein] [protein\_id=WP\_016529791.1] [location=3193960..3195984] [gbkey=CDS]

MNLQTLSWRTLPWVKATRPQWRYALRNGIAMCLALSIAYALDLDEPYWAMTSAAVVSFPTVGGVISKSFG

RIAGSLLGACAALLLAGHTLNDPWLFLFSISGWLALCTWACALFTNNVAYAFQLAGYTCAIIAFPVINIS

DSYELWVIAQSRVCEVIVGILCGGLMMMILPSTSDGSNLLTALKTMHARLLEHASLLWVPETTDAIRTAH

ESVIGQILTMNLLRIQAFWSHYRFRRQNPLLNYLLHQQLRMTSVISSLRRMLLNWPDAPANTRQVLESLL

AELATPHVDSYHVARILAPLAPRQDADYRHIAFWARLRYFCRIYLESSRWIRRVENASAIAEFNVPAAPP

LARHTDQAEALLNGVRTFCALVAIGAWGISTQWTSCAAALTLASICCVLYSVSASPFRSLTLLMQTLVLL

SLFSFVVKFGLMVQVTDLWQFLLFLFPLLTTMQLLKLQWPKYAGLWGQLIVFMGSFIAVTNPPVYDYAAF

FNDNLSKIVGVGFAWLAFAVLSPGSDARKGRRHIRALRRHFVDQLSRHPQHSEHEFESLVYHHVSQLSQS

KDALARRWLLRWGVVLLNCSHVVWQLREWETRSDPLAQVRDLCINLLRDVMSERGVQQRPLASTLQELQR

ICDALNHHHQPAARELAAAIWRLYCALSQLEQAPVAGTIGEGTT

>lcl|NZ\_FO834906.1\_prot\_WP\_002907759.1\_3136 [gene=sodC] [locus\_tag=BN49\_RS17255] [protein=superoxide dismutase [Cu-Zn] SodC] [protein\_id=WP\_002907759.1] [location=complement(3195977..3196498)] [gbkey=CDS]

MQRCILAILSLAFCAGAQAVSEDVQLNLVTNQGVGQTIGSVKITETDRGLEFAPTLRALPPGKHGFHIHA

EGSCQPAMKEGKAVAAGAAGGHYDPQHTGKHEGPLGAGHLGDLPLLVVNDAGVADQPIIAPRLKTLAEVK

GKALMVHVGGDNMADSPQPLGGGGERFACGVIK

>lcl|NZ\_FO834906.1\_prot\_WP\_002907760.1\_3137 [locus\_tag=BN49\_RS17260] [protein=aldo/keto reductase family oxidoreductase] [protein\_id=WP\_002907760.1] [location=complement(3196568..3197464)] [gbkey=CDS]

MVQRIAMAPQGPEFSRFVMGYWRLMDWKMSPGELVSFIEQHLDLGVTTVDHADIYGDYQCEAAFGEALKR

APHLRSRMEIVSKCGIATRARAENTIGHYITDRDHIVLSAEQSLRNLATDHLDLLLIHRPDPLMDADEVA

EAFLALHHSGKVRHFGVSNFTPAQFTLLQSRLPFTLATNQVEISPVHQPLLLDGTLDQLQQLRIRPMAWS

CLGGGRLFNEEGFQALRDELAQVAHELNADSIEQVVYAWVLRLPSQPLPIIGSGKIERVRSAIVAEKLSM

TRQQWFRIRKAALGYDVP

>lcl|NZ\_FO834906.1\_prot\_WP\_004189722.1\_3138 [locus\_tag=BN49\_RS17265] [protein=DUF1289 domain-containing protein] [protein\_id=WP\_004189722.1] [location=complement(3197513..3197755)] [gbkey=CDS]

MVAEQLEFFPVQSPCRGICQTDERGYCRGCFRSREERFNWQTMSDAQKQEVLRLCRQRLLRKIRANRPEP

AEEPQQPSLF

>lcl|NZ\_FO834906.1\_prot\_WP\_004175857.1\_3139 [locus\_tag=BN49\_RS17270] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_004175857.1] [location=3197895..3198494] [gbkey=CDS]

MNRHSDCDTREHILATGEQLCMHRGFTGMGLSELLKTAEVPKGSFYHYFRSKEAFGVALLEHHYTGYLQR

LVDHFDHGDGNYRDRLLAYYQHTLNQFCQQGIISGCLTVKLSAEVCDLSEDMRAAMDRGASQIIALLGDA

LEKGRQEGSLAFDGEAMTLSQVLYSLWLGANLQAKITRSATPLESALAHAKQIIAAPAV

>lcl|NZ\_FO834906.1\_prot\_WP\_002907763.1\_3140 [locus\_tag=BN49\_RS17275] [protein=alkene reductase] [protein\_id=WP\_002907763.1] [location=3198548..3199645] [gbkey=CDS]

MSEAKLFSPLKVGAVTVPNRVFMAPLTRLRSIEPGDIPTPLMGEYYRQRASSGLIITEATQISAQAKGYA

GAPGLHSPEQIAAWQKITAGVHAENGHIAVQLWHTGRISHSSLQPGGAAPVAPSALSAGTRTSLRDENGH

AIRVDTSMPRALETAEIPGIVNDFRQAVGNARDAGFDLVELHSAHGYLLHQFLSPSANQRTDQYGGSVEN

RARLVLEVVDAVSQEWSAERIGIRVSPIGSFQNVDNGPNEEEDALYLISELAKRGIAYLHMSEPDWAGGK

PYSEAFRQKVRDRFPGVIIGAGAYTVEKANDLINKGLIDAVAFGRDYIANPDLVARLQKKAPLNPQRPES

FYGGGAEGYTDYPTL

>lcl|NZ\_FO834906.1\_prot\_WP\_002907764.1\_3141 [gene=gloA] [locus\_tag=BN49\_RS17280] [protein=lactoylglutathione lyase] [protein\_id=WP\_002907764.1] [location=3199724..3200131] [gbkey=CDS]

MRLLHTMLRVGDLQRSIDFYTNVLGMKLLRTSENPEYKYSLAFVGYGEESETAVIELTYNWGVDSYELGT

AYGHIALSVDNAAEACERIRQNGGNVTREAGPVKGGTTVIAFVEDPDGYKIELIEEKDAGKGLGN

>lcl|NZ\_FO834906.1\_prot\_WP\_002907766.1\_3142 [gene=rnt] [locus\_tag=BN49\_RS17285] [protein=ribonuclease T] [protein\_id=WP\_002907766.1] [location=3200269..3200916] [gbkey=CDS]

MSENAQLNGLCDRFRGFYPVVIDVETAGFNAKTDALLEIAAITLKMDEHGWLMPDETLHFHVEPFEGANL

QPEALAFNGINPHDPQRGAVSEYDALHAIFKMVRKGMKESDCSRAIMVAHNATFDHSFTMTAAERAGLKR

NPFHPFVTFDTAALSGLALGQTVLSKACIAAGMPFDGAQAHSALYDTEQTAQLFCEIVNRWKRLGGWPLP

VATPE

>lcl|NZ\_FO834906.1\_prot\_WP\_002907768.1\_3143 [locus\_tag=BN49\_RS17290] [protein=Grx4 family monothiol glutaredoxin] [protein\_id=WP\_002907768.1] [location=complement(3200964..3201311)] [gbkey=CDS]

MSSTLEKIQRQIAENPILLYMKGSPKLPSCGFSAQAVQALSACGERFAYVDILQNPDIRAELPKYANWPT

FPQLWVDGELVGGCDIVIEMYQRGELQQLIKETAAKYHTDEPKAE

>lcl|NZ\_FO834906.1\_prot\_WP\_032104201.1\_3144 [locus\_tag=BN49\_RS17295] [protein=C40 family peptidase] [protein\_id=WP\_032104201.1] [location=3201652..3202524] [gbkey=CDS]

MARLNKIAISLCALLFTSISFTPLAQASGHTHASASPKALPAKSGSERKKKATSQKTKTTAKTTSKKSSR

TRLPTRTTAASQTALHRQAAGATKKCVLRKGYKKQCAKTVAAGAEPTLALNSVKSKCVVRKGYKKRCKPE

ASEANLTIADAHKVRVQKAQSTAMNKLMGQLGKPYRWGGTSPRTGFDCSGLVYYAYKDLVKIHIPRTANE

MYHLRDARPVDRDELQSGDLVFFRTRGRGAADHVGVYVGNGKFIQSPRTGRDIQITSLSEDYWVRHYVGA

RRVMTPKTIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004200127.1\_3145 [locus\_tag=BN49\_RS17300] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004200127.1] [location=complement(3202479..3202964)] [gbkey=CDS]

MAKTDEVVSAKMIPVVQGIVDWIEAHIFDTLSVSAIAKKSGYSHWYFQRQFAMVTGCTLASYVSRRKMTI

ATIYLTQTQASIQSISQCLGYEGQAAFCRTFHRHFGMSPTRYRRDTPGKESNLQYPLRVGMEMEQERRSA

AAAADRDQRMVFGVMTRRAPT

>lcl|NZ\_FO834906.1\_prot\_WP\_002907771.1\_3146 [gene=sodB] [locus\_tag=BN49\_RS17305] [protein=superoxide dismutase [Fe]] [protein\_id=WP\_002907771.1] [location=3203434..3204015] [gbkey=CDS]

MSFELPALPYAKDALAPHISAETLEYHYGKHHQAYVTNLNNLIKGTAFEGKSLEEIVRTSEGGVFNNAAQ

VWNHTFYWNCLAPNAGGEPEGELAAAIAKSFGSFADFKAKFTDAAAKNFGAGWTWLVKNADGSLAIVSTS

NAGTPLTTDAKPLLTVDVWEHAYYIDYRNARPSYLDHFWALVNWKFVAANLAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002907773.1\_3147 [locus\_tag=BN49\_RS17310] [protein=MFS transporter] [protein\_id=WP\_002907773.1] [location=complement(3204076..3205242)] [gbkey=CDS]

MKINFPLLALAIGAFGIGTTEFSPMGLLPVIAKGVDVSIPVAGMLISAYAIGVMVGAPLMTLLLSHRARR

NALIFLMGIFTVGNLLSSIAPDYTTLLLSRIITSLNHGAFFGLGSVVAASVVPKHKQASAVATMFMGLTI

ANIGGVPAATWLGETIGWRMSFLATAGLGLLAMVSLWFSLPKGSAGERPDVKKELSVLLRPQVLSALLTT

VLGAGAMFTLYTYISPVLNTLTHASSLFITAMLVLIGVGFSLGNYLGGKFADRSVSGTLKGFLLLLMAIM

LAIPLLAQSQAGAAISMIVWGAATFAVVPPLQMRVMRVAHEAPGLSSSVNIGAFNLGNALGAAAGGAVIS

GGLGYAFVPVMGAIIAGLALLLVWFSGRAQPEEAFASQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002907776.1\_3148 [locus\_tag=BN49\_RS30480] [protein=YnhF family membrane protein] [protein\_id=WP\_002907776.1] [location=complement(3205410..3205502)] [gbkey=CDS]

MMDTNLKFSLITTIIALGVIVAFSLTAILH

>lcl|NZ\_FO834906.1\_prot\_WP\_002907778.1\_3149 [gene=purR] [locus\_tag=BN49\_RS17320] [protein=HTH-type transcriptional repressor PurR] [protein\_id=WP\_002907778.1] [location=3205795..3206820] [gbkey=CDS]

MATIKDVAKRANVSTTTVSHVINKTRFVAEETRNAVWAAIKELHYSPSAVARSLKVNHTKSIGLLATSSE

AAYFAEIIESVEKSCFQKGYTLILGNAWNDLEKQRAYLSMMAQKRVDGLLVMCSEYPDSVLSMLEEYRHI

PMVVMDWGEAKADFTDAVIDNAFQGGYIAGRYLIERGHREIGVIPGPLERNTGAGRLAGFMQAMKEAHIS

VPENWIVQGDFEPESGYRAMQQILNQQHRPTAVFCGGDIMAMGAICAADEMGLRVPQDISLIGYDNVRNA

RYFSPALTTIHQPKDSLGEAAFNMLLDRIVNKREESQSIEVHPRLVERRSVADGPFVDYRR

>lcl|NZ\_FO834906.1\_prot\_WP\_009307704.1\_3150 [locus\_tag=BN49\_RS17325] [protein=DNA-binding transcriptional activator PunR] [protein\_id=WP\_009307704.1] [location=complement(3206747..3207751)] [gbkey=CDS]

MWSEYSLEVVDAVARNGSFSAAAQELHRVPSAVSYTVRQLEEWLAVPLFERRHRDVELTPAGVWFLQEGR

SVIKKMQITRQQCQQIANGWRGQLSIAVDDIVKPARMRQMIVDFYRHFPDVELIVFQEVFNGVWDALADG

RVELAIGATRSIPVGGRYAFRDMGMLSWDCVVASDHPLAKMDGPLSDDILRNWPSLVREDTSRSLPKRTT

WLLDNQKRVVVPDWESSATCLSAGLCVGMVPSHFARPWIDRGEWTALALENPFPDAACCLTWQQNDASPA

LNWMLDYLGDSDTLNREWLRAPERSAPARCLNDDNRQTGHPLPSGAQPDEGALR

>lcl|NZ\_FO834906.1\_prot\_WP\_002907785.1\_3151 [locus\_tag=BN49\_RS17330] [protein=purine nucleoside transporter PunC] [protein\_id=WP\_002907785.1] [location=3207864..3209045] [gbkey=CDS]

MSQPGKGFLVWLAGLSVLGFLATDMYLPAFAAMQQDLNTSAASISASLSLFLAGFALGQLFWGPLSDRYG

RKPVLLSGLAIFAAGCLGMLWVHNATLMLALRFLQAIGVCAAAVTWQAMVADYYPAQRTNRIFATIMPLV

GLSPALAPLLGSWLLVHFEWQAIFATLFAITLLLMLPALRLKAAAKSVVVTQQKITFLALLRSREYSGNV

LIYAACSASFFAWLTGSPFILHEMGYGPTAIGLSYIPQTIAFLVGGYGCRALLQKWSGQQMLPWLLVIFA

VSVAATWLVGLQTHASLVALMIPFCMMAVVNGGIYPIVVAQALKPFPQATGRAAALQNTLQLGLCFLTSL

LVSALIATPLLTTTSVMLVSIGLAGIGYRLQQTPELTPHSSHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002907788.1\_3152 [gene=cfa] [locus\_tag=BN49\_RS17335] [protein=cyclopropane fatty acyl phospholipid synthase] [protein\_id=WP\_002907788.1] [location=3209338..3210486] [gbkey=CDS]

MSSSCIEEVSVPNDDWYRIAAELLGRAGIEINGSAPSDLRVKNPLFFKRVLQEGSLGLGESYMDGWWECE

RLDIFFHKVLRAGLEKQLPHHFKDTLRIAGARLFNLQSKKRAWIVGKEHYDLGNDLFSRMLDPYMQYSCG

YWKEAQSLEAAQQAKLDLICRKLELEPGMRVLDIGCGWGGLAEYMARNYQVSVVGVTISAEQQKMAQARC

ADLDVEIRLQDYRDLHDSFDRIVSVGMFEHVGPKNYATYFEVADRNLKPNGRFLLHTIGSKVTDHNVDPW

IDKYIFPNGCLPSVRHIAEASEKHFVMEDWHNFGADYDTTLMAWYERFLASWPEIADNYSERFKRMFTYY

LNACAGAFRARDIQLWQVVFSRGIEHGLRVAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002907792.1\_3153 [locus\_tag=BN49\_RS17340] [protein=riboflavin synthase] [protein\_id=WP\_002907792.1] [location=complement(3210523..3211158)] [gbkey=CDS]

MFTGIVQGTAKVVSIDDKPNFRTHVVELPAHMLEGLETGASVANNGCCLTVTEINGARISFDLMKETLRI

TNLGDIQVGDEVNVERAAKFSDEIGGHLMSGHIMTTAEIVKILTSENNRQIWFKVQDPTLMKYILYKGFI

GIDGISLTVGEVTATRFCVHLIPETLQRTTLGAKKLGDRVNIEIDPQTQAVVDTVERVLAAKEMAAKVNE

A

>lcl|NZ\_FO834906.1\_prot\_WP\_004148609.1\_3154 [gene=mdtK] [locus\_tag=BN49\_RS17345] [protein=MdtK family multidrug efflux MATE transporter] [protein\_id=WP\_004148609.1] [location=3211388..3212761] [gbkey=CDS]

MQKYFVEARQLLALAIPVILAQVAQTAMGFVDTVMAGGYSATDMAAVAIGTSIWLPAILFGHGLLLALTP

VVAQLNGSGRRERIAPQVRQGFWLAGFVSVLIMVVLWNAGYIISSMHNIDPLLAEKAVGYLRALLWGAPG

YLFFQVARNQCEGLAKTKPGMVMGFIGLLVNIPVNYIFIYGHFGMPELGGVGCGVATASVYWVMFASMLW

WVRRARTMRDIRCAERFSGPDFAVLLRLVQLGLPIALALFFEVTLFAVVALLVSPLGIIDVAGHQIALNF

SSLMFVLPLSLAAAVTIRVGFRLGQGSTIDAQVSARTGVGVGVCLAVFTAIFTVLMRKQIALLYNDNPEV

VTLASHLMLLAAIYQISDSIQVIGSGILRGYKDTRSIFFITFTAYWVLGLPSGYLLALTDMIVPRMGPAG

FWCGFIIGLTSAAIMMMLRMRFLQRQPSSIILQRAAR

>lcl|NZ\_FO834906.1\_prot\_WP\_040024451.1\_3155 [gene=asr] [locus\_tag=BN49\_RS17350] [protein=acid resistance repetitive basic protein Asr] [protein\_id=WP\_040024451.1] [location=3212937..3213344] [gbkey=CDS]

MKKVLALVVAAAMGLSSVAFAANAASTTPSAAASHTTVHHKKHHKAAAKPAAEQKAQAAKKHHKAAAKPA

VAQKAQAAKKHHKAAAKPAVAQKAQAAKKHHKAAAKPAVAQKAQAAKKHHKTTHHAAKPAVKPAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004175848.1\_3156 [locus\_tag=BN49\_RS17355] [protein=TIGR00730 family Rossman fold protein] [protein\_id=WP\_004175848.1] [location=complement(3213485..3214063)] [gbkey=CDS]

MKSIGIFCGSSAGEHPLYLETARLVGRTLAQQGLALVYGGGKVGLMGAVADAALEAGGVVIGVMPRGLVE

REIAHRGLTELHVVEDMHERKTKMAALADGFIALPGGAGTLEEIFEQWTWAQLGIHEKPCAFLNIKGYYD

PLQAMVDNMVREGFMHPRYAEMLPFATSADEIIAGFRDYTPPARKWVQQPAI

>lcl|NZ\_FO834906.1\_prot\_WP\_077250274.1\_3157 [locus\_tag=BN49\_RS17375] [protein=hypothetical protein] [protein\_id=WP\_077250274.1] [location=complement(3214743..3214970)] [gbkey=CDS]

MNIKRTLLILLSRVIRGAGMGLGASGIALAGWFFFFSVNEYKFLWGLLSVVEFLVGYLIYRFAYAYIYDE

WNDYH

>lcl|NZ\_FO834906.1\_prot\_WP\_071609116.1\_3158 [locus\_tag=BN49\_RS29220] [protein=hypothetical protein] [protein\_id=WP\_071609116.1] [location=complement(3214967..3215428)] [gbkey=CDS]

MRNRLINDATSLVKQPPGQSRYRMVVLRRAQYRQPAESATVNPYGGRTEAAAPDAGRDEEEGNASRGVSA

FFAGSLAGLLLSVGAETSRAIYTSRYLKHRNPVLHDKLQNLGDLDLLYFLVEDIVKPFETACMVSDKNPA

EFNKICEYFFGGL

>lcl|NZ\_FO834906.1\_prot\_WP\_042940708.1\_3159 [locus\_tag=BN49\_RS17385] [protein=SDR family oxidoreductase] [protein\_id=WP\_042940708.1] [location=complement(3216254..3217006)] [gbkey=CDS]

MQTIMITGCSSGFGLETARYFLEQGWKVIATMRAPQEGVLPASDRLRLVRLDVTSAQSIAEAIAEVGEID

VLVNNAGVGMLNALEGAPREAIANLFATNTLGTIAMTQAVIPRFRERRSGTIVNITSAVTLQPMPLLAVY

TASKAAVNAFTESLALELLAFNIRVGLILPGRAPQTRFGENARRTMGQLPESYAALGQQIFDSMQDNASV

TQATDVAQAVWRMVHDADAPSRLPAGEDALAMAQASHRLV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043425.1\_3160 [locus\_tag=BN49\_RS17390] [protein=AraC family transcriptional regulator] [protein\_id=WP\_046043425.1] [location=3217105..3218031] [gbkey=CDS]

MSDPLAEVIAMLNLRAVLTKTIEGAGDWRVRRSDQGLSFYGVVLEGGCRLEIDQHEPQILRAGDFILIPA

AYRFSLTSLTPPPSPALETIPVQLAEGHFRLGALDKPAQMQALIGHCASGSTNASLLASLLPAFVVVRNQ

PRLATFVGLLKEEAQADRAGKSFVLARMVELLFTEAIRSSGTLATPGLMRGLSDPRVAQAIRLLHQAPAR

RWTVNALAADCALSRSTLFERFTDLTGMTPMGYLLGWRMTLAMQWLSETGISNADIAERIGYGSASAFSV

AFTRYTGISPGKYARQRAALNVSRPALT

>lcl|NZ\_FO834906.1\_prot\_WP\_002907799.1\_3161 [locus\_tag=BN49\_RS17395] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_002907799.1] [location=complement(3218028..3218912)] [gbkey=CDS]

MRRKIPSSAALLAFEAAARHGNFARAAAELALTEGAISRQIARLEALLDSKLFDRTGSRVRLNPAGARYA

RQVREILARLERDTHDVSGMPVDGRSLEIAVLPTFASRWLIPRLGRFAAQHPHIVVNIAARSDPFILPGS

GFDAAIHFEHPAWTGMEVTFLFAEYLLPVCHAALLTDDDLPGLLNRLTRIHRRQNPDAWLHYARECGLAL

DNPAQGPRYDLHEMAIAAVLSQQGVALVPKMYVESELSAGTLVAPWPGSPTLAKRFCLIKPGGGEGEPAL

QMFERWLQTEIAAG

>lcl|NZ\_FO834906.1\_prot\_WP\_032415066.1\_3162 [locus\_tag=BN49\_RS17400] [protein=hypothetical protein] [protein\_id=WP\_032415066.1] [location=3219069..3219584] [gbkey=CDS]

MLYVVECAYTDPQSEAAWNTFYNQEKLPALVSVPGFYASQRFRALSEGCPCYLALHDIHDATVIDSDAYR

RNGGGHFARWQSAIADWHRHLYLTNNTLREVAPDEVLLLGDTAEDLPVAAPILLQPGGLATEQSRYAAIV

SRDNLHHLATTAAVFIYQPITARLRNPAQRA

>lcl|NZ\_FO834906.1\_prot\_WP\_042940946.1\_3163 [locus\_tag=BN49\_RS17405] [protein=MBL fold metallo-hydrolase] [protein\_id=WP\_042940946.1] [location=3219592..3220428] [gbkey=CDS]

MSPAPFYTLTAGDLTVTAVSDGLMSAPLSLLSGISREEAEHLQRHSGLASPETIAIGAYLIRGRGNTVLV

DTGTGGANGVGGELIANLARLGVGPADIDAILLTHAHPDHIGGLLSAAGTPAYPNATVFLPTRESAYWLA

TSTFDNASDRGRRNVLLVRRVLANCAAQISGVDDEEVIAGIRPCPLPGHTPGHTGYRLEAGDTSLLIWGD

IVHFPSIQSARPEASVAFDVDPEQARRTREILLRQAASERWLIAGMHLGLPGFARVENTASGYCLRSV

>lcl|NZ\_FO834906.1\_prot\_WP\_002907802.1\_3164 [locus\_tag=BN49\_RS31090] [protein=hypothetical protein] [protein\_id=WP\_002907802.1] [location=complement(3220516..3220665)] [gbkey=CDS]

MVIATRKPLCNKRWSASPASQDLQLTQLRHPWVATKASCKSKKGWKSRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004143863.1\_3165 [locus\_tag=BN49\_RS17415] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004143863.1] [location=3221067..3221501] [gbkey=CDS]

MTKGYKLLGYKLADNIFYCLHHREIITLRGTRTQVQLRSTMACLLEYLLAHGRERLVSDEELMINVWEKN

NLRPSAQRLWQVIQSLKSRLHQAGVESALIIRVKCAGYYINNVYVAEIYSYKPPGMMNYINTSPADMNKL

LVRS

>lcl|NZ\_FO834906.1\_prot\_WP\_004210116.1\_3166 [locus\_tag=BN49\_RS17420] [protein=hypothetical protein] [protein\_id=WP\_004210116.1] [location=3221547..3222263] [gbkey=CDS]

MNILIHSNNIYFNIGIAQCFRDIQKTAPELKVIHSLPLSHLPELSGLDVIILSLENYHDYLAAAEIAQHF

QGLVIGFTSAGNVRRGRSFFADTLLWVSQREAVREVSRLLRCLAERRWPLVPRHQRQSVSFRQRAPLNRL

EMRMIDATMKGQSVHQMAATLGINRKRVYNGLERIKVNFRLVSHSHFHHFMTDRLSFSRLSADLRCLTTA

ANATLPPRAASRPAENHSYYLKEFRKLF

>lcl|NZ\_FO834906.1\_prot\_WP\_004210114.1\_3167 [locus\_tag=BN49\_RS17425] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_004210114.1] [location=3222348..3222557] [gbkey=CDS]

MNFIKTFVAVSALSLFSAASFAQSVSATASTLDRAEAKIAAQAAEQGASYKITSAQFNNRVHMTAELSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002907811.1\_3168 [locus\_tag=BN49\_RS17435] [protein=carbonic anhydrase] [protein\_id=WP\_002907811.1] [location=complement(3222870..3223505)] [gbkey=CDS]

MQHIIEGFLNFQKEIFPQRKELFRSLASSQNPKALFISCSDSRLVPELVTQQEPGQLFVIRNAGNIVPSF

GPEPGGVSATIEYAVVALGVTDIVICGHSNCGAMKAIATCQCLEPMPAVSHWLRYADAAKAVVEKKTWAS

ETDKVNGMVQENVIAQLNNIKTHPSVAVGLRDHTLRLHGWFYDIETGDIQALDKNTKSFVSLSENPDVFF

E

>lcl|NZ\_FO834906.1\_prot\_WP\_002907812.1\_3169 [locus\_tag=BN49\_RS17440] [protein=LysE family transporter] [protein\_id=WP\_002907812.1] [location=3223755..3224384] [gbkey=CDS]

MFLSSLMAIAAVLIMGVISPGPSFIFVARNAVARSRLHGMVTALGTGAGAAIFSIMAMLGLQKVLTAVPE

LFIGLKVAGGLYLLWLGYKIFRGSAQPMDFSASGMAGNRSLLKTFRDGLYTQLSNPKTALVFASIFTALL

PAQIPTAFYYIVPLMSFLIDVSWYSLVALVLSADRPRRVYLRLKRRIDIATATVLGALGLRLIATSLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_009307695.1\_3170 [locus\_tag=BN49\_RS17445] [protein=DeoR/GlpR family DNA-binding transcription regulator] [protein\_id=WP\_009307695.1] [location=complement(3224389..3225159)] [gbkey=CDS]

MLDYAAFPQQRQALICQILQENGRVVCAELAARLQVSEHTIRRDLHELSREGFCKKVYGGAVLSLPEAGD

YSQRKDKNRAIKLRIAQQCARLVKPGGTIFIDTGTTNLAMAEALPTELALTVVTNSPEIAAVLVKKPLYD

VVMLGGQVQRASGGCVGAAAVAQVQGMLFDQGFIGGCAMAPESGLTGFDYADCEFKKAVIKQCSEIIVGL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004175834.1\_3171 [locus\_tag=BN49\_RS17450] [protein=glyoxalase/bleomycin resistance/extradiol dioxygenase family protein] [protein\_id=WP\_004175834.1] [location=3225251..3225634] [gbkey=CDS]

MKIAHFALWTQQLDVQARFWVDFFAASINEKYLSQTNPGFASYFVTIDDEVVIELMTKPGLQQASADNNH

TGWAHLALSVGGAEQVDAIAQRAGAAGILISPPRTTGDGYYEAVIADPDGNLIEIVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004175829.1\_3172 [locus\_tag=BN49\_RS17455] [protein=CatA-like O-acetyltransferase, family 1] [protein\_id=WP\_004175829.1] [location=3225666..3226349] [gbkey=CDS]

MAHYRIIDTASWPRRDHFTFYRQFANPSFNLCVPIAAQRLYECAKDRRVSFFQLALYALLRAANGVPQLR

QRVRNDEVIEYDSLAVMTPVMTVGEGFRQVWCDNAPEFTAFSAAATPKIVAARETSPAPLIVDGEHFICA

SCLPWLHFTSMTHAEYAVGAAVPALTWGKLQNGVIPVAGRFNHAFVDGLHASRFYALVEEGFNDPERLWL

PLTETAPSLLPPAAKER

>lcl|NZ\_FO834906.1\_prot\_WP\_016529827.1\_3173 [locus\_tag=BN49\_RS17460] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016529827.1] [location=3226694..3228397] [gbkey=CDS]

MSRLQQGLKTRQTRFALALKVALLGGVVAFSSAVFAEGLLKEGITPATDASQIPASAKLRTDTVVAGISE

PQGIFNPYFFVNGWDENVTNVIFSRLIDWDSQGKLVPGLAESWTVSPDNKVYTIKLRPGLTFSDGSPLTA

EDVAFTLTVLLDPKYDGDTDITLANIAGGTDYKAGKADSVSGLKVIDPLTLQVTTTQPGATTLAKIGGPV

LSKAWYGKGYQRGNLDYLRSLHGKPLGNGPYVYDKYIPGQEIRFHANSHFYRGTPPTPRFIYRVTNPSTN

FQLFQTGETDYDAFTSRPDDIEQLKMLGFANINLYGSSDYSQVEFNVHRPALQDKRVRQALIYGLDRQKL

IDVVYQGYGKVAIEPIAPISWAFNAEGVNPYPYDPAQAKKLLDEAGWKAGADGIRAKDGQRLELTLLVSK

KVLNDALIPIAKENWRQIGVLLKPQVVDFNALMAQRKAGNYDLASFSTSTLNDPHDGVWDFYSSEAKESG

YHNAEVDKLINAGNAVLDIEQRKPIYHQLYKVLADDPPVILLGYREILSASSARVSGFKPDIYNGLTGSL

PDVKIVK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043426.1\_3174 [locus\_tag=BN49\_RS17465] [protein=ABC transporter permease] [protein\_id=WP\_046043426.1] [location=3228441..3229400] [gbkey=CDS]

MRNFILRRLLQTLPMLLLASFIIFLLFAKTPGDFIDGNITLTAARAAELKAIYGLDQPLLTRYLHWLGQL

LRGDLGFSLQYQIPVSQLLNQYIWNSFLLASVALVFYWGIGLAVGVVSALRPGSWFDHLVSVAVFAAMSF

PTFFLCLLLIKWFAVDLHWLPVGGMTNTGSDESGWQYVLQVAAHLALPVLALVMLQAGSLTRYVRASMLD

VVKMDFIRTARAKGLQERTVILKHALRNALLPIITLLGFKLPGLFSGAIITEKVFNWPGAGHIHIDSLAA

RDYPVLMGFTLFLAVLTIVGNLLADVLYAWADPRIRVRS

>lcl|NZ\_FO834906.1\_prot\_WP\_162263764.1\_3175 [locus\_tag=BN49\_RS17470] [protein=ABC transporter permease] [protein\_id=WP\_162263764.1] [location=3229397..3230347] [gbkey=CDS]

MMILSYLASRRRQRQAAIPALAHITPSPWRQGWRQLRRNRLAMFCLILLAVMAVWCVLGPVWSPWSDDAT

DALSINQPPGAEHWLGTDFLGRDVYTRLLLAGRISLIIGLLTMVMSVCLGYLLGALSGYVGGLTDKLIMR

VADLVMTVPGLPLLIVAGAMLSELDFSPDSRIYMVVVMLSLLEWPRLARLVRGQCLSLRERDFMLATQVL

GLSARRRLFGHLLPNTIPILVVMATMAVANAILSESALSYLGLGVVPPTPSWGNMMDAANSLIDFQRRPW

LWMPPGIAIFITVIAINVLGDGLRDAMDPNMKPRLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004151192.1\_3176 [locus\_tag=BN49\_RS17475] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004151192.1] [location=3230344..3231324] [gbkey=CDS]

MTTPLVSFNHLSVSFAGERSRVRAVQEVSFTIQAGQTVGVVGESGCGKSVTAMALMGLLPPQTARIDGGE

IRFADRDLLRLKARQMADLRGHQLAMIFQEPMSALNPVLTIGEQLCEPPIRHLGATPKAAWHQAIQLLSE

VGLARGDSLMTRYPHQLSGGMLQRVMIAMALSCRPKLLIADEPTTALDVTVQAQILRLLRDRARASQMAM

MLITHDLGVIAQMAEQVVVMYAGRIVEQGATAEVLRHPQHPYTRGLIASRPVPGERRRRLYSIPGQVPDL

AALPAGCAFAGRCERATARCREAIPPLLGDRQRAACFYSEFAEVTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004898655.1\_3177 [locus\_tag=BN49\_RS17480] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_004898655.1] [location=3231321..3232292] [gbkey=CDS]

MSERYVIEVDGLKKYFPLRDGLFGQQTGELRAVDGVSFNIRPGTIFGLVGESGSGKTTVGRTLLGLYEKS

AGSVKFHGQELADLTAPALRAIRPRMQLVFQDPYSSLNPRLRIGDAIGEAMLEHKLCARNELYDRVIDVM

KICGLAPEHYARFPHQFSGGQRQRIGIARALILNPDFIVADEPISALDVSIQAQIINLFSDLRDNRGVTF

LFISHDLGVVEHLCDDVAVMYLGQLVESASRDALFSRPLHPYTRALMAAVPTLDPHSEPQALVQGEIPDP

ANPPAGCRFSSRCPLASERCRREPPALREVAPGHRVACHWVAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002907918.1\_3178 [locus\_tag=BN49\_RS17485] [protein=anti-virulence regulator CigR family protein] [protein\_id=WP\_002907918.1] [location=3232658..3233185] [gbkey=CDS]

MLKRRTLKTALAAVISLAVMAAPAYANPGNGNGNGGGNHGNSGNHGNSGNHGNNGNSGDHGNKGQNKGQS

TEDHGKRKNYGKPDHVDSDISFSRARSLAVNYGLVGYQALPPGIAKNVARGKPLPPGIAKKTLPASMIND

LPYYPGYEWRAVGDDLVLVALSTAIVTAVINGVFD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530053.1\_3179 [locus\_tag=BN49\_RS17490] [protein=DinB family protein] [protein\_id=WP\_016530053.1] [location=3233303..3233791] [gbkey=CDS]

MDKDTVVTLLKYKRWIDLATLQAIRAIDGTVHGEKRHLTIRLMNHIHVVDMIFRANLRSRPHGYTALNTP

ETPTVDELETAMTACTDEYIQYVSAMTPADFHERIAFKFVDGGDGNMTAMEMLNHMLFHGAYHRGAVGWM

IGECGGVPPKEVLTVFLRDHHS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043427.1\_3180 [locus\_tag=BN49\_RS17495] [protein=hypothetical protein] [protein\_id=WP\_046043427.1] [location=complement(3233828..3234112)] [gbkey=CDS]

MAIDPELIYIEILETVLMATLDPDLWKSALQKLAFLTGSALMELFNVKPAENAVAELLVRGMTPYIWAYL

SPRSEPTLAPCTRKPILEIRQSSC

>lcl|NZ\_FO834906.1\_prot\_WP\_171819478.1\_3181 [locus\_tag=BN49\_RS31095] [protein=MFS transporter] [protein\_id=WP\_171819478.1] [location=complement(3234257..3235018)] [gbkey=CDS]

MLELSLLRHPRFVGVLLLPVATCCCYVVLLIIVPLHFMGGEGMSEPQSALYLMALTTPMLVFPSVAALLT

RWFSPGQVSTAGLMMASVGLLLLGNAFHSHHLPQLVLALILCGAGAAFPWGLMDGLAISAVPMAKAGMAA

GLFNTVRVAGEGIALAVVSAVLTASNNLTLQSRVHGYAPEVIDRAAGWLGAGNMPQAAALLPDFSLRALR

ESYDSAYTLLFSGLAVVTLVCALMVWRTLCRKAGAIQTRDSGC

>lcl|NZ\_FO834906.1\_prot\_3182 [locus\_tag=BN49\_RS31100] [protein=MFS transporter] [pseudo=true] [location=complement(3235166..3235784)] [gbkey=CDS]

MLLTARTPSRYASALAALSVFMAALLLPLSFTGGVMTTPAIQQSLGGSPAALSWLTNGFMLTFGSFLLAA

GVTADAIDRKRIFIAGAALFCLSSLLFCLTHNLFLSGVLRALQGLAAAMILASGSAALAQLYDGAQRTRA

FSILGTVFGIGLAFGPLLIGFMIDAVGWRGVYALFALLSAGVLLIGLVSLPATEKSEPRTPDNLGL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530688.1\_3183 [locus\_tag=BN49\_RS17505] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530688.1] [location=3235901..3236818] [gbkey=CDS]

MDSLTSLTSFVRTAETLSFVQAARLLGISASAVGKNVARLEHKLGVRLFNRSTRNVSLTAEGAAFLTRCQ

SILEQIQEAESELTSSLSQPTGKLRISLPVIGYRLLLPALTAFSRLYPQVELDLDFSDRLVNLIDEGVDV

AIRSGELADSRLIARTLGGFRFVLCASPAYLAEYGVPGSPAELAAHKCIFFRFPATGLIQPWELRGMRLT

GDFRAAAVMTVNNIEAAIRLSAAGMGIAYVPDFVVREAMDEGQLQEVLPGCCVKDGHFSVLWPASRYLSP

RIRCFIDFIAAAEIPLSPASVSPTT

>lcl|NZ\_FO834906.1\_prot\_WP\_004898666.1\_3184 [locus\_tag=BN49\_RS17510] [protein=APC family permease] [protein\_id=WP\_004898666.1] [location=complement(3236880..3238406)] [gbkey=CDS]

MSNEILANPAPAAEKHVVQRLRPNAVGLGGVLFMTIATAAPITAMLGNVPIAVGSGNGQFAPAGFMVATL

ILALFAIGYAQMARFITATGAFYGFISHGLGRIVGMASGVTVTMTYIVFEAALVGIFAFFCEDLINTVFS

VHIPWLILAFAMLMTTGVLSYFDISLTSRVLGLCLVLEILILTAVAVAVLIHGGGPQGFVPESINPLNAF

TPAKGVVGASAGIGLFFAFWSWVGFESSAMYGEESKNPKKIIPLATLLGVIGIGVFYVFISWMAIAGTGP

EQAIALAQDPNRAGEIFYGPARQYLGEWAVGVFKLLVITGSFACGMAFHNCAARYLYALGRENLFPFAGR

TLGRSHSRHGSPHVASTVQTVIATLIVLLFFITGKDPYADIYTLLALLGTMGIMIVQALCAFAVIVYFHG

NKENIGKGHWFKTGVAPLLGGMGMIYIVYLLFKNMAFAAGAAASSSFYHAIPWIVLACFCFGAAIAVWFY

LFDAQKYRVIGRIVLTDD

>lcl|NZ\_FO834906.1\_prot\_WP\_024264438.1\_3185 [locus\_tag=BN49\_RS17515] [protein=SDR family oxidoreductase] [protein\_id=WP\_024264438.1] [location=complement(3238421..3239194)] [gbkey=CDS]

MMSDFMNKHVLVTGGSSGIGLGIALGFARAGAKVTITARTPSRIDSAIGQAAEQGLTLRGLTCNVSHAEE

VKACVAEAAQQWGGLDIVCCNAGIFPSAPLADMSEQQWDEVQAINSKGTFLTVQAALPWLKRAEYGRIIL

TSSITGPVTGYPGWAHYAASKAAQLGFMRSAALELAGDNITVNAVLPGNIVTEGLRDMGEDYIAGMASAV

PLKRLGTVEDIAAAALFFASRQAGYITGQSLIVDGGQILPESAACLN

>lcl|NZ\_FO834906.1\_prot\_WP\_223203120.1\_3186 [locus\_tag=BN49\_RS17520] [protein=phosphotransferase] [protein\_id=WP\_223203120.1] [location=3239617..3240672] [gbkey=CDS]

MSFQIEDSMFNDEYLTTLTLKLRPLLPRWGLSEGAEIGLLTVSENATFLVSDKMTQRKIVLRVHRPNYSS

AVEIHSELMWLNALHARGDINIAVPLVLDDGTCIASLIDGETVTHVVGFTFVAGSEPDTGSHLTGWYHAL

GRVAGELHRHSEGWVKPEGFHRKVWNTETIIGRHAWWGDWRKMTQLSADDITLLEAVEATVVARLEAYGQ

GADRYGLVHCDMRLANLLVNENSLTVIDFDDCGICWFGWDFATAVSFIEDDPALADYRAAWLAGYRSVRP

FSQQDEVMLPVLVMLRRLQLTAWLASHSETATARRYSPQWGAITVRLAQAFLLQASPLSATVNCKEPADE

Q

>lcl|NZ\_FO834906.1\_prot\_WP\_016532206.1\_3187 [locus\_tag=BN49\_RS17525] [protein=aspartate aminotransferase family protein] [protein\_id=WP\_016532206.1] [location=3240662..3241999] [gbkey=CDS]

MNNKTPILQLNRFDALTGVADENLSRQIARRHATQGTGSVLFYPQPIVMASASGAWMEDSAGNRYLDMYN

NVPGVGHCHPHITQAMVRQAGLLNTNTRYLFPVLEQYADSLLATFPAGLSNVIFTCTGSESNDIALRMAR

FISGRQGIIVTESAYHGNTTAVMEVSPSGHKEALLPPWVHTIPAPDLRRLSAGQTLSDLFAADVERAMDE

LDERGYGCAALLVDTIFSSDGVFADPPGFLAQAVARVQARGGLFIADEVQPGFGRTGSHFWGFQRHSVQP

DIVTLGKPMGNGFPMAAVITRPAILQAFSEKTEYFNTFGGNPVAAAVGLAVLEVIEQEALMNNAKRNGDY

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PLCFSRDDADFFLERLAKVMGRLNG

>lcl|NZ\_FO834906.1\_prot\_WP\_004898673.1\_3188 [locus\_tag=BN49\_RS17530] [protein=DeoR/GlpR family DNA-binding transcription regulator] [protein\_id=WP\_004898673.1] [location=3242092..3242874] [gbkey=CDS]

MSKRKEDRQQQILRELAETPTLRIGDMARTHGVSTETIRRDLDELTRRGVLNRTYGGAVRAMNSEPTVTE

RHQLFTEERERIARDAVHCMREGKIFMIGSGATTVHVARRMASELRDITVITHAFGVATVLSMNPTIRVI

VAPGEYCATEGAMTGAQTLQFLSQFTADYTLLGASGIAADGPSEALIDSGTVYRAMIQRAAKSIVVADHS

KFDLTYPYHYAGWSGISRLITDQPLPDHLATVLGREKVVVARGHAAPEQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004898677.1\_3189 [locus\_tag=BN49\_RS17535] [protein=isopenicillin N synthase family oxygenase] [protein\_id=WP\_004898677.1] [location=complement(3242890..3243879)] [gbkey=CDS]

MNATTQNQRYALQELEKEALMGAEGEEIFAREVRCIDLSNFAARKNDIAEQLWEAAVEIGFFQVSHHGIP

LADIRQAFSMTEAFFDLPDEVKRQYPLAGNAGWESKAQVRPSTRTPDQKESYQITRPLMAGRWPSDRELP

AFQQTMLGFESQCWQLGMKILSCFALKLGFPESFFTTAHDPQRDTYQSTLRMLHYYATEQSQQGMWRAGA

HTDFDCLTLLFQRPGQGGLQVCPGKDRESQQWTSIEPREEVITCNIGDMLMRWSDDQLPSNFHRVRNPLP

HEYQGPRYSLAFFCQANKDVEILGPQRKYPPISAEDYLQQRIQANFAKG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043442.1\_3190 [locus\_tag=BN49\_RS17540] [protein=amidohydrolase family protein] [protein\_id=WP\_046043442.1] [location=complement(3243900..3245318)] [gbkey=CDS]

MSLIIKNAHAILSGLPGEAARLAGPDIRIRDGKIAAIGSLTPLPEERQIDARDCVIYPAWVNTHHHLFQS

LLKGEPQGLNQSLTAWLSATPYRFRAAFDEHTFRLAVRIGLVELLRSGCASVADHNYLYWPDMPFDTSEI

VFSEGEALGMRIVLCRGGATQGRAVEQDLPVALRPETFDSYMADVERLVSRYHDPRPESLRRVVMAPTTV

LHSAPGAQLREMAKLARQLRIRLHSHLSETVDYLDAARQKFAMTPVQYCAEHDWLGNDVWYAHLVKLLPE

EIALLGRTGTGIAHCPQSNGRLGSGIADLLALEQAGVPVSLGVDGAASNEAADMQSEAHAAWLLQRARKG

MLAQPRYAGGTFEGGADAATVEDVVRWGSAGGAQILGLAQSGTLQVGMQADLAIYRLDDPRYFGLHDMAI

GPVACGGRAALKALLLNGRPIVEDDAIPGLDLDAMRHDALAAVRTLQQRAAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529197.1\_3191 [locus\_tag=BN49\_RS17545] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016529197.1] [location=complement(3245330..3246319)] [gbkey=CDS]

MKTGARLPRGIRWLGLMALGSVSLAVQAEEKIVLLTSWYAQAEQGGYYQAQATGLYKKYGLDVEIRSGGP

QVNGMQLLLSKRADVIIGYDLQLLEGIQRGFQAKAIAAPFQYDPQGLLTHADVTSLQGLKDKTLLVSSSG

QATWWPWLKAQYQLSDAQVRPYTFNIQPFVVDDAVAQQAYVSSEVFQVQKAGVKAHFFLFSEHGYPPYGG

ILIARPDTIAERKAAMAKFVRASMEGWVSYLKDPAPGNALIKQDNPKMTDDLLAWGVTQIREHHLIDGGD

AASQGWGTMTDARWQKTRDFMVSAGLLAAATDWKQAYTTEFVQAMQVKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002908057.1\_3192 [locus\_tag=BN49\_RS17550] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002908057.1] [location=complement(3246614..3247513)] [gbkey=CDS]

MFAFSRFLLYFTEVARQGSFRKASEALHVSASSIDRQILRVEQELAMPLFERHPTGLRLTAAGELLLHAA

NNWKKDFTRVCEQLDDLRGLRRGHVRIATIDAINRHFFSTMLKEVHKHYPNISFTLTTINNIHIQQALIS

GEADFGIMLNPQTSRELQVRAFAEMNMGIVVPTGHPLASRSAVRFSQCLDYPFILPSAPLMISEPVEALV

NISGNEVKEVAVSNNIHMIRTLIKEQMGIGILCRLDILDEIESGQLAFVPLTDPQLKPFTLALCVSPARQ

LSLAASMMLNQLEMLFSQL

>lcl|NZ\_FO834906.1\_prot\_WP\_004199282.1\_3193 [locus\_tag=BN49\_RS17560] [protein=PDR/VanB family oxidoreductase] [protein\_id=WP\_004199282.1] [location=3247721..3248689] [gbkey=CDS]

MHSHDLISVSVGEIRPNGQGNLSLILQAAAGEILPAYSAGAHIDIIIPGVGPRQYSLCGTPDRSNTYEIC

VRLTDASTGGSRYLHQQLKAGDRLAISPPRNHFPLPQAGRYLLFAGGIGITPLLAMAEAIAARKGALELH

YYVASSRQTAFSPRLNQLTANGTVAIHCSEEGASLRQRVPECLTVPHPDTAVIACGPEGFIQRLRSVMEE

YRWSPSQFVFERFTPAAENNTAAKNAFYIELASSGQRLQVAADQTIAQVLQHAGVEVMLSCEQGMCGSCI

TGVLDGIPEHRDSVLTAEEKAGNDQITLCCSRAKSPGLVLDL

>lcl|NZ\_FO834906.1\_prot\_3194 [locus\_tag=BN49\_RS17565] [protein=amidohydrolase family protein] [pseudo=true] [location=3248701..3249938] [gbkey=CDS]

MTLPSSCAPLTGISRARLPAWALPDGWPTQANGEPLLADLAFRDSRIAALTPTDQPTPGLWDLAGALTLP

GLVEPHAHLDKTFTIERCRPAQAGLLPAIHAMHEDRRHWSRADIQRRASTALARAAANGVTHLRSHVDWF

TADAPDAWQEIARLDTVGLTLERVALVPLPLFREPAQAEAIARTVANSGERCLLGGFIHSSNWDATAMEN

LLYSAARWDLDLDLHIDEELSEVSQGLTWLADHLSRHPFPGHICCSHGCALAAGSDEQAAPILRQLAAHG

VTLIALPMTNLLLQDATFGRTPRQRGITLLHEAQAAGVATLLGCDNVQDVFCPAGSYDPLDTLACGLFSA

QLSDLFDRQSRRLLPSGRRPA\*\*FSRVATVLPGL\*TAPPVWWLTTAG\*PTGACGRRRWHMSL

>lcl|NZ\_FO834906.1\_prot\_WP\_016528844.1\_3195 [locus\_tag=BN49\_RS17570] [protein=RidA family protein] [protein\_id=WP\_016528844.1] [location=3249928..3250407] [gbkey=CDS]

MSLEAGAGAPLARYAAWRRAGDFIFLSGIIPVNPLTGTIVNGFQDVPEPVRELLGATGEFSTDAKQGPIL

AQSWYVLESIRRTVASAGGQMSDVIKLVQYFRNLDHFPYYSRVRKLFYPDQPPVSTVLQVSEMLPDATVL

IEVEATVWLPPSFNSEAPR

>lcl|NZ\_FO834906.1\_prot\_WP\_016528843.1\_3196 [locus\_tag=BN49\_RS17575] [protein=creatininase family protein] [protein\_id=WP\_016528843.1] [location=3250404..3251285] [gbkey=CDS]

MINGYIPAARFLPFLSWTDVAALPDKSNTVIVLPTGAIEQHGLHLPCSVDSVISSGVAGHALARLPATIP

AYAIPPIVYGKSEEHLHFPGTLTLSGDTLLHTLLEIAESLYRAGFRKLLMINGHGGQPQILQIACREMRL

RHGDFIAIPHDVFNVPNCEKQFLSPHEQRMAMHAGHSETALMLALAPECVHMERAVANFPPEFPCPTLSK

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SLPPSFAAESREP

>lcl|NZ\_FO834906.1\_prot\_WP\_004184312.1\_3197 [locus\_tag=BN49\_RS17580] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004184312.1] [location=3251285..3252268] [gbkey=CDS]

MNTRLTPVFTLLTVAALATSASCFAAEKFTFLTNWYAQAEHGGFYQAQATGLYQHAGLDVEIKMGGPQIN

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FWPWAKSELGLAGSKVRPYTFNVQPFLADKNLVQQGYVTSEPFSVAKGGQPFYVYPLSDWGYPPYGNSII

CMADTIRKRPAAVAAFVKASMEGWKSYLQDPAPGNSLIGKANPQMGAEQIAFGIAQMKQYQLVTGGDAKS

GGIGIITEPRLKKTWDMLVKNKLIDASKVPFEQTYTLEMVKDAGVMP

>lcl|NZ\_FO834906.1\_prot\_WP\_016528842.1\_3198 [locus\_tag=BN49\_RS17585] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016528842.1] [location=3252265..3253095] [gbkey=CDS]

MNTAPKLTVMSDTRFMPAAATPAIEVLSAEKIYSNGTRALLPVNLTINQGEFITLLGPSGCGKSTLLKMV

AGLVEPSDGKLMLWRRDSREKAQHPLSFVFQEATLMPWSSVRNNVRLPLDLAGVPRAEGNTRVSEVLELV

GLGKFADVLPRELSGGMQMRVSIARGLVTRPKLLLMDEPFGALDEITRNKLDSDLLRLWQEQNLTVVFVT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528841.1\_3199 [locus\_tag=BN49\_RS17590] [protein=ABC transporter permease] [protein\_id=WP\_016528841.1] [location=3253097..3253912] [gbkey=CDS]

MKNTTATPWIQHPRFLKILYPTLVAVAMVLLWQGAVSYFRTPAFLVPSPLVMLESLWTHLTPLLLALLFT

LKITLISFLLSIVIGAAVAFILVQNRFVETALFPYIVFLQVTPIVAIAPLIIIWVKDATLSLVVCATLMA

VFPIISNTTQGLRSVSPGLLSYFRLNHASRWQTLVRLRIPSALPYFFGALRISSGLSLIGAVVAEFVAGT

GGTNTGLAYQILQAGYQLDIPLMFAALLLISLAGIALFGVMSWVSRRALSAWHESEAVQSH

>lcl|NZ\_FO834906.1\_prot\_3200 [locus\_tag=BN49\_RS17595] [protein=FAD-binding oxidoreductase] [pseudo=true] [location=3253939..3255326] [gbkey=CDS]

MMTDEQRQHAVAAIQQALPALEWTLQPAKIKRLSRDFHWFSPLLTEQLAGKQADAVVRPRDEEELRQLVC

AAAPPATTDSWSPSKAGCWWI\*PGSTRSSPSATAQ\*GPRPAFAWRTLKPPPARRVGSCAVCHRPIDWRAW

AVSTAAGSAVSAPSTMGRWRRPAMCSASK\*\*PSSRSPAC\*PSRLPKRCCCITPTAPTALSWRLSWRWHLR

TSGLNVWTCLTISPMR\*TMPTPASARRGW\*SARWRCWPRRLPIILATSTIVIAPGSMRLSA\*SPRRAKDS

APACYSAIAGATPSVRPATRPGRKTPR\*WNTAGTIPPCMRSRWTIR\*LISRRRLIRCAIRSKFYRWSSTS

PGR\*FPILNSCAISKATSPPAVCSWCAIPRPRGSTPSCRYFATTTSRLTTPTCCRLRTANRA\*FAPTSWR

\*NSLSTRRDCLTPASCAAGRCATSWNWTATRWREPPAKAPRP

>lcl|NZ\_FO834906.1\_prot\_WP\_015958547.1\_3201 [locus\_tag=BN49\_RS17600] [protein=hypothetical protein] [protein\_id=WP\_015958547.1] [location=3255711..3256187] [gbkey=CDS]

MSDAISSQLENIITMLIAISIASERLVEIIKGYFPWLNLENQDPVIEGRRKSALQILAVVAGIVTAFLTQ

PFVAGSFSAIKHPDLMTLCIGLMASGGSAFWNVILNYLLQVKNLKKQQVSSVKTDPVADPAPPSPVHQDV

VHGAEPVSSNPCFNPEGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528804.1\_3202 [locus\_tag=BN49\_RS17605] [protein=hypothetical protein] [protein\_id=WP\_016528804.1] [location=3256189..3256425] [gbkey=CDS]

MVWRVAKSLLILRDQINQYAPHRNTDSDGTIGDEHHAHTNSDHNPQVIDGNIGVVTAIDITHDPQHKCDA

QAIVRLAP

>lcl|NZ\_FO834906.1\_prot\_WP\_115217266.1\_3203 [locus\_tag=BN49\_RS17615] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_115217266.1] [location=join(3256501..3256816,3256816..3257729)] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_WP\_218976471.1\_3204 [locus\_tag=BN49\_RS17620] [protein=hypothetical protein] [protein\_id=WP\_218976471.1] [location=3257714..3257953] [gbkey=CDS]

MSGNIGANPIVDALVASKDKRIKYIIWNKRIISASVQPWVWRDYHGVSPHDKHFHLSVVPVKALYDYTLP

WLLFNPHKE

>lcl|NZ\_FO834906.1\_prot\_WP\_023301844.1\_3205 [locus\_tag=BN49\_RS17625] [protein=hypothetical protein] [protein\_id=WP\_023301844.1] [location=3257986..3258285] [gbkey=CDS]

MTQQIDIEKIKAALNAIEELEQIARSTQPADIKNFCVEYNKTWKKKVDTLLALIDEPISSLLVKLVPYLP

TLLVIINMLKAGVEQYCQLHLAEEPPVDK

>lcl|NZ\_FO834906.1\_prot\_WP\_023278927.1\_3206 [gene=chrA] [locus\_tag=BN49\_RS17630] [protein=chromate efflux transporter] [protein\_id=WP\_023278927.1] [location=complement(3258376..3259743)] [gbkey=CDS]

MSKTVVLPQSDSPSVVASVPFWQAIRFWLKLGFISFGGPAGQIAMMHQELVDNRRWISEGRFLHALNFCM

VLPGPEAQQLATYIGWLMHKTWGGVIAGVLFILPSLVLLIALAWIYLVWGDVAVVAGIFYGIKPAVAAIV

LQAAHRIGSRALKNGAYWAIAAAAFVAIFALNVPFPLIVLAAALVGFIGGRLAPTIFGKADAHRAQSHPG

GAAIIDDTTPIPAHAIFSWRRTSQVLIAGMLLWLVPMAALTLMLGWAHPLTQMSWFFTKAALMTFGGAYA

VLPYVYQGAVTHYGWLTAGQMMDGLALGESTPGPLIMVVTFVGFVGGYTKAVLGVDDVLLGGIAAACLVT

WFTFLPSFIFILAGGPFIETTHNKVGFTAPLTAITAAVVGVILNLALFFIWHSVWGPSGFDPWSAAIALG

AAGLLFRYKWKLTWVLAAAAAVGLIVHMAGLSGAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016531581.1\_3207 [locus\_tag=BN49\_RS17635] [protein=chromate resistance protein] [protein\_id=WP\_016531581.1] [location=complement(3259712..3260680)] [gbkey=CDS]

MHLLILNLTTSQATLRMRVWRTLKQSGAVVLRDGVYMLPDVRQGYDTFLSACQAIRAEGGAGYVFTIESA

EEEALRPLFDRREQYDALLQDLQDLQALQGALSADGLAAQLKQLRKIQRDYRRIEAIDFFPGAAREQAAE

RLATLEQAINQRLSPDEPQAVAGELSLLDREAFRGRLWATRRRPWVDRLASAWLIQRFIDPEARFLWLAA

PEDCPATAVGFDFDGAPFSHVGTRVTFEVLVRRFALEAAIPDALGRLIHFLDVGGEPTPEAAGVESILAG

LRETITDDDQLLAAACSLFDGLLKSCEMRSGNHEQNGRSSAE

>lcl|NZ\_FO834906.1\_prot\_3208 [locus\_tag=BN49\_RS17640] [protein=MFS transporter] [pseudo=true] [location=complement(3260810..3262000)] [gbkey=CDS]

MSTEHMLPLAVQNKNIFRLAAAQALAGANSVVFYATGAIVGNAIAPSPSLATLPITLFVLGMAASILPFG

ALARTRGRKAAFRLGTGAGMVTGLAAALAVVLGSFLLFCFAAMLGGAYAAVALSFRFAATDGVAPERRAR

ALSLVMGGGVAAGIIGPMLVTGTMHLWPTHTFAFTFLAQALVAALAAILLAGVTSAEPAASSVRGGRPLR

EIVRQPGFATTVFSGAVAYMVMNFLMTAAPLSMHMHGLSQQAANLGIQWHVMAMYGPGFVTGRLIQRFGA

VRMAAGLLITGASVAVGLSGVGVYHYWLSLILLGIGWNFGFTGASAKIIDFHRPEEKTQV\*SLNDFLVFG

VMIVGSFSSGVLLNAFGWNAVLWGSLAPVGVALFTLLLRPLSPPRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004175772.1\_3209 [locus\_tag=BN49\_RS17645] [protein=tautomerase family protein] [protein\_id=WP\_004175772.1] [location=complement(3262187..3262435)] [gbkey=CDS]

MPFVNVQTIKGIMTAEQKSELLRRMTDLLVEIEGQGDPQFRQSVWIRIDEHDPEQWSLGGVQPTAAMIAA

KFAAARRDGSPE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531583.1\_3210 [locus\_tag=BN49\_RS17650] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_016531583.1] [location=3262496..3262957] [gbkey=CDS]

MSKNKSLPYLDPALCGLAEGAKILGDRWVLLILREAFYGVTRFETMLSHTHITRQTLTTRLKTMTETGLL

SKVPYREAGSRERYEYVLTDKSRSLALVLFALMEWGHQHVLHSAPHIALVDSASGEAVHPGFITASGAVA

SPAALQIVKADER

>lcl|NZ\_FO834906.1\_prot\_WP\_046043446.1\_3211 [locus\_tag=BN49\_RS17655] [protein=MFS transporter] [protein\_id=WP\_046043446.1] [location=3263135..3264352] [gbkey=CDS]

MSLRSLRALCLTSFFIADVRDGLGPFLGIFLTQRHWQAEDIGLLMSVGGIAGLLATLPAGFITDSSRHKR

LLLAGVCLVITLTTLLLWFSQKTSVVALSQVASGICAAFVGPLIAGITLGLARQRGFSAQMGKNEAFNHA

GNFFTALMAGAIAWYWGIGGIFILMACTTLLTLVALLAIRGGDIDDDAARGIEAASTPSLPGFAILFRHT

PLLIAGVTLMLFHLANAALLPMLSMRIAAAPGHLNPGLFAAATVIISQVVMIPVAIRVAGSIDKYGYWRC

ILLALVIMPIRAALAASSDAPAMMVPVQILDGLAAGILGVAVPSFIVLLLRGSGHVNAGQSVVMLMQGAG

AAMSPALTGSIAGHYSFATAFGVLSVIAIVALMVWWRSAQLLTASASPPIGESGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004145368.1\_3212 [locus\_tag=BN49\_RS17660] [protein=DUF535 family protein] [protein\_id=WP\_004145368.1] [location=complement(3264435..3265343)] [gbkey=CDS]

MEHTVAGAIKEWRKHNKVIGQVKISYKKILRKCRELSLAGGKYREYQGLCAKYQCARLTAVTKGLVPFED

KPFKAYLNKRLSKRRKLDIAHGSLNFIEKTFHPDVLPQLYNVADFGREMFSIPLKNGDKLDVKLLASPFQ

EEGELMLQLFLGDRRVYSVCFSCTDDGRAYIGGIQGGKDITNDEVKVLTKELHGARPKNIIMSVLYGLLR

YFNISTVYAIDSDYHVKSDLVKASYSSLWLEMGGEKQARGWYKLPAQEIKKSIEEVKSKHRSQFIKREGL

KELIQINMANALQQITLSARVN

>lcl|NZ\_FO834906.1\_prot\_WP\_002908189.1\_3213 [locus\_tag=BN49\_RS30485] [protein=hypothetical protein] [protein\_id=WP\_002908189.1] [location=3265633..3265773] [gbkey=CDS]

MEIDLDNLVFSGLDEAEERNAERLEEADKKAQAIVADDDCGDACKI

>lcl|NZ\_FO834906.1\_prot\_WP\_004180250.1\_3214 [locus\_tag=BN49\_RS17670] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004180250.1] [location=complement(3265818..3266708)] [gbkey=CDS]

MRMSVKQLRAFLAVAHTLNFAHASERLNLSQPALSLTIKGLEEALGGALLQRSTRKVTLTQEGELFLPMA

RQLLADWDNVEEAMRQSFTLQRGKISVAAMPSFAANVLPEALKAFRDRYAGVNVTVHDVINEQVIEMVRE

GRVEMGIAFEPSPNHNLLFTPLAVDRFVAIVPQQSPLAKKKQLSWQELLTLDFITLQRPSAVRLMLEEAL

ARSGRQLDVALESHQLVTVGRMVASGLGGSAVPALCKTQMASLGAVCIPLSDPPIEKCVGAIHAGHLPLS

KAAQALLDTLKGFLPT

>lcl|NZ\_FO834906.1\_prot\_WP\_004175762.1\_3215 [locus\_tag=BN49\_RS17675] [protein=CoA transferase subunit A] [protein\_id=WP\_004175762.1] [location=3266849..3267556] [gbkey=CDS]

MAGLDKRVASYEAALEGLTDGMTLLAGGFGLCGIPENLIAEVQRRQVQGLTVVSNNCGVDGFGLGMLLES

RQVSKVVASYVGENALFEQLVLSGELAVELTPQGTLAEKIRAGGAGIPGFYTATGYGTPVAEGKEVRQFD

GRHYILEEAIRGDFALVKGWKADWYGNVVYRHTAQNFNPLMATAGRITVVEVEEIVPPGELPPSAIHTPG

IYVDRLIVGQFEKRIEQRTLRAGGH

>lcl|NZ\_FO834906.1\_prot\_WP\_002908192.1\_3216 [locus\_tag=BN49\_RS17680] [protein=CoA transferase subunit B] [protein\_id=WP\_002908192.1] [location=3267558..3268214] [gbkey=CDS]

MLTREQMAMRVAQELRDGDYVNLGIGIPTLVANYIPAGIEVMLQSENGLLGMGEFPDEETIDADMINAGK

QTVTAQTGAAIFDSAQSFAMIRGGHVDLTVLGAFEVDVAGNIASWMIPGKMVKGMGGAMDLVAGAQNIIV

VMTHASKNGESKLLPQCTLPLTGVGCIRRVLTDLALLEIVDGAFVLREVAPGVSPDEVIRKTAGRLIVAD

DVREMRFS

>lcl|NZ\_FO834906.1\_prot\_WP\_032420148.1\_3217 [locus\_tag=BN49\_RS17685] [protein=acetyl-CoA C-acetyltransferase] [protein\_id=WP\_032420148.1] [location=3268224..3269405] [gbkey=CDS]

MTDIAIVAAVRTPIGSFRGAFAPLSAVDLGAAVVRGLLERCQLPAAAVDELIFGQVLTAGCGQNPARQTA

LRAGLPVDTPAVTVNLVCGSGLKAVQQAVQAIRCGDAGIVIAGGQESMSNAPYLMHGARDGLRFGHASLQ

DSMIQDGLWDAFNDYHMGITAENLADAFDISRERQDAFAASSQRKAAAAIAAGRFREEIVPVSVPQGKKP

PRVVTDDEQPRPETSEQQLAQLRPAFRPADGSVTAGNASSLNDGAAAVLLMRVDKARELGLPVLARIVSS

AVAGVDPSVMGIGPVSACRQALQRAGWTLDEVDLIEANEAFAVQALAVGQLLEWDSEKVNVNGGAIALGH

PIGASGCRILVSLVHEMQRRGASKGLATLCVGGGQGIAMTLQR

>lcl|NZ\_FO834906.1\_prot\_WP\_023282682.1\_3218 [locus\_tag=BN49\_RS17690] [protein=3-hydroxyacyl-CoA dehydrogenase family protein] [protein\_id=WP\_023282682.1] [location=3269417..3270340] [gbkey=CDS]

MFTPRLAVLGAGLMGVGIACHFARHGHAVRLYDTDPQRLAEVPAVASAILRELEASGQQDPADRDAVLAR

LTPTPTLNALADATLLIEAIPERLALKHALYAELETLIADETIIASNTSGLPPDRLAQGMRHPERLLIAH

FWHPPHLIPLVEVVPGSATLPHLARQVSDFCAACALEAVVLNRAAPGFVGNRLQFALLREALHIVHSGIA

SPEVVDQVMRASLGRRYAMVGPLEAADMTGLATVQDICQHLLPELASGTEMMSLVAEKVARGDTGARSGQ

GFYRWDEARHQRIQSRREHQLRFALKP

>lcl|NZ\_FO834906.1\_prot\_WP\_198409054.1\_3219 [locus\_tag=BN49\_RS17695] [protein=GntP family permease] [protein\_id=WP\_198409054.1] [location=3270385..3271779] [gbkey=CDS]

MMSVIIALAALALLMLAAYRGYSVILFAPIAALGAVLLTDPGAVGPAFTGLFMEKMVGFVKLYFPVFLLG

AVFGKLIELSGFSRSIVAAAIRILGRRHAIPVIVLVCALLTYGGVSLFVVAFAVYPFAAELFRQSGIPKR

LIPATVALGAFSFTMDALPGTPQIQNIIPTSFFGTNAWAAPWLGLIGSLFIIIFGLLWLERQRRKAQARG

EGYGTDLQNEPETPDDIDLPHPLIAIAPLLLVGVLNLLFTHWIPQWYGASHELNLPGLAKPVVTEVGKIT

AIWAVQAALLSGIVLVLVCGYRNIRGRLAEGSRTAVGGAILAAMNTASEYGFGAVIAALPGFLVLSKALA

AIPNPLLNEAISVTALAGITGSASGGMSIALAAMSETFVAAAHAANIPLEVLHRVAAMASGGMDTLPHNG

AVITLLAITGLSHRQAYGGIFAITVIKSLAVLFVIATFYVTGIV

>lcl|NZ\_FO834906.1\_prot\_WP\_004189574.1\_3220 [locus\_tag=BN49\_RS17700] [protein=3-hydroxybutyrate dehydrogenase] [protein\_id=WP\_004189574.1] [location=3271803..3272573] [gbkey=CDS]

MNLHGKTALVTGSTSGIGLGIAKVLAQAGAQLVLNGFGDSSHARAEVAALGKIPGYHDADLRDVGQIEAM

MHYAESTFGGVDIVINNAGIQHVAPVEQFPVDKWNDILAINLSSVFHTTRLALPGMRQRNWGRIINIASV

HGLVASKEKSAYVAAKHAVVGLTKTVALETARSGITCNAICPGWVLTPLVQQQIDKRIAEGVDPEQASAQ

LLAEKQPSGEFVTPQQLGEMALFLCSDAAAQVRGAAWNMDGGWVAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530164.1\_3221 [locus\_tag=BN49\_RS17705] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530164.1] [location=complement(3272593..3273465)] [gbkey=CDS]

MELRYLRYFVAVARTRHFTQAAKELGISQPPLSQQIQRLEREVGTPLFRRLTRGVELTEAGESFYEDARQ

ILAMSDAALEKAKGIARGMNGSLSLGITSSDAFHPQIFTLLHRFQLDHPGVTLHQMEDNMANLMAALSEA

ELDIAFVRLPCESSKAFNLRIIDEEPMVIALPRDNPLATQPTLALEQLRDVAPILFPREVAPGLYELVYN

SCLRAGIDMERAWQSSQISSSLSMVNAGFGFALVPQSMTCIQQPNVSYHPLSGAPLKTDIAIAWRRFERS

RTVKRFLAMF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530165.1\_3222 [gene=budA] [locus\_tag=BN49\_RS17710] [protein=acetolactate decarboxylase] [protein\_id=WP\_016530165.1] [location=3273572..3274351] [gbkey=CDS]

MNHSAECTCEESLCETLRAFSAQHPESVLYQTSLMSALLSGVYEGSTTIADLLKHGDFGLGTFNELDGEL

IAFSSQVYQLRADGSARNAQPEQKTPFAVMTWFQPQYRKTFDHPVSRQQLHEVIDQQIPSDNLFCALRID

GHFRHAHTRTVPRQTPPYRAMTDVLDDQPVFRFNQREGVLVGFRTPQHMQGINVAGYHEHFITDDRKGGG

HLLDYQLDHGVLTFGEIHKLMIDLPADSAFLQANLHPDNLDAAIRSVES

>lcl|NZ\_FO834906.1\_prot\_WP\_004175750.1\_3223 [gene=alsS] [locus\_tag=BN49\_RS17715] [protein=acetolactate synthase AlsS] [protein\_id=WP\_004175750.1] [location=3274361..3276040] [gbkey=CDS]

MDKQYPVRQWAHGADLVVSQLEAQGVRQVFGIPGAKIDKVFDSLLDSSIRIIPVRHEANAAFMAAAVGRI

TGKAGVALVTSGPGCSNLITGMATANSEGDPVVALGGAVKRADKAKQVHQSMDTVAMFSPVTKYAVEVTA

PDALAEVVSNAFRAAEQGRPGSAFVSLPQDVVDGPVSGKVLPASGAPQMGAAPDDAIDQVAKLIAQAKNP

IFLLGLMASQPENSKALRRLLETSHIPVTSTYQAAGAVNQDNFSRFAGRVGLFNNQAGDRLLQLADLVIC

IGYSPVEYEPAMWNSGNATLVHIDVLPAYEERNYTPDVELVGDIAGTLNKLAQNIDHRLVLSPQAAEILR

DRQHQRELLDRRGAQLNQFALHPLRIVRAMQDIVNSDVTLTVDMGSFHIWIARYLYSFRARQVMISNGQQ

TMGVALPWAIGAWLVNPERKVVSVSGDGGFLQSSMELETAVRLKANVLHLIWVDNGYNMVAIQEEKKYQR

LSGVEFGPMDFKAYAESFGAKGFAVESAEALEPTLRAAMDVDGPAVVAIPVDYRDNPLLMGQLHLSQIL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043453.1\_3224 [locus\_tag=BN49\_RS17720] [protein=(S)-acetoin forming diacetyl reductase] [protein\_id=WP\_046043453.1] [location=3276064..3276834] [gbkey=CDS]

MKKVALVTGAGQGIGKAIALRLVKDGFAVAIADYNDATAKAVASEINQAGGRAMAVKVDVSDRDQVFAAV

EQARKTLGGFDVIVNNAGVAPSTPIESITPEIVDKVYNINVKGVIWGIQAAVEAFKKEGHGGKIINACSQ

AGHVGNPELAVYSSSKFAVRGLTQTAARDLAPLGITVNGYCPGIVKTPMWAEIDRQVSEAAGKPLGYGTT

EFAKRITLGRLSEPEDVAACVSYLASPDSDYMTGQSLLIDGGMVFN

>lcl|NZ\_FO834906.1\_prot\_WP\_004200175.1\_3225 [locus\_tag=BN49\_RS17725] [protein=hypothetical protein] [protein\_id=WP\_004200175.1] [location=3277229..3277870] [gbkey=CDS]

MISVIKDLFSNQVVSAVILTIIGAITKKYIQFHRRDFFSRSSSEQIKAVEWLRTSSVPISDPLAKAEQQF

RLQSFGLHRDWHLSYKIICLSSDYAQSLIPSLKAVLRYQGMYTITNGNIYPHKFHKWIIPFVLISLLLYI

GAEIYRGSSQSDGIEILKSLYVVIVAFIVWCWVAACALRVSSISKKLNAYIPPANDFKSKTYDFSSILNN

RYP

>lcl|NZ\_FO834906.1\_prot\_WP\_004189572.1\_3226 [locus\_tag=BN49\_RS17730] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004189572.1] [location=complement(3277999..3278535)] [gbkey=CDS]

MTIITTQRLIIRHFKEEDAAALFDYLSSPRTPCFKDEKLHSLAEAEVDVAKRASDPTQFAVCLKETDTLI

GHLFADNSNEPDNNTWSVGWHFNQRFEHQGYASESVAALFDYLFKVKGARRLYAWVEDYNYSSQKLCERL

LMRREGCFKEFVSFENEEGKARYDDTYIYALLHKEWTK

>lcl|NZ\_FO834906.1\_prot\_WP\_004151177.1\_3227 [gene=kexD] [locus\_tag=BN49\_RS17735] [protein=multidrug efflux RND transporter permease subunit KexD] [protein\_id=WP\_004151177.1] [location=complement(3278611..3281727)] [gbkey=CDS]

MPHFFIERPIFAWVIALFIVLTGLLSIPRLPVAQYPEVAPPGIIISVSYPGASPEVMNTSVVSLIEREIS

SVDNLLYFESSSDTTGMASITVTFKPGTDIKLAQMDLQNQIKIVESRLPQSVRQNGINVEAANSGFLMMV

GLKSPSGAYQEADLSDYFARNVTDELRRVPGVGKVQLFGGEKALRIWLDPMKLHSYGLSVTDVLSAISQQ

NVIVSPGRTGDEPATSSQEVTYPITVKGQLSSVEEFRNITIKSQVSAARVTLADVARVESGLQSYAFGIR

ENGVPATAAAIQLSPGANAISTASGIRARLTELSGVLPEGMTFTVPFDTAPFVKLSILKVVETFVEAMVL

VFFVMLLFLHKIRCTLIPAIVAPVALLGTFTVMLLSGYSINILTMFGMILAIGIIVDDAIVVVENVERLM

EDKKMSPQDATREAMREITPAIIGITLVLTAVFIPMAFASGSVGIIYRQFSISMAISILLSAFLALTLTP

ALCATLLKPHGIHQGKSSVFSAWFNAHFHRLTSFYATGLGFVLKRTGRMMMIYAALCLALFAGLSTLPSS

FLPDEDQGYFMSSIQLPSDATMQRTLKVVDTFEEEIAHRQAVESNIMILGFGFSGSGQNSAMAFTTLKDW

RQRKGTTAQEEADHIRSQMANVPDAVTMSLLPPAISDMGTSSGFTYYLQDRGGKGYQALKKAADELIVQA

NHNPHLADVYIDGLGEGTSLSLHVDREKAEAMGVSFDEINQTISVAAGSNYVNDYTNNGRVQQVIVQADA

PYRMQPEQLLALSVKNRLGQMLPLSTFVTLSWNVAPQQLIRYQGYPAIRITGSSAQGKSSGTAMAAMDNL

AKHLPPGFAGEWAGSSLQEKESASQLPGLIVLSVLVVFMVLAALYESWSIPFAVMLVVPLGLLGAVLAVS

VTNMTNDVFFKVGLITLIGLSAKNAILIIEFARQLMKEGKSLIDATLTAAKLRLRPILMTSLAFTLGVVP

LMLASGASDSTQHAIGTGVFGGMISGTLLAIFFVPVFFVTITRFTGMRKYRLGNSRNG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151176.1\_3228 [locus\_tag=BN49\_RS17740] [protein=ABC transporter six-transmembrane domain-containing protein] [protein\_id=WP\_004151176.1] [location=complement(3281765..3282649)] [gbkey=CDS]

MAPGVAISLKRLAWRHRKKLCITFMLVIAENVAFLLYPVLAGMAINAILGGQTSHAALYGLMVLFMWCMG

AARRSVDTRTFARIYASLAVTVVLSQRKYSLNHSTIAARVTLSREFVDFFELHLPVLITSIISLFGAAIM

LLWIEFWTGIACLIIVAILMCFVSSYASKNETFYRRLNNRLEKEVDYVNKASFGALKRHYDTLARLRVVL

SDREAWGYLSIGLLVSALFSMTIIRMSMESGINAGHIYSVMTYMWMFATSLDDAPQLLEKFSQLRDIGKR

VSTDDETSLSGKPC

>lcl|NZ\_FO834906.1\_prot\_WP\_032448046.1\_3229 [locus\_tag=BN49\_RS17745] [protein=transporter] [protein\_id=WP\_032448046.1] [location=complement(3282879..3283268)] [gbkey=CDS]

MVLTKCFFRRENLMASLLFCIVSYGLLSTWLYLVHSINEKVESTLPSSLLIRVLIIITALSFIIQKKPGV

FKNFIAITFGLILLFIHTIIVLHLLLNTFPDIYDFVFYYEFFLMVFFCGLPLCLCIRMV

>lcl|NZ\_FO834906.1\_prot\_WP\_004151175.1\_3230 [locus\_tag=BN49\_RS17750] [protein=response regulator] [protein\_id=WP\_004151175.1] [location=3283551..3284255] [gbkey=CDS]

MNNNNLIIVAEDDDDIAAILTGYLRKAGMKTLRAEDGEQAINLTRLNKPDLLLLDIHLPVYDGWNVLTTL

RKETNVPVIMVTALDQDVDKLMGLRLGADDYVIKPFNPSEVIARVEAVLRRTRPVAESTHSRPLRTPFLT

IYPDEFYVEITAQGEVSTPVLTTTEFKLLTYLARNPRKVCSREELLDACLPEGDSLDRTVDSHMSKLRKK

LEHAGLKGIPESIRGLGYRLGDKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004184324.1\_3231 [gene=ccrB] [locus\_tag=BN49\_RS17755] [protein=HAMP domain-containing histidine kinase CrrB] [protein\_id=WP\_004184324.1] [location=3284252..3285313] [gbkey=CDS]

MNKETILSRQILTYMLLLTFVIIAIAILGSYLFYSFLIYYLPGGMNEGSEDAMTFLDWMWILMASITSLV

VALFFTVKLSARIFNPLNDVAYSLKQISQGNLSARAFNSSSKLGEMNRLVNDFNEMAEKLQTLDAQRNLW

NAAIAHELRTPVTILRGRLQGLVDGVFEPEPSLFRNLLKQTEGLTNLIEDLRVVSSSGGAGYSLMLSEVD

LKATISNALDTFWPDFDKKHFKIVTEINQQYCVCDPLRIIQCLTVLFDNALKYSTSQTLLIKNGITGNDN

FIIVQDQGPGIPEELQKSLFQPFQRGEYAKNINPEGCGLGLSVVKAIMCAHGGDVSYSLTPENGSLFKLS

WPV

>lcl|NZ\_FO834906.1\_prot\_WP\_004148636.1\_3232 [locus\_tag=BN49\_RS17760] [protein=glycosyl transferase] [protein\_id=WP\_004148636.1] [location=complement(3285310..3286245)] [gbkey=CDS]

MNKINYQIKYIEYLLRKCRTILTNDISFHADRLREISGTYPDLLNPVTLNEKICHRILFIHNPFYTLLAD

KLLVRQYVEKRTNLIKLIPLVGVYNRVDDIDFDKLPSKFVLKCNHDSGSAVICTDKTNIDPAKVKSKLKL

SLKKNMYYTTREWQYKNIPPVILCEMYLDLFSSKHRNITPEMIRIHCFHGVACFIEADFTDSDGNEFINV

YDRAWNLQPFQMEYPNTPLPVDEPESFHKSVIAAQDLAKEIDYCRVDLMLKGDDIYFSEITLSPKRGKLK

ITPSIWDAKLGSMWDLSLAKTGSIEPVYSCP

>lcl|NZ\_FO834906.1\_prot\_WP\_004898730.1\_3233 [locus\_tag=BN49\_RS17765] [protein=LD-carboxypeptidase] [protein\_id=WP\_004898730.1] [location=complement(3286482..3287519)] [gbkey=CDS]

MSVLFPPRLAPGDVIGVTAPSAGVPEHLHPRLELAIKNLKKRGYQVREGRCLRLQHKNKSATKFSRVEEL

MSYLTDPDIKAVMPPWGGDLAMELLDLIDFDLLSRSKPKWFVGFSDLSTLHFPLTMISGWATLHGPNLMD

LGAQKLDATTQAVWEILESNRGTVIKQYSSTAFQADENQWGTASDGGFNLTQKTQWKRLDGVTSSLTFSG

KLIGGCLEIISRLAGTPFGNVPLFKASNSPQGIILYFENVEMAPCELTRALFSLRLQGWFDNLNGVLIGR

SAAPDVSDPTKHNYLDALKAAFENIAVPVLYDVDIGHIPPQISLVNGADATVFFAENGSWVTQQL

>lcl|NZ\_FO834906.1\_prot\_WP\_016946436.1\_3234 [gene=ccmI] [locus\_tag=BN49\_RS17770] [protein=c-type cytochrome biogenesis protein CcmI] [protein\_id=WP\_016946436.1] [location=complement(3287917..3288759)] [gbkey=CDS]

MSLLVVIVALLLAGALGLLYFPWSGKGAVDRDALNRALYQSRLQELAQERGEDNPALVVELQRTLLTDIP

PQPLPGERPLNRWALFPGALLLVVLSLGLYLKTSDIGQVLLWQQAERHYPALLQQVKDPTAAPLRMDELA

ELRLGLRSHLQDTPNDLAGWQLLGRLGLLLNDGETAIGAFGRAHALAADDPAAAFDYASALVRAGDSGQV

RMGELLLRDLHQRQPNSLPVLEMLALSAVRNEDYPEAVAALQALLARLPKGDARREAIVRQLAQAQQQAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004200187.1\_3235 [locus\_tag=BN49\_RS17775] [protein=cytochrome c-type biogenesis protein CcmH] [protein\_id=WP\_004200187.1] [location=complement(3288756..3289202)] [gbkey=CDS]

MVILLALMLTGQAWAAIDTWQFKDEAQEQAFREITSQLRCPKCQNNSIADSNAMIAADMRQKVYELMQQG

KTKGQIVDYMVARYGHFVSYEPPLTAGTVLLWLGPGLFVLAGAGVIIARARRRDIPDAALTAEERQRLAA

LLQEGKER

>lcl|NZ\_FO834906.1\_prot\_WP\_004184329.1\_3236 [locus\_tag=BN49\_RS17780] [protein=DsbE family thiol:disulfide interchange protein] [protein\_id=WP\_004184329.1] [location=complement(3289214..3289768)] [gbkey=CDS]

MNRKLLFIPLVLFLALAAALFWQLMRNAEGDDPTTLESALIGKPLPEFRLEALSTPGQTLDRRTLIDGKP

LLLNVWATWCPTCRAEHQFLNGLAQQGVRVVGMNYKDDRQKAMSWLQRLGNPYRLSLYDGNGMLGLDLGV

YGAPETFLIDGQGIIRWRHAGDLNERVWREELQPLWDQYNRRAG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043461.1\_3237 [locus\_tag=BN49\_RS17785] [protein=heme lyase CcmF/NrfE family subunit] [protein\_id=WP\_046043461.1] [location=complement(3289765..3291717)] [gbkey=CDS]

MMPELGNFLLCLAAGLALLLSVYPLWGAARQDRRLMALARPLACGLFACIGGAFLLLVHAFVVNDFTVRY

VAENSNSALPVWYRVAATWGAHEGSLLLWVLLLSVWTFAVALFSRRMPLDAVARVLAVMGMIAFGFLLFI

LFTSNPFSRGLPQYPIDGRDLNPLLQDIGMIFHPPILYMGYVGFSVAFAFAIASLLAGRLDTAWARWSRP

WTQAAWMFLTLGIVLGSAWAYYELGWGGWWFWDPVENASFMPWLVGTALLHSLAVTEKRGSFRAWTVLLA

IAAFSLCLLGTFLVRSGVLVSVHAFASDPSRGLFILVLLIVAIGGSLLLYALKGGRVRARVEHTLWSRET

FLLGNNILLMAAMLVVLLGTLLPLVHKELGLGSISIGEPFFNTMFTALMAPFALLLGLGPLIRWRRDDVA

RQIKRLIIALLVTLSLSLALPWLLQDRITAMAVIGLMMALWVLIFALMEVHERATHRHGFWRGLRTLTRS

QWGMVLGHVGVAVTVIGITFSQNYSVERDVRMRPGDSIDIHRYHFVFNGVRNIVGPNWTGGEGIIAVTRN

GRPEATLYAEKRFYTASRMMMTEAAISGGLTRDLYAALGEELSDGSWAVRLYYKPFVRWIWYGGVLMALG

GLCCMLDPRYRMRKKLQEAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004143391.1\_3238 [gene=ccmE] [locus\_tag=BN49\_RS17790] [protein=cytochrome c maturation protein CcmE] [protein\_id=WP\_004143391.1] [location=complement(3291714..3292172)] [gbkey=CDS]

MQARRKTRLYIVLAVLAGLGLTVSLTLYALSSNIDLFYTPGEIIYGKTETRALPHTGQRLRVGGYVQPGS

LQRDPQTLDVRFKLYDARGVVDVSYKGILPDLFREGQGVVAQGVLDGERHITAQQVLAKHDENYTPPEVK

NAMTPEKTGAQP

>lcl|NZ\_FO834906.1\_prot\_WP\_004143390.1\_3239 [gene=ccmD] [locus\_tag=BN49\_RS17795] [protein=heme exporter protein CcmD] [protein\_id=WP\_004143390.1] [location=complement(3292156..3292386)] [gbkey=CDS]

MSPAFSSFAAFLNMGGYAVYVWLAVAVTVAAFGLLTVHTLWARRALFHEVRRQQARERRIAAAREHDKEA

ADASAS

>lcl|NZ\_FO834906.1\_prot\_WP\_016531818.1\_3240 [locus\_tag=BN49\_RS17800] [protein=heme ABC transporter permease] [protein\_id=WP\_016531818.1] [location=complement(3292383..3293120)] [gbkey=CDS]

MWKALHQLAIPERLYRLCGCWIPWLAALSALLLVIGLGWGFGFAPADYQQGESYRIMYLHVPAAMWSMGL

YLAMAVAAFVGVVWQIKMADLAIAALAPVGAVCTLVALVSGAAWGKPMWGTWWIWDARLTSELVLLFLYA

GVIALWHAFDDRRLAGRAAGILVLVGVVNLPIIHYSVYWWNTLHQSSTNLQQTIDPSMRLPLRICIFAFL

TLSVTLTLMRLRNLILQLERRRPWVVALVNKGAAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151166.1\_3241 [gene=ccmB] [locus\_tag=BN49\_RS17805] [protein=heme exporter protein CcmB] [protein\_id=WP\_004151166.1] [location=complement(3293170..3293829)] [gbkey=CDS]

MMRALLARELRLAWRSGAEILNPLWFFLIVITLFPFGVGAAPQLLAQIAPGVVWVAALLAALLVMDRLFR

DDWQDGSLEQLMLLPTPLVAVVLVKVVAHWMMSGLPLLIVSPLAALLLGMSLHDAGVLALTLLLGTPTLS

FLGAVGVGLTVGLKRGGVLLSLLVLPLAVPLLIFATAACQAAAAGLPVGGYLAMLAAFLTASATLCPFAT

AAALRLTVR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151165.1\_3242 [gene=ccmA] [locus\_tag=BN49\_RS17810] [protein=cytochrome c biogenesis heme-transporting ATPase CcmA] [protein\_id=WP\_004151165.1] [location=complement(3293826..3294449)] [gbkey=CDS]

MLHAERLTCIVDDRPLFAALTLSLAAGELLQVAGDNGAGKTSLLRILCGLARPESGVVSWQGQPLAKVRE

SFHRQLLWLGHKPGVNAALTADENLRFFFPASRLQQRESALAAVGLAGYEDLPLSQLSAGQQRRVALTRL

WLTDAPLWILDEPFTALDATAMETLTRRLEQHARQGGCAILTTHQPLRPLGCPLRTLRLGGDAGGGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004184337.1\_3243 [locus\_tag=BN49\_RS17815] [protein=cytochrome c] [protein\_id=WP\_004184337.1] [location=complement(3294533..3295873)] [gbkey=CDS]

MMKMQWLSALVLGALSCAAFAEEAPADSNLIKQGEYLARAGDCVACHTNGKAGKPFAGGLPMETPIGTIY

STNITPDKEHGIGGYTFEEFDDAVRKGVRKDGSTLYPAMPYPSFARISEADMRAMYAYFMHGVEPVNVAN

KDTDIPWPLSMRWPLAFWRGIFAPTPSDFVANPQVDPVLERGRYLVEGLGHCGACHTPRSLTMQEKALSE

SEGDDYLAGSNAPIDGWVASSLRGENRDGLGTWSEAELAEFLKTGRNDKSVVFGGMSDVVEHSLQYLSDD

DITAIARYLKSLPPRGGKQTPAPVEDSVAKDLWKGNDSKTGAALYVDNCAACHRTDGVGYKRAFPSLKGN

PVVQTEDATSLIHIVLTGSTTPAVKDAVSNLTMPSFGWRLDDQQVADVVNFIRTSWGNNAPAVSASDVAK

VRKETAAHDEKALGNADISKLPGAGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002908285.1\_3244 [locus\_tag=BN49\_RS17820] [protein=GMC family oxidoreductase] [protein\_id=WP\_002908285.1] [location=complement(3295884..3297668)] [gbkey=CDS]

MATVLKKTDVAIVGFGWVGAIMAKELTEAGLNVVALERGPMRDTWPDGAYPQVIDELTYNIRRKLFQDLS

KSTVTIRHNTSQQAVPYRQLAAFLPGTGVGGAGLHWSGVHFRVDPIELRMRSHYEERYGKNFIPQDMIIQ

DFGVTYDELEPFFDKAEKVFGTSGTAWSIKGKVVGKGRGGNAFAPDRSDDFPLPAQKNTWSAQLFEKAAL

EVGYHPYNLPSANTSDSYTNPYGAQMGPCNFCGFCSGYACYMYSKASPNVNILPALRQEKRFELRTNANV

LKVNLTDDKSRATGVTYVDGQGREMEQPADLVIIGAFQFHNVHLMLLSGIGKPYNPETGEGVVGRNFAYQ

NMTTIKAIFDKDTYTNPFIGAGGNGVGVDDFNADNFDHGAAGFVGGSPFWVNQAGTKPISGFPVPPGTPA

WGSKWKAAVADTYTHHLSMDAHGAHQSYRQNYLDLDPNYKNVFGQPLLRMTFDWQENDIKMAQFMFDKMA

PIAKAMKPKYILGSPKNANSHFDTTTYQTTHMNGGAVMGEDPKTSAVNRYLQSWDVHNVFVIGASAFPQG

LGYNPTGTVAALAYWSAKAIREQYLKNPGPLVQA

>lcl|NZ\_FO834906.1\_prot\_WP\_074187644.1\_3245 [locus\_tag=BN49\_RS17825] [protein=gluconate 2-dehydrogenase subunit 3 family protein] [protein\_id=WP\_074187644.1] [location=complement(3297671..3298426)] [gbkey=CDS]

MMSSEKTNNSRRDFLVKSMALIPTVVIGGAGAGAIGVATSATAQAAPASEPASGNTAAASDWKPQFFNDR

EWAFINAAVARLIPADELGPGAKEAGVPEFIDRQLNTPYATGSIWYMQGPFNPDVPKEMGYQLPLVPKQI

YNLGIADAEAWCQDKYHKTFAELSSEQQDEALGLWESGKAEFKQLPASLFFTYLLQNTREGFFSDPIHGG

NKGMVGWTLINFPGARADFMDWVERGERYPFPPVSINGERV

>lcl|NZ\_FO834906.1\_prot\_WP\_002908289.1\_3246 [locus\_tag=BN49\_RS17830] [protein=VOC family protein] [protein\_id=WP\_002908289.1] [location=3298928..3299299] [gbkey=CDS]

MFDHVKFGVSDYAASKAFFLQALAPLGVTLVGEGEPSYGAELAGSGDASLCLYQSAEKPAPLHIAFRADS

REQVDAFWQAALAAGGKDNGAPGLRPNYHASYYAAFVIAPDGHNIEAVCHLAG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043465.1\_3247 [locus\_tag=BN49\_RS17835] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_046043465.1] [location=complement(3299307..3300377)] [gbkey=CDS]

MIELSVENLHLTYSDNPVLKGVSMTLGRGEVVSLLGPSGSGKTTLLRAVAGLEKPTSGRIAIGNRTVYDG

TPRSEIPAEERNLGLVFQSYALWPHKTVFDNVAYPLKLRKVAAGEIKERVQRVLDQLGLGHLGNRHPHQL

SGGQQQRVAIGRALVYNPPVILLDEPLSNLDAKLREEARVFLRELIIKLGLSALMVTHDQNEAMAISDRI

LLLNNGVIEQQGTPQEMYGSPATLFAAEFMGSNNRLHGKVMALENGRARIEGASWSLWGRAGEGVSVGEP

ATAVIRVERLRLDGAAQDNSLQLPLLTSMYLGDRWEYLFRTEGDDFPLRAYGTALRDAEHCHLTLPAEDV

WIFPQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002908294.1\_3248 [locus\_tag=BN49\_RS17840] [protein=iron ABC transporter permease] [protein\_id=WP\_002908294.1] [location=complement(3300370..3302139)] [gbkey=CDS]

MNVLRRKWQGLPRGVVVCITALVIYVPLLFIVVQSFLSAPFFSRSKSWSLEAFAFIFTDPDFYLALRSGF

ILAFGLVIIAIPLGGILAFLMVRTDLPGRRIIEPLILVPIFVSPMVLGFGYVVAAGPVGFFSQWAQQLIG

FVPWNIYSMFSIVVIAGLTHVPHAYLYISSALRSVGSDVEEAARTVGATPLQVMTSVSLPMVRPSILYAC

VLLFFLGLEVFGLMLVLGDPEGNMVLATYLYKLTNKLGTPSYHLMAAVAVVLICITIPLVMLQRRLMRTA

NRFVTMKGKASQARALPLGKWRWVAGAVVVAWLTVTIGVPLLGVALRAFISNWGVGVSLWDELSLATFHN

IWQQPNLLRAIVNSMAIGIIGGALAVICYLFVGIAMHRKADNVTRFLDYSVLVPRAVPGLLAGLAFLWVF

LFVPMWLDQSLKHGWLSALPVADWLREHLIVQLRALRNTIFSVWLAYTVVWMAYGLRLISSTLLQVGPEL

EEAARSTGASRGQITRHVTVPLSRYGLIGSWLLMFLIFEREYSTGVYLLSPGTETIGSMLVSLWAAGAID

IVAALSFINILLVVIGLGIALRFGVKLHD

>lcl|NZ\_FO834906.1\_prot\_WP\_004891285.1\_3249 [locus\_tag=BN49\_RS17845] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_004891285.1] [location=complement(3302213..3303301)] [gbkey=CDS]

MYKKISGLVVSLTAVFACAAWAEVPAGYPADYQKTVDAAVKEGKVVVYSTTDTKAAGPLIKGFEAQYPGV

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TYEPVVFIYNKRLIPQNEVPDSHTALAKLIASQADKFKGKVTTYDIEKSGLGFMLAVQDSQADANYFADL

ANIAKGGLTVQSSTGTMMERVSSGENLIGYNILGSYAEARAKNDPSLGIAYPKDYVLVLSRVSFISQESE

HPNAAKLWLDYVLSEKGQQILASQADIPSIRRDIAGKNDIDGMTALLGKALKPIPVNETLLDYLQPQKRL

QFIKQWRSAAAK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043467.1\_3250 [locus\_tag=BN49\_RS17855] [protein=malate/lactate/ureidoglycolate dehydrogenase] [protein\_id=WP\_046043467.1] [location=3303604..3304614] [gbkey=CDS]

MPTGHRFLATDLHQFVVSLFTHLGSTPGEATLVADHLIAANLAGHDSHGVGMIPSYVKSHAGGFLQLNRH

ATVTKDAGAVVTLDGNAGFGQVVAHEAMQLGIEKAKQHGMAAIALRNAHHVGRIGYWAEQCAAAGLISIH

FVSVIGDPMVAPFRGKDSRFGTNPLCVVFPRAGHPPLLLDYATSAIAFGKTRVAWHKGEAVAPGCLIDAE

GRPTTDPAVMQTSPLGALLTFAQHKGYALATLCEVLGGALSGGQTTHQESLQTSVDAIFNCMTTVILRPD

AFDAPVLAPGEWEAANREARLAQGIPLDAGSWQAICAAARDVGLSESHFDRCRPLA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043469.1\_3251 [gene=fdhF] [locus\_tag=BN49\_RS17860] [protein=formate dehydrogenase subunit alpha] [protein\_id=WP\_046043469.1] [location=3304861..3307011] [gbkey=CDS]

MKKITSVCPYCGAGCKLKLVVDNNKIIRAEAADGVTNQNQLCLKGYYGWDFLKDTQLLTPRLKQPMIRYQ

KGGAFTPVSWQEAIRYTASKLKEIKEKHGPRAIMTTGSSRGTGNETNYVMQKFARAVLNTNNVDCCARVC

HGPSVAGLQQALGNGAMSNSISDIENSKCLLVFGYNCADSHPIVARRVIKARDNGAKIIVCDPRRIETAR

IADRHLQLNNGSNMALVNAFGYVLLEEELYNKTYVERYTEGLDAYREAVKDYAPEAVEGIVGVSAREIRE

AMRMFAAAPSATIMWGMGVTQFGQAVDVVRGLASLALLTGNLGRPNVGVGPVRGQNNVQGACDMGVLPNL

FPGYQEVTDPAVRAKFAAAWGIDPALMDDQVGTRITEVPHKALTGEIKAYYIMGEDPLQTEADLGLVRKG

IEALDFVVVQDIFMTKTAEMADVLLPATSWGEHGGVFTCADRGFQRFEQAIPPAGNVKRDWEIISLLASE

LGYPMHYENNQQIWDEMRELCPLFYGVTWEKMGDMGHVQWPCPTLDHPGTPWLYKDNRFDTPSGKGQLFA

TAWRAPAERPDDEWPLVLCTVREVGHYSCRSMTGNCAALQSLADEPGRVQMNPADAQRLGIADKQLVWVS

SRRGKVISRADLSDRINPGAVYMTYQWWVGACNELTQDNLDPISKTPETKYCAVKVEAIADQQWAERYAW

TAYSDMKARLKAAADV

>lcl|NZ\_FO834906.1\_prot\_WP\_021313974.1\_3252 [locus\_tag=BN49\_RS17865] [protein=M20 family metallopeptidase] [protein\_id=WP\_021313974.1] [location=complement(3307054..3308211)] [gbkey=CDS]

MAVSPSLIAEAVGWRREFHAAPELGYQEQETSRRVAELLASFGLQVHRGLAGTGVVATLENGPGPVIGLR

ADMDALPITELGSVSYRSRRAGVMHACGHDGHTAMLLAAAAHLAQTRHFSGTVHFVFQPAEENLGGARKM

VEEGLFERFPMDAIYALHNWPGIPLGEVALSDGAMMASLDAFEITLRGKSCHAAMPESGADPIVAAAQLI

MALQTIPSRRLSPQDSAVVSITQINGGEAINVLPDTVVLRGTFRCLSNRVRARVRELIERYVATQPQVSD

VQGEISWFPGYPVTKNHALQAQQVREVAVATLGAQAVRWNQAPSMASEDFACMLEACPGAYFWIGTDGET

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043471.1\_3253 [locus\_tag=BN49\_RS17870] [protein=MFS transporter] [protein\_id=WP\_046043471.1] [location=3308507..3309706] [gbkey=CDS]

MFNPDQNRLAPTLAMIMAASLVGFITGYTVPLISLELAQQQIAPLYVGLLAALPPAGMMISSFLSPALCR

RVEMGALLSGSLILLALATIASCMTTDMTLLLLPRLLTGLASGVIIVLGESWITGGAAGSQRATLTGLYA

SAFTGCQLAGPLLISVGPAWQTSALIAIVAVTAVCLLMLRHLPTGTRESLGERASWRSLGAFLPVLASGV

FCFAFFDASILALLPLYGMDKGLNEGLAVLLVTVVLTGDAMFQTPLGWLADRVGIRRVHLSCAVVFSLSL

LALPLMLGSRIQLMAICLLLGAAAGALYTLSLVRAGKTFNGQKLIMINALFGFFWSAGSVAGPVVSGMLI

GITGYDGLIVTLVASGVLFLLIQCLCKNEKTLLASEQEDDMDEATESAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004175720.1\_3254 [locus\_tag=BN49\_RS17875] [protein=VOC family protein] [protein\_id=WP\_004175720.1] [location=3309823..3310257] [gbkey=CDS]

MESNTLHRGRLIDHILLVVEDFEASKNFYTAVLSALEIPVITTANEYLLADELVVASRHSPEAAGKLTGR

HHLAFQARDRDMVDAFYHAALTHGGRDNGAPGERHYHPGYYAAFVLDPQGNNIEAVYHGKAERSAGSVAI

SFTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016532387.1\_3255 [locus\_tag=BN49\_RS17880] [protein=multidrug efflux MFS transporter MdtM] [protein\_id=WP\_016532387.1] [location=3310823..3312055] [gbkey=CDS]

MKLALGPYIRFSRILLFPLAMVIYDFSAYLTTDLIQPGIIHIIREFETDVALAPASVSLYLAGGLALQWL

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IMAALTSIVLLAPVIGPLAGAGLMNFLHWKLLFAIIGAMSLLAWALLIFNMPETVTSQGRGFRPGEVFSE

FVRALKQPVVLTGALALSFSNLPIITWVALSPVILIDDGGMSRGAYAWTQVPVFGGVIIASIIVARFIKE

PTSPRFIWRTIPIQLTGLLVLLAGNIAWPHTWWWSVSGTSLYALGTGLLFPVLFRFALFSHSLPKGTVSA

TLNIVALSFMAASVEVARWVYFQAGGRIAFHCLALIAGIVVIMLVSRLLKLRQQHLLQPA

>lcl|NZ\_FO834906.1\_prot\_WP\_002908370.1\_3256 [locus\_tag=BN49\_RS17885] [protein=VOC family protein] [protein\_id=WP\_002908370.1] [location=3312092..3312484] [gbkey=CDS]

MFSYIMLGTNDLPRAIKFYDPLMALLGHVKAGRNEQGASWGTFNGNHTCGLCVGVPFDQQPAGVGNGTMV

ALNARSVAHIAELHALALQLGGRDEGGPGHRPQYGDGFHSAYVRDPDGNKLAFVYYASAD

>lcl|NZ\_FO834906.1\_prot\_WP\_072158538.1\_3257 [locus\_tag=BN49\_RS17890] [protein=DUF1062 domain-containing protein] [protein\_id=WP\_072158538.1] [location=complement(3312613..3313200)] [gbkey=CDS]

MGYQHIAKRCPACNVKRDFAPSGAIRVNSQKKLLDIWSIYKCTRCDYTWNIALFSRLHVSKINRELLQRL

LKNDAAMVHYYAADLATLKRNRAEPSGQPDFRIHEQWSVTLMACQRITVRVRVSQPFRISLLSILKKQLK

LSTAEIRWLVATGHIEGIPLKQLKTKKLKAMEYDFQLAAETLYARRRITLSLCGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002908374.1\_3258 [locus\_tag=BN49\_RS17895] [protein=amino acid ABC transporter ATP-binding protein] [protein\_id=WP\_002908374.1] [location=complement(3313499..3314221)] [gbkey=CDS]

MIHINNLHKRFGDSHVLRGISCDIKPQEVVCIIGPSGSGKSTFLRCMNALETVSEGEVVVNGFAAHDRTT

DLNKMRESVGMVFQRFNLFPHMTVLENLIMAPMNLRNMPRQQAVDLAEALLAKVGLSDKRDAWPSSLSGG

QQQRVAIARALAMKPSIMLFDEPTSALDPELVGDVLEVMKNLASEGMTMVIVTHEMGFAREVADRVIFID

QGVIQEEGKPGQIFSAPSNPRTAAFLSKVL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151161.1\_3259 [locus\_tag=BN49\_RS17900] [protein=amino acid ABC transporter permease] [protein\_id=WP\_004151161.1] [location=complement(3314208..3314972)] [gbkey=CDS]

MTGFRWEIIEEYGPLFVDGALMTIKCTIICVILGTLWGLTLGLGRMAKAEHGPWKYILRYLVQFPVRFYV

SAFRGTPLFVQIMVVHFALVPLFINPRDGLLVTSGLMSADFARELRASYGAFLSCIVAITLNAGAYVSEI

FRAGIQSIDKGQMEASRALGMPWWKTMRKVILPQAFRRILPPLGNNAIAIVKDSSLASAIGLADLAYAAR

TVSGAYATYWEPYLTISLVYWVITFLLAQLVNRLEKRFGKSDSH

>lcl|NZ\_FO834906.1\_prot\_WP\_016532382.1\_3260 [locus\_tag=BN49\_RS17905] [protein=basic amino acid ABC transporter substrate-binding protein] [protein\_id=WP\_016532382.1] [location=complement(3315036..3315803)] [gbkey=CDS]

MVKNLLKACCMIAALTAAGQATAETYTVGSGGTYRPFEFENSQKQLEGFDIDIIKAIAKAEGFDVKLVNT

PWEGIFATLNTGDRDIIISGITITDKRKQMVDFSAPYFPAEQSIVVAQDSQVDSLAALKNEKVGVVNSST

GDIVVSEVLGKNSTAIKRFDNTPLMLQELFEDGVSAAVGDVGVVKYYIKQHPEKQFKLVPDAKFERQYFG

IAVAKGNSELLGKINAGLQKIVADGTYAKIYKTWFDDNVPTLPAQ

>lcl|NZ\_FO834906.1\_prot\_3261 [locus\_tag=BN49\_RS17915] [protein=MurR/RpiR family transcriptional regulator] [pseudo=true] [location=complement(3315896..3316829)] [gbkey=CDS]

MPAGRSRRRPNEKRGKKREGQSRSVRRTLSRPGAPALPPAAGGGQLYQRQPRGGAGAYGDGDRHRDPDLR

RHGGACHPGAGLRRAARA\*ADHGALVRHLGHLGGKDALDGYRALQRRQLQY\*FCA\*RPSAGVRGPVAGRQ

PCGGGSGGGIAQRRAPGGDLRYRRLGDPRRIHRPVVQPYWPSGVRDEPHGL\*PCRTAYRPAARRCADHDG

AKIPPSRRVDHPARGEAAGYSDHPADPGGGLALQPGGAGGDRRPARRGQ\*PDAAARYGAGLSRDDCPVGG

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>lcl|NZ\_FO834906.1\_prot\_WP\_171819495.1\_3262 [locus\_tag=BN49\_RS17920] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_171819495.1] [location=complement(3316795..3317772)] [gbkey=CDS]

MPFNQEGSMRWFVSLLLLLTGVVSAAAPQTQTFADDLGRTVTVPLHPQRIVSMHDLDITIPLIELGAPPI

ASHGRTRPDGSHYLRASAQLTGVDFDNSDIRFIGTADIDLEAVAAARPDLIITEPSRHVSVEQLEKIAPT

VSIDHLQGSAPEIYRKLAQLTGTQPRLAILERRYQEQIKQLKAMVNPPQYSVSVIQANNGKVTVHHSYHA

LGRVLRDAGFRFPPLIERIPDGQRIDVSAEQLPELDADFVFATWRSDTGGKPQDELQAMEGVMPGWCDFM

RACRTGHCILLPREEVISNSYAALSLMVAQVQSHIAGRPIPAEAK

>lcl|NZ\_FO834906.1\_prot\_WP\_032103733.1\_3263 [locus\_tag=BN49\_RS17925] [protein=iron ABC transporter permease] [protein\_id=WP\_032103733.1] [location=complement(3317762..3318814)] [gbkey=CDS]

MTRAVHRAGFRPLAFASRHLLLRPAALKIAASIVLTLLALGLYSLCRGSYPLPASTLARALLAPQEMGEQ

PRFILFDIRLPRILMALLCGAMLGLAGAAMQSITRNGLADPGLIGVKEGASIVVLALVLFFPAVGLVWRP

LAGMVGGIAVALLVLTLARDCSRPRFILIGIGVSWSLAAAVGIFMTTADVRDVQTAMIWLAGSLQAATWP

LLAVAFCWALPGAIILFCTARAADVALLGDRTAIGLGVRLQQLTVLRFFAPVLLTSASVSCVGSLGFVGL

MAPHMARFVLRGGQVSLLCGSALIGALLVLATDTLGRLAFAPLQIPAGIVIALVGCPFFVVLLWRRRDAL

>lcl|NZ\_FO834906.1\_prot\_WP\_023316974.1\_3264 [locus\_tag=BN49\_RS17930] [protein=iron ABC transporter permease] [protein\_id=WP\_023316974.1] [location=complement(3318811..3319836)] [gbkey=CDS]

MSVAILLSARRRPRPRLALLLLTLLLIAASLVHLGLGARWIAPQTVLQALLEYDPRNFEQRIIIDLRLVR

LAAALLTGAALGVAGLLLQTVIRNPLGEPHILGLNAGASLAVVATSALGLSFGAFPAGRPLTAACGAGLL

FGGVMALASAGRGGATPLRITLCGVALSGFASAVTAAILILDEQTLLAMRTWLAGDLAGLNWSTLQTALV

PALIGLGVALLIAPRLNVLALGDKVALGLGVNLVQTRLLGLLAIALLCGAAVAVAGPIGFVGLVVPHVVR

RLVTEDIRLALPLAAPVGALVLVLADIAARTLVAPQELATGAMTALVGAPLFIFIAARFFK

>lcl|NZ\_FO834906.1\_prot\_WP\_004143331.1\_3265 [locus\_tag=BN49\_RS17935] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004143331.1] [location=complement(3319833..3320654)] [gbkey=CDS]

MPQRVKPAEQGIVLDALSAGYGQTLIVDDINLTIPTGKMTVLAGANGSGKSTLLSTIARMLKPLGGCVRL

DGQAIHQMPTKTVSRQLGILPQSPLTPEGLTVFELVSRGRYPWQGLMRQWSEADELAVEEALRLTGTAEF

AHLPVDSLSGGQRQRCWIAMALAQQTATILLDEPTTWLDLRYQVDILELLQTLTREHGRTVVTVLHDLNF

AVNYADLLVFLKQGRIAGTISDNDVCSPELIKRVFDVDVQMSINPQTGKPFFMPFRARQAAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_128972593.1\_3266 [locus\_tag=BN49\_RS17940] [protein=TonB-dependent siderophore receptor] [protein\_id=WP\_128972593.1] [location=3321160..3323232] [gbkey=CDS]

MAADNRAAKSTNDAEETITVVADGAQQSATSGYQPLSSATATLTSMPLLDIPQVVNTVSDRVLEDQHATS

LDEALYNVANVVQTNTLGGTQDAFTRRGFGANRDGSIMTNGLRTVLPRSFNAATERVEVLKGPASTLYGI

LDPGGLINVITKRPERQFSGSVSGTSTSFGGGTGSVDITGPIEGTNLAYRLIGEYQNEDYWRNFGKNKSS

FIALSLTWFGERATVTASYSHRDYSAPFDRGTIFDLNTGHAVNVDRKTRFDEAFNITDGYSDLAQLNAEY

RLNDAWTARFDYSYSQDHYNDNQARVMAYDSATGNLTRRVDGTHGSTQKMHSTRADLQGNVVVGGFYNEL

LTGVAYENYDLLRTDMLRCKNVKGFNIYHPVYGTLDTCNTVSASDSDQRIQQESYAAYVQDALYLTDNWI

AVAGVRYQYYTQYAGKGRPFNVNTDSRDEKWTPKAGLVYKVTPNVSLFANVAQSFMPQSSIASYIGELPP

EESTSYEVGAKFDLLNGITANIALFDIHKRNVLYTESIGDETVAKTAGKVRSQGVEVDLAGSITDNLSVI

ASYGYTDAKVLEDPDYAGKPLPNVPKHTGSLFLTYDIHNVYNSNTLTVGGGGHAVSKRSGTNGADYYLQG

YAVADVFAAYKMKLQYPVTLQVNVKNLFDKTYYTSSIGTNNLGNQIGDPREVQFTVKMDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004175711.1\_3267 [locus\_tag=BN49\_RS17945] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004175711.1] [location=complement(3323578..3324351)] [gbkey=CDS]

MVTETIARGAAVSISHLHHAFTLGKQTVPVLENISLQLRPGESVALLGPSGCGKSTLLRLLAGLEAPQSG

QMQIDGAAPGAPGPERILVFQDPTLYPWLTVRQNVLLGPQAQGKKGLEAKADALIDRIGLQAFSEAWPRQ

LSGGMAQRAALARALLNEPRLLLLDEPLGKLDSLTRISMQRELIALWQQQGYTSLLVTHDIEEALLLCER

VLVMSPRPGRIIAEFALPLAFPRHRDNPQLLQHRQDILRILGQEADW

>lcl|NZ\_FO834906.1\_prot\_WP\_016532314.1\_3268 [locus\_tag=BN49\_RS17950] [protein=ABC transporter permease subunit] [protein\_id=WP\_016532314.1] [location=complement(3324345..3325340)] [gbkey=CDS]

MPTYSPEQALARPTGRAPLWGEGLLAATLWLLGGLFTLTWPDAGRRWPFSEGWALAQFTLGGGLLLLALS

YRYWRARGARVLHAGKWLALLPVLFAVWEGLTAKTAVLPVPFFAPPQALIEVLHDDWPRLLDSLLHSLGL

LGLGVLLGTSSGFITGLAIGWSQRIGYWVHPVLRLLGPVPSTALLPLCLFIFPSSFGASVFLIALSTWFP

VTVLTWSGVMGIDKAWYDVARTLGASQRFLILRVAIPAALPNVFVGLFMGLGASFSVLIVAEMVGVKSGI

GFYLQWAQGWAAYPNMYAALLVMALLCSGLISGLFMLRDRLLSWQRGGMQW

>lcl|NZ\_FO834906.1\_prot\_WP\_016946421.1\_3269 [locus\_tag=BN49\_RS17955] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016946421.1] [location=complement(3325321..3326358)] [gbkey=CDS]

MTRTPFSRRRFLQLSGGLALAGVSLPLWAHDMADMAGGDTHPALRLPQPYKIKLAINKSAVCLAPVAVAE

QQKIFSKYNLDVEFVNFGNSTDVLLEAIATGKADAGVGMALRWLKALEQGFDVKLTAGTHGGCLNLLTAK

DSPFGGLESLKGQTIGVTDMAGPDKNFFAILLKRHGIDPISDVQWKVYPADLLSVALDKREIAAISGSEP

FSYRLLETGKYQLIASNMTGDYANLSCCVLGVSGSLARDHKPAAAALTQAILEAHSYAAAHPESVAQSFL

AHALNTSEAEVSGILHGQGHGHHAVGEAFVKELTQYAVDLQRVQVIKPGTDPHQFAESIYANVFA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043480.1\_3270 [locus\_tag=BN49\_RS17960] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_046043480.1] [location=complement(3326355..3327317)] [gbkey=CDS]

MRLSFSGRVAAALMLLVLGGYATAQERLTLRIADQKGGMRSQLEAANALQNLPYDIKWAEFPAAAPLAEA

LNAGAVDAGIIGDAPLLFALANGAPVKAIAVDKSNPAGTAVLVFPGSTLKSGADLKGKRIATGKGSIGHF

VALKALEQAGISPKEVQWVFLGPVDAKVALLNGSVDAWATWEPYTTQMVKTNEGQILVSGKGLLPGNTFL

AATDSALNDPQKRAALQDYLQRLAGAERWAYANLDSYGKTLGEIIRFPAEIARAQFANRQSQWQPLAEET

VAQQQATADFYLANGLIRTRLDVKPTFDRRFSVPAAEVTP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043482.1\_3271 [locus\_tag=BN49\_RS17965] [protein=acyl-CoA/acyl-ACP dehydrogenase] [protein\_id=WP\_046043482.1] [location=complement(3327323..3328474)] [gbkey=CDS]

MIHPERDDWARQLTALRQQMAEQAASLDASGEFPWRNIDHLRAGGWLSLAVPPSCGGAGASLAQLQQVIA

AIAWGEPATALIVCMQYLHHLRLAENDAWHAPLRQQVFHDAVEHGGLINSLRVEPELGSPARGGLPDTVA

TRRAEGWDISGHKIYTTGIEGLRWLAVWARSDDNPPLVGTWLVPGDSPGISVVKSWDHAGMRATGSHEVI

FNHVRVAAEHAVDVWPADAPPAAQAEPFRLFANRQTALLAAIYDSIAHAAHDWLVRWLAGRVPAGLGHPL

SRLPRVQEKVGQIAGRLLVNRSLLEQAAALRFSAIEANLAKVTITDNAIQAVNIALELTGNHGLSRQNPL

ERHYRNVLCGRVHTPQSDSAWLAAGNFVFQSQG

>lcl|NZ\_FO834906.1\_prot\_3272 [locus\_tag=BN49\_RS17970] [protein=LLM class flavin-dependent oxidoreductase] [pseudo=true] [location=complement(3328461..3329556)] [gbkey=CDS]

MSIQFLGMIGHRLSSETIAPVGPIFDRDYIVRLAQTHEAAGFDRLLVGHWSDQPDGFLVTALAGLSTQKI

QYLLAHRPGFVSPTLAARKFATLEHLLGGRLAVHIISGGNDAEQRRDGDYLDHDQRYARTDAFLDIVRQV

WTSEQPVDIHNDFYQAEQAWSAIRPLQKPHLPIYFGGSSEAAIAVAGKHADVFALWGESLAQTGETIQRV

RAEAAKHQRDIGFSVSFRPIIADSEAEAWEKAEHILHVATEQAAQRGGGFKAKPDSIGAQRLRATAAQGR

VVDKRLWTGIAQLVGGGHNSTALVGTPEQVADALLDYYDLGVRNFLIRGFDPLNDAADYGRALLPIAREK

AARRAVAERAS\*SIL

>lcl|NZ\_FO834906.1\_prot\_WP\_009307638.1\_3273 [locus\_tag=BN49\_RS17975] [protein=LysR family transcriptional regulator] [protein\_id=WP\_009307638.1] [location=complement(3329701..3330594)] [gbkey=CDS]

MRIDDIDALLATVQFSSLNQAAEYLGITQSAITRRLQRLEQELNVTLLERQTRPLTLTAAGHRVYEQCLS

IKRETKKLYSLLDPQGEPRGALRLGVPQSLSEIALPAALSALSQQFPGLSPQITCGWSGQLQRRLENGEL

DGMLAMGPAQQSFAEGYSGRLLCPLEVVPIVGRRLNLRASSLRECAERGWILNPDGCGLRAGLIRELQSQ

GLRLTLNVESAGAQLQIALVAQGLGLGLVPRAALASSPWRDEVAVLSLSDFQPAVSLWLIHAQYLANLQP

PLTFFASKVMQQLTVSD

>lcl|NZ\_FO834906.1\_prot\_WP\_227504851.1\_3274 [locus\_tag=BN49\_RS17980] [protein=cysteine dioxygenase] [protein\_id=WP\_227504851.1] [location=3330755..3331303] [gbkey=CDS]

MHREHHQTAPLLDAVAQRLAALVRYDDWLPEEYTLPHPHHYQQYLLHADSGERFSIVSFVWGPGQATPIH

DHRVWGAIGMLRGAEENQRYQLDADGIPRALGAATLLEAGQVEKVSADDGDIHRVSNALADRVSISIHVY

GGNIGAVKRAVYTPEGQQKPFISGYSNRHLPNIWDSSREHQG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043485.1\_3275 [locus\_tag=BN49\_RS17985] [protein=rhodanese homology domain-containing protein] [protein\_id=WP\_046043485.1] [location=3331309..3332889] [gbkey=CDS]

MSTYAYRQAAGIRQALLDHRELALIDVREEADFATAHPLFAVNLPLSKLELEVRRRIPRFTTPLTVYDNG

EGLAEIAVERLRSWGYQDVALLAEGLAGWRRSGGELFHDVNSASKAFGELVESVRHTPSLSAQEVQALID

SRQEVVIVDARRFDEYQTMSIPGSISVPGGELALRVESLTPSPQTPVIVNCAGRTRSIIGTQSLINAGVP

NPVHALRNGTIGWTLAGQTLAHQQQRQYDPSARASGARAAEVAHFAERAGVAVIDEATLQRWLQQSDRTT

FLFDVRSPEEYAAGHYPGSLSAPGGQLVQETDHFASVRGARIVLLDDDGIRAAITGSWLAQMGWETARLS

ALSTSQLSERGVPAAEVPPGPQAEEISPTQLAQQLEEPGTVVLDFTTSANFVARHIPGAWWLTRSQLRQA

LEAIPPAQRYVVTCGSSLLARYAVPEVAALTGKPVQLLTGGTLAWIAAGLPLAHGDSGLAVERRDRYRRP

YEGTDNSAEAMQAYLEWEYGLVDQLARDGTHGFRVL

>lcl|NZ\_FO834906.1\_prot\_WP\_009307636.1\_3276 [locus\_tag=BN49\_RS17990] [protein=polyphenol oxidase family protein] [protein\_id=WP\_009307636.1] [location=complement(3332902..3333627)] [gbkey=CDS]

MAYTSRLLNAIPGIRHAFLDVHETAAFPYAELAPVKLVHGNEVHHYQQPLPTRPHADAVFTAVAGQKVGV

VTADCLPLLIASRDGRYVCSVHAGWQGLVSGIVDNSLACFRQQGVALADLVIAVGPYIHPCCYEVSAGFY

QQLLDQPGGDRVARHRQRLFHSRSGPVSDPLKAAARGSDNLWFDLRAFAEAIFAEAGVAPASVEWLGSCT

YCTPQSLGSYRRRTHFPAPKSFQYSWIMREA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529739.1\_3277 [gene=mhpT] [locus\_tag=BN49\_RS17995] [protein=3-(3-hydroxy-phenyl)propionate transporter MhpT] [protein\_id=WP\_016529739.1] [location=complement(3333730..3334887)] [gbkey=CDS]

MTKITTATPSRLVVTIGLCFMVALMEGLDLQAAGIAAVGMAQAFALDKMQMGWIFSAGILGLLPGALVGG

MLADRHGRKRILLGSVLLFGLFSLATALAWSFPTLLLARLLTGVGLGAALPNLIALTSEAAGSRFRGRAV

SLMYCGVPIGAALAAALGFSGLAAAWQIIFWIGGVVPLLLIPLLMRWLPESQAFQRAEASVPLRTLFAPG

QAAATLLLWLGYFFTLLVGQGFRASQAAGVMFSLQIGAACGTLLLGALMDKLTPLRMSLLIYSGILASLL

ALGSASSLTGMLLAGFVAGLFATGGQSVLYALAPLFYPAAIRATGVGTAVAVGRLGAMSGPLLAGKMLDL

GTGTVGVMAASAPGIVLAGVAVFWLMHRQQRAAMV

>lcl|NZ\_FO834906.1\_prot\_WP\_004898794.1\_3278 [gene=dmpG] [locus\_tag=BN49\_RS18000] [protein=4-hydroxy-2-oxovalerate aldolase] [protein\_id=WP\_004898794.1] [location=complement(3334963..3335979)] [gbkey=CDS]

MNGKKLYISDVTLRDGMHAIRHQYSLAQVQQIASALDKAGVDSIEVAHGDGLQGSSFNYGFGAHSDIAWI

EAAADVVSQAKIATLLLPGIGTLHDLKAAYQAGARVVRVATHCSEADVAAQHIAFARELGMDTVGFLMMS

HMISPQALAQQALKMESYGATCIYVVDSGGAMNMNDIRDRFRALKAVLKSETATGMHAHHNLSLGVANSI

VAVEEGCDRIDASLAGMGAGAGNAPLEVFIAAADKLGWQHGTDLYALMNAADELVRPLQDRPVRVDRETL

ALGYAGVYSSFLRHSEAAAKRYGLSAVDILVELGKRRMVGGQEDMIVDVALDLLNRNK

>lcl|NZ\_FO834906.1\_prot\_WP\_032425055.1\_3279 [locus\_tag=BN49\_RS18005] [protein=acetaldehyde dehydrogenase (acetylating)] [protein\_id=WP\_032425055.1] [location=complement(3335976..3336926)] [gbkey=CDS]

MRKRKVAIIGSGNIGTDLMIKILRHGQHLEMAVMVGIDPQSDGLARARRLGVATTHEGVGGLMQMAEFVD

IDFVFDATSAGAHIKNDAALREAKPGIRVIDLTPAAIGPYCVPVVNLAANLHQGNVNMVTCGGQATIPMV

AAVSRVAKVHYAEIVASIASQSAGPGTRANIDEFTETTSQAIEKVGGAGKGKAIIVLNPAEPPLMMRDTV

YVLSELASQEAIAASIAEMAAAVQAYVPGYRLKQQVQFEVIPEDRPVNLPGVGCFSGLKTAVYLEVEGAA

HYLPAYAGNLDIMTSAALATAEQMAGAMHSAAGATA

>lcl|NZ\_FO834906.1\_prot\_WP\_002908598.1\_3280 [gene=mhpD] [locus\_tag=BN49\_RS18010] [protein=2-keto-4-pentenoate hydratase] [protein\_id=WP\_002908598.1] [location=complement(3336919..3337725)] [gbkey=CDS]

MTFSLDALARQLRDAEQSGQAIAPLRDILGVDNADAAYAIQRLNVQHHVAHGRRVVGRKVGLTHPKVQQQ

LGVNQPDFGTLFADMCYGDNAEVPFGRVLQPKVEAEIALVLKQDLPHADTTFDELYNAIEWVLPALEVVG

SRIRDWSIGFVDTVADNASCGLYVIGGPAQRPAGLDLKQCAMHMTRNQELVSSGRGSECLGHPLNAAVWL

ARKLASLGEPLRAGDIVLTGALGPMVTINEGDSFVAHIEGIGSVAARFVAAGEGDRDA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151837.1\_3281 [locus\_tag=BN49\_RS18015] [protein=alpha/beta fold hydrolase] [protein\_id=WP\_004151837.1] [location=complement(3337736..3338602)] [gbkey=CDS]

MSYQPQTEAATSRFLNVDEGGRTLRIHINDCGDGKETVVMLHGSGPGATGWANFSRNIDPLVEAGYRVLL

LDCPGWGKSDAIVNSGSRSDLNARILKSVVDQLGIDKVHLLGNSMGGHSAVAFTLSWPERVAKLVLMGGG

TGGMSLFTPMPTEGIKLLNALYREPTIENLKKMMSIFVFDTRDLTEALFEARLNNMLSRRDHLDNFVKSL

EANPKQFPDFGPRLGEISAPTLIVWGRNDRFVPMDAGLRLLAGIAGSELHIYRDCGHWAQWEHADSFNQL

VLNFLARA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531258.1\_3282 [gene=mhpB] [locus\_tag=BN49\_RS18020] [protein=3-carboxyethylcatechol 2,3-dioxygenase] [protein\_id=WP\_016531258.1] [location=complement(3338620..3339564)] [gbkey=CDS]

MHAYLHCLSHTPLVGFVDPEQAVLDEVNGVIADARRRIAEFDPELVVLFAPDHYNGFFYDVMPPFCLGVG

ATAIGDFASAAGDLPVPAELAEACAHAVINSGIDLAVSYNMQVDHGFAQPLEFLLGGLDRVPVLPVFING

VAAPLPGFQRTRLLGEAMGRFLNTLNKRVLILGSGGLSHQPPVPELAKADAHLRDRLLGGGKQLPPDERE

RRQQRVISAARRFTEDPHSLHPLNPVWDNRFMSLLEQGRLSELDAIGNDELSAMAGKSTHEIKTWVAAFA

ALSAFGRWRSEGRYYRPIPEWIAGFGSLSATTEI

>lcl|NZ\_FO834906.1\_prot\_WP\_046043492.1\_3283 [locus\_tag=BN49\_RS18025] [protein=bifunctional 3-(3-hydroxy-phenyl)propionate/3-hydroxycinnamic acid hydroxylase] [protein\_id=WP\_046043492.1] [location=complement(3339566..3341230)] [gbkey=CDS]

MTTSTPDIQPAVQHTAQVAIVGAGPVGLMMANYLGQMGISVLVVEKLATLIDYPRAIGIDDESLRAMQAV

GLVNDVLPHTTPWHAMRFLTPKGRCFADIQPMTDEFGWSRRNAFIQPQVDAVMYHGLQRFPQVRCLFSRE

VEAFSQTGDGVTLNLKGPDGERETVRADWLVACDGGASFIRRTLNIPFEGKTAPNQWIVIDIANDPLATP

HVYLCCDPVRPYVSAALPHGVRRFEFMVMPGETEAQLSEPHNMRRLLSKVLPDPDRVELIRQRVYTHNAR

LAERFRIDRVLLVGDAAHIMPVWQGQGYNSGMRDAFNLAWKLALVVNGKAGETLLDSYQQERRDHAKAMI

DLSVTAGYVLAPPKRWQGAVRDGLSWLLNYLPPVKRYFLEMRFKPMPQYREGALLTDGAGKTSPVGKMFI

QPQVTLESGESVLLDEVIGANFAIIGWGCNPQWGLNAGQIARWRAIGVRFIQVVPEVQIHREQDNAPGTL

RVGDTQNRLKSWFVLHNTAIAVVRPDRFVAALAIPQTLGAQLTALAEKMTLATGDTAHAEEKVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004215282.1\_3284 [locus\_tag=BN49\_RS18030] [protein=DNA-binding transcriptional regulator] [protein\_id=WP\_004215282.1] [location=3341408..3342220] [gbkey=CDS]

MRDDGSAAYKTVRGLSRGLLLLKLLNKFDGGATPGLLAEFSGLHRTTVRRLLETLQEEGFVRRSRSDDSF

RLTINVRQLSDGFRDEHWISALATPLLGELLREVQWPTDITTLDVDAMVVRETTHRFSRLSFHRAMVGRR

LPLLLTASGLTWLAFAPDAERDAVVSMLAARPEAEYQLAREPERLAAILARTRQNGYGENFRGWRQEEKI

ASIAVPVCSQQRVIGCLNLVYIASAMTIEQAAQKHLPALQRVARQIEARMEEEEVWYEMP

>lcl|NZ\_FO834906.1\_prot\_WP\_016530930.1\_3285 [locus\_tag=BN49\_RS18035] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016530930.1] [location=3342312..3343370] [gbkey=CDS]

MSKHPLLLGLTLLSASLFTGQTFADRTVTDQLGRQVTLPDHVTRVVVLQHQTLNLLVQLHAAEDIVGVLS

SWQKQLGPQFARFMPEIGQLATPGDLTQVNIESLLALRPQVVFVANYAPPAMIAQIQQAGIPVVAISLRH

DAAGEKNKMNPTMADEEQAYNAGLMEGIRLIGEVVERQPEAEALIHYTFEARKQANAPVADIPQNQRVRV

YMANPDLNTYGAGKYTGLMMAHAGALNVAAASVKGARQVSLEQVLEWNPQVIFVQDRYPQVVKQIENDPQ

WQAIDAVKHHRVWLMPEYAKAWGYPMPEALALGELWMAKKLYPARYQSIDVDSKARDYYQRFYRVAWMPD

AR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530931.1\_3286 [locus\_tag=BN49\_RS18040] [protein=iron ABC transporter permease] [protein\_id=WP\_016530931.1] [location=3343360..3344367] [gbkey=CDS]

MPANSQPWLVQGSLALATLAIAVASLCFGQYPLSLSAVGHTLVHLPPGEGVIGQIVWSVRLPRVVMALLA

GGALGLCGATLQGVFQNPLVDPHIIGVTAGSAFGGTLAILLGVGSLLMMASTFFFGLVALGLIYALAALQ

GRDSTLGLILSGIILSGFFAALVSLMQYLADSEETLPNIVFWLLGSFATASWHKVLLMSLPMALAAGVLW

KLRWRINLLALEERDARSLGVPVAALRRGVLVCCAVLVAAQVAVSGSIAWMGLVVPHLARLLVGADHRRL

LPTAFWLGAALMLVVDDLARTLTQAEIPIGIITALLGAPLFTVLLVQSRRRSTTR

>lcl|NZ\_FO834906.1\_prot\_WP\_029884122.1\_3287 [locus\_tag=BN49\_RS18045] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_029884122.1] [location=3344364..3345113] [gbkey=CDS]

MNSSLSLQALRYGHRQPLFAPLTLACRPGEIWAVLGANGRGKSTLLDTLTGVLPPLGGEMQCEGGVALVP

QSFRPAFCWRVSDVVLMGRARHVDLFAQPDEEDARRVEQALAQLGIAALAEDDFGALSGGQQQLVLIARA

LVSASQNILLDEPCSALDLGNQQVVLQLIVDLAHRQTRTVLFTTHDPNHALQVASHTLLLLPEGQWLAGE

TADVLSETHLRQAYGLPVRLIHHAASAFPLLASGFTLRR

>lcl|NZ\_FO834906.1\_prot\_WP\_029884123.1\_3288 [locus\_tag=BN49\_RS18050] [protein=substrate-binding domain-containing protein] [protein\_id=WP\_029884123.1] [location=complement(3345097..3345840)] [gbkey=CDS]

MANTTLTLLAAGSLRSAFLPLVAHFQQHTGLAVDAQFGPAGLLRERIEAGAPCAVFASANAAHPQALLQA

GLAQECQGFASNQLMLTARRSPDNDGLDWLALLSTPRLRLATSTPGCDPSGDYTWQLFARIEARYPGLGN

AMAGRAQQLVGGRDSLSVPPGEIAGAWLIRQNLADLFIGYAHYGPALATCDVLRTLTIPAPWNIRCDYQL

ARLRADPAALALYRFILGDVGQGYLRQAGFMPFSDAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004215272.1\_3289 [locus\_tag=BN49\_RS18055] [protein=shikimate dehydrogenase] [protein\_id=WP\_004215272.1] [location=complement(3345897..3346733)] [gbkey=CDS]

MVISGNTRLIAHLGYPTASFKAPMIYNPWFVDQQVDVKVVPMGVRPEDYAAFIPPLFTMTNIIGALVTMP

HKIATCDLVQRLSPTAAIAGACNAIRREADGSLSGDMFDGEGFVLGLRRKGFNPQGTRALVVGSGGVGSA

IAASLAAAGVSALTLYDTRPEVAHALAGRLHQHYPQLDITLMQPDPAGHELVVNATPLGMKASDPLPLDV

DRLAPGAWVGEVVMTQEYTPLLRAAQARQCHIQRGTDMLFEMIPAYLRFFDLPVATPEQLRALAEIRY

>lcl|NZ\_FO834906.1\_prot\_WP\_016530159.1\_3290 [locus\_tag=BN49\_RS18060] [protein=MFS transporter] [protein\_id=WP\_016530159.1] [location=complement(3346749..3348071)] [gbkey=CDS]

MSSYSPNPTAAAQPAVTVRRSRRRIGILALLAIGTMINYLDRTVLGIAAPKLTAELGIDPAIMGILFSAF

AWTYALAQIPGGLFLDRFGNKVTYFLSLTLWSLFTLFHGMAVGLKTLLLCRFGLGISEAPCFPVNSRVVS

AWFPQQERAKATAVYTVGEYLGLACFAPLLFWIMDGFGWRVLFVSVGAVGILFALVWWRCYREPHEDPRL

SQQEREHIENGGGLSAPTDQHVAFSWPLVRQLLSKRQIIGASIGQFAGNTVLVFFLTWFPTWLATERHMP

WLKVGFFSILPFVAAAGGVMFGGWLSDKLLKATGSANLGRKLPIVAGLLMASCIITANWLESDLAVLLVM

SFAFFGQGMVGLGWTLISDIAPKGLGGLTGGLFNFCANLAGILTPLVIGFIVAGFGNFFYALIYIGGAAL

LGVVAYLFILGDVKRIELSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_023301812.1\_3291 [locus\_tag=BN49\_RS18065] [protein=sugar phosphate isomerase/epimerase and 4-hydroxyphenylpyruvate domain-containing protein] [protein\_id=WP\_023301812.1] [location=complement(3348143..3349996)] [gbkey=CDS]

MLRSIATVSISGTLPEKLHAIAAAGYQGVEIFENDLLYYTGTPAEIRQLAADLGLKITLFQPFRDFEGAS

RAQFAANMARARRKFALMRELGCETLLLCSNVQPDCSADSELQVADLRALATLAEEEGIAIGYEALAWGT

HVNRWQQAWERVRRVDSPALGLVLDSFHILARGDTLDALPSVPVEKITFVQLADAPYMKMDLLEWSRHFR

CFPGQGELPLEAFAEQITRCGYRGPWSLEIFNDGFRASPNGATAKDGYRSLLWLEEQTRRRLPTCDADLF

SPPPLPVYHGLEFIEFAASAAEAQRLGQHLQALGFQHEGSHRSRRVTLWRNGGARIVINHQPHSWADHFY

QRHGVSLCAMALRVEHSASLVARARALGYATWQGDAGPNETPIPAICAPDGSLIYLIDAGEAIYERDFHL

RDGVTVREDYLGIDHLALGMEADSRDNWVMFFRTVFGFSLEHEQTLPDPYGLVRSLAVRSPQGDIRLALN

ISQSRATQIARSVACYQGAGLQHAAFACRDLPAACDQLAEVARHTLPIPANYYDDLLARFGGELDVGQLQ

RQQLLYDRDPQGGDFLHLYTRPFTAGRFFFELTERRAGYALYGAANAAVRLAAMQYC

>lcl|NZ\_FO834906.1\_prot\_WP\_002908844.1\_3292 [locus\_tag=BN49\_RS18070] [protein=TetR family transcriptional regulator] [protein\_id=WP\_002908844.1] [location=3350123..3350761] [gbkey=CDS]

MTVVAHDEAQSLKARIFSAAIAVFAEHGLSGARMEQIATEAQTTKRMVVYYFKSKEQLYQEVLQHVYARI

RETEQQLGLENVPPVEALVRLVRWSVRYHATHADYMRVICMENMQRGKWLKSSGELKPLNRTALSILEDI

LLRGQQQGVFQAGLDARDVHRLISSFSFYQVSNFYTFSSLYLDDPLPAIDDEAMVAHHCDIAVRAVIRFV

IS

>lcl|NZ\_FO834906.1\_prot\_WP\_004180357.1\_3293 [gene=fumD] [locus\_tag=BN49\_RS18075] [protein=fumarate hydratase FumD] [protein\_id=WP\_004180357.1] [location=complement(3350779..3350991)] [gbkey=CDS]

MGNKAKDDDLYQEMCRVVGKVVLEMRDLGQEPKHIVIAGVLRTSLANRKIQRSPLTVEAMEKVIHALSGH

>lcl|NZ\_FO834906.1\_prot\_WP\_004143246.1\_3294 [locus\_tag=BN49\_RS18080] [protein=hypothetical protein] [protein\_id=WP\_004143246.1] [location=complement(3350981..3351139)] [gbkey=CDS]

MKKGKRNGLFRHHEPVKCVIEPLKWRWFALCGKSINNDLIDNDKIRAKFYGK

>lcl|NZ\_FO834906.1\_prot\_WP\_004217210.1\_3295 [locus\_tag=BN49\_RS31110] [protein=hypothetical protein] [protein\_id=WP\_004217210.1] [location=complement(3351228..3351359)] [gbkey=CDS]

MCAGGSAHEMWQGVMRFIMQSNALKPFKKESKRIIRCRNQKGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002908859.1\_3296 [gene=pykF] [locus\_tag=BN49\_RS18090] [protein=pyruvate kinase PykF] [protein\_id=WP\_002908859.1] [location=3351497..3352909] [gbkey=CDS]

MKKTKIVCTIGPKTESEEMLTKMLEAGMNVMRLNFSHGDYAEHGQRIQNLRNVMSKTGKKAAILLDTKGP

EIRTIKLEGGNDVSLKAGQTFTFTTDKSVIGNNEIVAVTYEGFTSDLAVGNTVLVDDGLIGMEVTAIEGN

KVICKVLNNGDLGENKGVNLPGVSIALPALAEKDKQDLIFGCEQGVDFVAASFIRKRSDVVEIREHLKAH

GGENIQIISKIENQEGLNNFDEILEASDGIMVARGDMGVEIPVEEVIFAQKMIIEKCIRARKVVITATQM

LDSMIKNPRPTRAEAGDVANAILDGTDAVMLSGESAKGKYPLEAVTIMATICERTDRVMTSRLDFNNDNR

KLRITEAVCRGAVETAEKLEAPLIVVATQGGKSARAVRKYFPDATILALTTNETTARQLVLSKGVVPQLV

EEIASTDDFYHLGKDLALKSGLARKGDVVVMVSGALVPSGTTNTASVHVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002908860.1\_3297 [locus\_tag=BN49\_RS18095] [protein=major outer membrane lipoprotein] [protein\_id=WP\_002908860.1] [location=3353221..3353457] [gbkey=CDS]

MNRTKLVLGAVILGSTLLAGCSSNAKIDQLSSDVQTLNAKVDQLSNDVNAMRSDVQAAKDDAARANQRLD

NQAHSYRK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043501.1\_3298 [locus\_tag=BN49\_RS18100] [protein=L,D-transpeptidase family protein] [protein\_id=WP\_046043501.1] [location=complement(3353519..3354505)] [gbkey=CDS]

MKRKMMITLALLSALGASSAAWAVDYPLPPANSRLIGQNQYWTVQEGDRNLQAIARHFDTAAMLILEAND

TIAPVQPKPGTQVLIPSQMLLPDVPREGIVVNLAELRLYYFPPGENQVQVYPLGIGQLGLETPEMTTRVG

QKIPNPTWTPTAGIRARSLEKGVTLPAVVPAGPNNPLGRYALRLAYGNGEYLIHGTNSPDSVGLRVSSGC

MRMNADDIKALFSQVKTGTPVRIINQPVKFAVEPDGKRYVEVHRPLSQTEGENTRTIAYTLPAAFHAFAE

DKAVDDLQLKKAMSRRAGYPVVVSAGAGSTAASLSAQNSSSDNGLLTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002908865.1\_3299 [gene=sufE] [locus\_tag=BN49\_RS18105] [protein=cysteine desulfuration protein SufE] [protein\_id=WP\_002908865.1] [location=complement(3354605..3355021)] [gbkey=CDS]

MAALPDKDKLLRNFSRCANWEEKYLYIIELGQRLAPLSPEEHSVQNIIQGCQSQVWIVMDQDPTGVITLR

GDSDAAIVKGLIAVVFILYDRMTAQDITEFDVRPWFEKMALTQHLTPSRSQGLEAMIRAIRAKAANIS

>lcl|NZ\_FO834906.1\_prot\_WP\_016532585.1\_3300 [gene=sufS] [locus\_tag=BN49\_RS18110] [protein=cysteine desulfurase SufS] [protein\_id=WP\_016532585.1] [location=complement(3355033..3356253)] [gbkey=CDS]

MTFSVEQVRADFPVLNREVNGQPLVYLDSAASAQKPEAVIGAEAEFYRHGYAAVHRGIHTLSAEATARME

AVRQQAATFLNAGSAEEVVFVRGTTEGINLVANSWGNANVGAGDNIIISEMEHHANIVPWQMLCARVGAE

LRVIPLNPDGTLQLDVVPGLFDPRPRLLAITEVSNVLGTENPLAALIALAHQHGAKVLVDGAQAVMHHPV

DVQALGCDFYVFSAHKLYGPTGIGVLYARSELLQTMAPWEGGGSMIATVSLTEGTTWNQAPWRFEAGTPN

TGGIIGLGAALTYVSQLGLTQIAEYEQTLMRYALDALRAVPDLILYGPAQRKGVIAFNLGQHHAYDVGSF

LDNYGIAVRTGHHCAMPLMARYQVPAMCRASLAMYNTTEEVDRLVAGLQRIRKLFG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532586.1\_3301 [gene=sufD] [locus\_tag=BN49\_RS18115] [protein=Fe-S cluster assembly protein SufD] [protein\_id=WP\_016532586.1] [location=complement(3356250..3357524)] [gbkey=CDS]

MAGLPNSSNALQQWHHLFEAQGGPRTPEASQHLQQLLRLGLPTRKHEDWKYTPLDALLNGRFVADEGASL

SAEQRDALALPLDAWRLVFIDGRYHPQLSDDLAASGVEVSVDNQRQHLPDALQPEVFLHLIESLAQTVTR

IRVPRNRRLDKPLLLMHITSGLAGDALNTAHYRHHLALESGAEATIVEHYLSLNEQPHFTGGRLTMTVAD

NAHLQHIKLAFENARSYHFAHNDLLLGRDASAFSSSFLLGGQVLRHQTSTRLGGENSNLRLNSLAMPVKN

EVCDSRTWLDHQVGYCTSRQLHKTIVSDKGRAVFNGLINVAPLALKTDGQMTNNNLLLGRLAEVDTKPQL

EIYADDVKCSHGATVGRIDEEQLFYLRSRGIEQQAAQQMILYAFAAELTEAIRSDALREQVLARIGQRLP

GGTV

>lcl|NZ\_FO834906.1\_prot\_WP\_016532587.1\_3302 [gene=sufC] [locus\_tag=BN49\_RS18120] [protein=Fe-S cluster assembly ATPase SufC] [protein\_id=WP\_016532587.1] [location=complement(3357499..3358245)] [gbkey=CDS]

MLSIQDLHVAVEDKAILRGLNLEVRPGEVHAIMGPNGSGKSTLSATLAGREDYEVTGGRVEFKGKNLLEL

AAEDRAGEGIFMAFQYPVEIPGVSNQFFLQTALNAVRNYRGLEALDRFDFQDLMEEKIKLLQMPEDLLTR

SVNVGFSGGEKKRNDILQMAVLEPELCILDESDSGLDIDALKIVSQGVNALRDGKRAFIIVTHYQRILDY

IKPDYVHVLYQGRIVKSGDFSLVKQLEEQGYGWLTEQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016532588.1\_3303 [gene=sufB] [locus\_tag=BN49\_RS18125] [protein=Fe-S cluster assembly protein SufB] [protein\_id=WP\_016532588.1] [location=complement(3358262..3359749)] [gbkey=CDS]

MSRNTEATDDVKTWTGGPLNYKEGFFTRLQTDELAKGINEEVVRAISARRNEPQWMLEFRLNAYRAWLEM

EEPHWLKAHYDKLNYQDYSYYSAPSCGNCDETCASEPGAVQQTGANTFLTSEVEEAFNQLGVPVREGREV

AVDAIFDSVSVATTYREKLAEQGIIFCSFGEAIHDHPELVKKYLGTVVPGNDNFFAALNAAVASDGTFIY

VPKGVRCPMELSTYFRINAEKAGQFERTILVADEGSYVSYIEGCSAPVRDSYQLHAAVVEVIIHKDAEVK

YSTVQNWFPGDNNTGGILNFVTKRALCEGENSKMSWTQSETGSAITWKYPSCILRGDNSIGEFFSVALTS

GHQQADTGTKMIHIGKNTRSTIISKGISAGHSQNSYRGLVKIMPTATNARNYTQCDSMLIGPDCGAHTFP

YVECRNNSAQLEHEATTSRIGEDQLFYCLQRGISEDDAISMIVNGFCKDVFSELPLEFAVEAQKLLAISL

EHSVG

>lcl|NZ\_FO834906.1\_prot\_WP\_004143232.1\_3304 [gene=sufA] [locus\_tag=BN49\_RS18130] [protein=Fe-S cluster assembly scaffold SufA] [protein\_id=WP\_004143232.1] [location=complement(3359752..3360129)] [gbkey=CDS]

MEVQAGTFNPADFSWQGLTMTPAAAAHIRDLMRKQPDKKGLRLGIKTSGCAGFGYVLEMIAEPAPDDLLF

ESDGAKLFAPLQAMPFIDGTELDYVREGLNEIFKFHNPKAQHECGCGESFGVQAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002908880.1\_3305 [locus\_tag=BN49\_RS18135] [protein=hypothetical protein] [protein\_id=WP\_002908880.1] [location=complement(3360613..3360810)] [gbkey=CDS]

MKDKDEQTALIGMAIGAAVISLVATQKQINQGSIVDELVRLGRQKGDGVEDEVFVQAARLVSKGT

>lcl|NZ\_FO834906.1\_prot\_WP\_020314287.1\_3306 [locus\_tag=BN49\_RS31115] [protein=hypothetical protein] [protein\_id=WP\_020314287.1] [location=3360809..3360946] [gbkey=CDS]

MVSLRLSSRERLAKDTICSISNSPSLRLTQSLRQGTWQEKNKLSG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532589.1\_3307 [locus\_tag=BN49\_RS18145] [protein=DoxX family membrane protein] [protein\_id=WP\_016532589.1] [location=3361047..3361382] [gbkey=CDS]

MPNSTLFFITLCLSRVLVTFFFWMAGIYGVFHFAELVQEMVTVGLPWPALFAAGTIFCQLAGSALIVFNP

SGYGWIGSGMLIVFTLLTIPLGHAFWAFSEPRRTEEFHIAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002908882.1\_3308 [locus\_tag=BN49\_RS18150] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_002908882.1] [location=3361439..3362071] [gbkey=CDS]

MSETPRQKGRPKDPLKTQAILQAARKLFLEQGLEVTTAEIARVAGVAKATLYANFSDKEHLIEAVLRQES

DLTISDHDFAQRHHLPLIEVLTAFGYRFVRFINQRELTGWDRLIASAAVRHPDLPGRFYAAGPGRAQQML

EAIIAEAIEAGTLRACDPQEAADELAGLWLGMTSLAIKLGARPPLSDDEIKQRVERALDVFLRAYSLAPG

>lcl|NZ\_FO834906.1\_prot\_WP\_021313475.1\_3309 [gene=lldD] [locus\_tag=BN49\_RS18155] [protein=FMN-dependent L-lactate dehydrogenase LldD] [protein\_id=WP\_021313475.1] [location=3362326..3363510] [gbkey=CDS]

MIVSAPSDYREAARRRLPRFLFDYIDGGAVAENTMNANAAELASVALRQRVLCGAGEPTLATTILDAPWA

MPVALGPVGATGMYARRGEVQAARAASRAGIPYTLSTVSVCSIEEVASHASGALWSQLYVLKDRGYMRNA

LERAWAAGMKTLVFTVDMPIPGSRYRDNRSGMSGPHATLRQYLQACTHPRWAMNVGLAGRPLSFGNIEAY

TGHKMTMDDYMGFISNNFDPSIAWHDLEWIRDSWQGKLIIKGILDADDARNAVRLGADGIVVSNHGGRQL

DGAIPTARALPRVVDAVGDDLTVLADSGVRSGVDVIRLLALGAKGVLLGRAYIYALAAAGEAGVAHLLRL

FAEDMKVTMTLTGATSPSAISLDCLDRLEQDQYRTHAVPVSLPA

>lcl|NZ\_FO834906.1\_prot\_3310 [locus\_tag=BN49\_RS18160] [protein=efflux RND transporter permease subunit] [pseudo=true] [location=complement(3363566..3366648)] [gbkey=CDS]

MSAGRFNLSALAVRERSVTLFLIILISVAGLVAFFGLGRAEDPPFTVKQMTVITVWPGATAQEMQDQVAE

PLEKRLQELKWYDRTETYTRPGIALLTLSLQDQTPPSEVPEQFYQARKKLGDEAKNLPAGVSGPMMNDEF

ADVTFALFALKARGEPPRQLVRDAEALRQQLLHVPGVKKVNILGEQAERIYLSFSHDRLATLGLSPEAIF

AALNSQNVLTAAGAIETRGGQIFIRLDGAFDRLQQIRDTPIIAGGRTLKLADVATVERGYEDPATFLIRH

QGEPALLLGVVMREGWNGLALGKALDAETASINQNLPLGMSLTKVTDQSVNISAAVDEFMIKFFVALLVV

MAVCFVSMGWRVGVVVAAAVPLTLAVVFVVMAATGKNFDRITLGSLILALGLLVDDAIIAIEMMVVKMEE

GYDRLKASAYAWSHTAAPMLAGTLVTAVGFMPNGFAQSTAGEYASNVFWIVGIALIASWIVAVIFTPWLG

VHLLPDRKPAAAGHAALYDTPRYQRFRRLLTRVIARKWRVAAGVVALFIVAILGMSVVKKQFFPTSDRPE

VLVEVQLPYGSSISQTSAAAAKIEHWLQRQPEAKIVTSYIGQGAPRFYLAMAPELPDPSFAKLVVLTDGQ

GAREALKRRLREAVANGLAPEARVRVTQLVFGPYSPYPVAWRVMGPDPHALLDIAERVKSVLQASPLMRT

VNTDWGSRVPVMHFSLNQDRLQASGLSSQSVAQQLQFLLSGIPITTVREDIRAVQVIGRAAGDIRLDPAK

IADFTLVGSGFPCHRLATCRSGWRTRCFAVATARRPSPSAEMLRRTCSRRMSPPR\*\*SRCSPLSTRCRLA

IASRRRGRLRNPARPPGRWCRYFR\*\*SPSRC\*SLSCRCVRCRRWSWFS\*PRRWG\*LAWSRRCCCSISRLA

SMPWWA\*SPCRGS\*CAIR\*S\*LAKSIITNRRGSIRSTRWWRRRCSAPARFC\*PRWRRSWRSFLSPSRSSG

ERSPIR\*LAGRWEEPS\*PLSSCRPCTRSGSASARRTRYNRQSCTFRG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043512.1\_3311 [locus\_tag=BN49\_RS18165] [protein=efflux RND transporter periplasmic adaptor subunit] [protein\_id=WP\_046043512.1] [location=complement(3366645..3367700)] [gbkey=CDS]

MLRLNAVHLAVCLLPLALAGCGEPAAHDDPRIRPPLVRVATVERAEAGSRAFTGVVVARTQSDLGFRVAG

KVLERRVETGQSVKRGQLLLRLDPADLALQAQSQQRVVDAARARAKKAANDLARYRGLVASGAISAAEFD

QINAAAEAARADLSAAQAQANVAQNATGYAGLLADADGVVVETLAEPGQVVSAGQVVIRPAVGSEALATR

YGSESQPVTATLRLLSDAADATTRTFEARYVLNGALANAPLGSTVTLRIGNDQAPGQVLAVPLASVYDPG

NGPGVWRIASRPATVSWQPVTVLGLDDETARVTGPLKPGEPIVALGAHLLHQGEAVRLAERREHNAAGSQ

P

>lcl|NZ\_FO834906.1\_prot\_WP\_015958592.1\_3312 [locus\_tag=BN49\_RS18170] [protein=TetR/AcrR family transcriptional regulator] [protein\_id=WP\_015958592.1] [location=complement(3367775..3368311)] [gbkey=CDS]

MAHFSRYGYEKTTVTDLAKAIGFSKAYIYKFFDSKQAIGEAICASRLEKIMVAVSAAIADAPSASEKLRR

LFRALTEAGSELFFEDRKLYDIAAVAARDKWPSTEQYAGHLQQLIGQILVEGRQAGEFERKTPLDEATLA

VYMVMCPFINPVQLQYNLDTAPTAAVLLASLILRSLSP

>lcl|NZ\_FO834906.1\_prot\_WP\_016530780.1\_3313 [locus\_tag=BN49\_RS18175] [protein=NAD(P)H-binding protein] [protein\_id=WP\_016530780.1] [location=complement(3368485..3369480)] [gbkey=CDS]

MNSSGKVLILGASGGIGGEVARRLVADNWQVRALKRGAQIRDPEDGIQWIAGDALDGGQVAAAAAGCDVI

VHAVNPPGYRHWRQQVLPMLHNTLQAAERQRALVVLPGTVYNYGPDAFPLIAEEAAQQPVTRKGAIRVAM

ELALKDYVQRGGRALIVRAGDFFGPRAGNNWFSQGLVKPGQLPRIISYPGAIGVGHQWAWLPDVAATIAA

LLARRHELEPFARFHMQGHWDPDGSEMSQAIQRVVARYGGRAVAKSFPWWLVKLAAPFNATLREMVEMHY

LWRLPVRLRNDKLVDFLGAEPHTPLDSAVYQTLQGLGCLPAGAINQEAGEA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530779.1\_3314 [locus\_tag=BN49\_RS18180] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530779.1] [location=3369577..3370488] [gbkey=CDS]

MNTSIPWEWYRTFLAVLREGSLSGASRTLNITQPTAGRHIAGLENALGQALFTRSQTGLLATDAALALRV

HAEAMDNTARALERTAANFSRDRAELRGVVRVAASEVVGAEVLPPLVARLRQACPNIVIELMLSNRFQDL

LHREADIAVRMVAPQQEQLIARRLGRIELGLHATAAYLTRQGLPTTLDDLASHALIGFDSAPPLVRRALQ

AYPRFQREAFAMRTDSDLAQLSLIRAGAGIGICQVPLADGIIPLQRVLAADFSLYLDTWLVMHEDLRHSP

ACKRVFDFLAQGLQAYIRGPLAS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530778.1\_3315 [locus\_tag=BN49\_RS18185] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016530778.1] [location=3370647..3371642] [gbkey=CDS]

MKKVLCALGLMFTAVSSALATTYPLTIENCGYQETFTRPPERVVALGQNTVEILLLGLQKQVVASAFWPT

SVLPQLAEQNAKIKTLTVEIPSLESVLAQNPDFVPAQLPLLLGPESKVARREDLATVGVNSYVSPGMCAT

KKATGDMYGSRQKLWDMTWLYQEISDFARIFNVEDRGQALIADFKKREADLRQEFGKSKKDLSFVFWFSS

ASPSADAYVGGKNSASGFIASVLGGHNAITSETEWPTVSWESIIAANPDVIVVASLDRNRWALDKAEEKI

KFLKSDPAVSQLEAVKKGHIVVMDGQAMNPTIRTLYGAEQVGEQLRKMGLN

>lcl|NZ\_FO834906.1\_prot\_WP\_002908998.1\_3316 [locus\_tag=BN49\_RS18190] [protein=iron ABC transporter permease] [protein\_id=WP\_002908998.1] [location=3371642..3372679] [gbkey=CDS]

MSVAAIETRRSILLTGWCLLAAIVLALVIAVGVSVGELAIPLQNVFYAISNRTGLTAEPLNRIYESVIWD

FRLSRALVAACCGAGLAICGVVLQSLLKNALAEPYVLGVSAGASTGAVSIVVLGLGAGAISLSAGAFAGA

FAAFAFVALLTNGARGGNERTILAGVAASQLFNAITAYTISTSASAQQARDVMFWLLGSFSGVRWPEFQL

VIVVVLAGLAVCLWYARALDAFTFGDDAAASLGIAVPRVRLILFTTAALITATIVSMAGSIGFVGLVVPH

VMRFFFGPLHRTLLIASALAGAILMVLADIASRLLIAPQSLPVGVVTALVGVPFFAVIIYRSRNK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530777.1\_3317 [locus\_tag=BN49\_RS18195] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016530777.1] [location=3372679..3373440] [gbkey=CDS]

MSICAENITWKAGKKVIVNNVSLRVPRGETVGLLGPNGCGKSSLLRVLAGLRRPDAGRVTLDGQDIARMA

KKQLARRVAFVEQHGMTEANMRVRDVVRLGRIPHHSPLSNWSAQDDEAIAAALQRVAMLEKSEQGWLSLS

GGERQRVHIARALAQSPSEILLDEPTNHLDIHHQMQLMQLISELPVTSIVAIHDLNHAAMFCDSLIVMQQ

GQILASGTPEEILSEGLLWDVFRVKTKIEISPYHGKKHIHFIV

>lcl|NZ\_FO834906.1\_prot\_WP\_020317066.1\_3318 [locus\_tag=BN49\_RS18200] [protein=MFS transporter] [protein\_id=WP\_020317066.1] [location=3373497..3374684] [gbkey=CDS]

MLLGSQFVFNIGFYAVVPFLALFLRDDMLLSGGLIGLILGLRTFSQQGMFILGGTLADRYGAKAIILAGC

VVRVAGFLLLACGASLWPIILGACLTGVGGALFSPSIEALLARAGTLSQANGKRSRAEWFALFAVCGELG

AVIGPVAGGVLSGIGFRHIALAGAGIFLLALAVLFFCLPADGHTTTTRRRVPWWTPLRQPRFVAFILAYS

SWLLSYNQLYLALPVEIQRSGGREQDLAPLFMLASLLIITLQLPLARFARRMGAVRILPVGFLLLSASFA

SVALFAAAPPAEGWLRLMPAAGFVTLLTLGQMLLVPAAKDLIPLFAEESTLGAHYGALATAGGCAVLAGN

LLLGHLLDQALIPSPQAVYPWLLLALFPLCSAVALRAICRPLAAT

>lcl|NZ\_FO834906.1\_prot\_WP\_002909005.1\_3319 [locus\_tag=BN49\_RS18205] [protein=methionine synthase] [protein\_id=WP\_002909005.1] [location=complement(3374767..3375798)] [gbkey=CDS]

MKTWLPTSTAGSLPKPSWLAQPETLWSPWKLSSEELLAGKRDALRLSLDDQLRAGIDIVSDGEQTRQHFV

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LYDNHYKSREKLAWEFAKILNQEAKELEAAGVDIIQFDEPAFNVFFDEVNDWGIAALERATEGLKCETAV

HICYGYGIKANTDWKKTLGSEWRQYEEAFPQLQKSSLDIISLECHNSRVPMDLLELIRGKKVMVGAIDVA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530324.1\_3320 [locus\_tag=BN49\_RS18210] [protein=DUF1852 domain-containing protein] [protein\_id=WP\_016530324.1] [location=complement(3375822..3376802)] [gbkey=CDS]

MNNKFTYTIKRTRFDENYNPAENTRITTNFANLARGGNREENLRNTLIMMNNRFNSLAHWDNPHNDRYAV

ELDIISVEMNIAQDSASFPVIEILQTHIVDKKSGERHAGIVGNNFSSYVRDYDFSVLLLEHNKDQSRFSV

PENFGELHGNIFKDFVQSSAWRANFSKAPVICLSVSSKDVYHRTGNEHPVLGIEYAQEGVSLTERYFSKM

GLQVRYFMPKNSVAPLAFYFTGDLLSDYTSLELIATISTMETFQKIYRPEIYNANSPAGQYYQPNLSHLD

HSLTKIVYDREERSLLAIEQGKFTQQHFINPHKTLLEQWSANFALC

>lcl|NZ\_FO834906.1\_prot\_WP\_004184563.1\_3321 [locus\_tag=BN49\_RS18220] [protein=hypothetical protein] [protein\_id=WP\_004184563.1] [location=3377372..3377692] [gbkey=CDS]

MKKALLALFAIATVTAASAFAADKTDVPAPVVDNGVRPPMERDRGPLPPFPPQLPPHRPVLFSATVATDT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002909014.1\_3322 [locus\_tag=BN49\_RS18225] [protein=GlsB/YeaQ/YmgE family stress response membrane protein] [protein\_id=WP\_002909014.1] [location=complement(3377790..3378038)] [gbkey=CDS]

MGILSWIIFGLIAGILAKWIMPGKDGGGFIVTVILGIIGAVVGGWISTLFGFGKVDGFNFGSFVVAVIGA

LVVLFIYRKVRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002909015.1\_3323 [gene=menI] [locus\_tag=BN49\_RS18230] [protein=1,4-dihydroxy-2-naphthoyl-CoA hydrolase] [protein\_id=WP\_002909015.1] [location=complement(3378243..3378653)] [gbkey=CDS]

MIWKRQATLEQLNRLGEGNMVGLLDIRFETVTDDTLEATMPVDSRTQQPFGLLHGGASVVLAETLGSVAG

YLCSEGEQKVVGLEVNANHIRSARGGRVRGVCKALHVGTRHQVWQIEIFDEQSRLCCSSRLTTAVI

>lcl|NZ\_FO834906.1\_prot\_WP\_016530323.1\_3324 [locus\_tag=BN49\_RS18235] [protein=FAD-binding oxidoreductase] [protein\_id=WP\_016530323.1] [location=complement(3378650..3381706)] [gbkey=CDS]

MIPQISQAPGVVQLVLNFLQVLEQQGFTGDTATSYADRLTMATDNSVYQLLPDAVIFPRSTADVALLARV

AAEPRFKSLIFTPRGGGTGTNGQALNGGIIVDMSRYMNRIIEINPEEGWVRVEAGVIKDQLNQFLKPYGY

FFAPELSTSNRATLGGMINTDASGQGSLVYGKTSDHVLGLRAVLMGGDILDTQAVPVALAETLGNTPSTV

GRIYNTVYQRCKAQRDLIIDKFPKLNRFLTGYDLRHVFNDEMSEFDLTRILTGSEGTLAFITEARLDITR

LPKVRRLVNVKYDSFDSALRNAPFMVEAKALSVETVDSKVLNLAREDIVWHSVSELITDVPDKEMLGLNI

VEFAGDDAALIDQQVTTLCQRLDELMAASEAGVIGWQVCHDLEGVERIYAMRKKAVGLLGNAKGAAKPIP

FAEDTCVPPEHLADYIVEFRALLDSHGLSYGMFGHVDAGVLHVRPALDMCDPQQEVLMKQISDEVVALTA

KYGGLLWGEHGKGLRAEYSPAFFGETLYAELRKIKAVFDPDNRLNPGKICPPEGIDAPMMKVDAAKRGTW

DRQIPIAVRSSWRGAMECNGNGLCFNFDVKSPMCPSMKVSNQRIHSPKGRATLVREWLRLLADRGVDPNQ

LGKALPEQGVSLRSLVARTRNSWHARKGEYDFSHEVKEAMSGCLACKACSTQCPIKIDVPEFRSRFLQLY

HSRYLRPVRDHLVASVESYAPLMAQAPKTFNFFINQPWLKKLSEKHIGMVDLPLLSAPSLKQQMAGHRSA

NMTLEQLEALSAEQKAKMVLVVQDPFTSYYDAQVVADFIRLVEALGYQPVLLPFSPNGKAQHIKGFLTRF

ARTAQKTADFLNRVAQLGMPLVGVDPALVLCYRDEYKQTLGDKRGDFQVLLVHEWLPKALTSDARPDLGG

EPWYLFGHCTEVTALPAATKQWADIFAHFGAKLENVSVGCCGMAGTYGHEVKNHANSLAIYALSWQQAMQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_004148729.1\_3325 [gene=ydiK] [locus\_tag=BN49\_RS18240] [protein=AI-2E family transporter YdiK] [protein\_id=WP\_004148729.1] [location=3381925..3383037] [gbkey=CDS]

MINPHQPRDIPQILLSVLFLALIIISCLWVVQPFILSFAWAGTVVIATWPVLLRLQRVLFGKRLLAVLAM

TLLLFLLFVIPIALLVNSLVDNSVPLIKLISSGNVTLPDFAWLNSVPLVGDKLYSAWHGLLDMGGSAIMA

KVRPYIGTTTSWFVGQAAHIGKLLVYCGLMLLFSALLYWRGEQVAYGFRYFATRLAAKRGDAAVLLAGQA

VRAVALGVVVTALTQAVLGGIGLAVSGVPYAALLTVVMIFTCLVQLGPLLVLVPSIIWLYWSGDTTWGTV

LLVWSCVVGTMDNVIRPVLIRMGADLPMILILTGVIGGLIAFGMIGLFIGPVLLAVSWRLYDAWVHEVPP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002909055.1\_3326 [gene=ppsA] [locus\_tag=BN49\_RS18245] [protein=phosphoenolpyruvate synthase] [protein\_id=WP\_002909055.1] [location=complement(3383420..3385798)] [gbkey=CDS]

MSNNGSSPLVLWYNQLGMNDVDRVGGKNASLGEMITNLSGMGVSVPNGFATTADAFNQFLDQSGVNQRIY

ALLDETDIDDVSALAKAGAQIRQWIIDTPFQSELENAIRDAYDLLSADDAEASFAVRSSATAEDMPDASF

AGQQETFLNVQGFDAVLVAVKHVFASLFNDRAISYRVHQGYDHRGVALSAGVQRMVRSDLASSGVMFSID

TESGFDQVVFITSAWGLGEMVVQGAVNPDEFYVHKPTLAAGRPAIVRRTMGSKKIRMVYAPTQEHGKQVR

IEDVPQAQRDIFSLSNEEVQELAKQAVQIEKHYGRPMDIEWAKDGHTGKLFIVQARPETVRSRGQVMERY

TLHAQGQIIAEGRAIGHRIGAGPVKVIHDISEMNRIEPGDVLVTDMTDPDWEPIMKKASAIVTNRGGRTC

HAAIIARELGIPAVVGCGDATDRIQENQNVTVSCAEGDTGYVYAELLDFSVKSSSVGDMPDLPLKVMMNV

GNPDRAFDFACLPNEGVGLARLEFIINRMIGVHPRALLEFDDQEPGLQNEIRELMKGYDSPREFYVGRLT

EGIATLGAAFYPKRVIVRLSDFKSNEYANLVGGERYEPEEENPMLGFRGAGRYVSESFRDCFALECEAMK

RVRNDMGLTNVEVMVPFVRTVAQAKAVVEELERQGLKRGENGLKIIMMCEIPSNALLAEQFLEYFDGFSI

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>lcl|NZ\_FO834906.1\_prot\_WP\_002909058.1\_3327 [locus\_tag=BN49\_RS31120] [protein=hypothetical protein] [protein\_id=WP\_002909058.1] [location=3385874..3385993] [gbkey=CDS]

MKLKKTVNRSSKLFFHFSDCSPDIANLMIFRNSDEKRWK

>lcl|NZ\_FO834906.1\_prot\_WP\_002909061.1\_3328 [locus\_tag=BN49\_RS18255] [protein=kinase/pyrophosphorylase] [protein\_id=WP\_002909061.1] [location=3386138..3386971] [gbkey=CDS]

MESAVDRHVFYISDGTAITAEVLGHAVMSQFPVAISSVTLPFVENISRARAVKEQIDAIYQQTGIRPLVF

YSIVIPEIRDIILQSEGFCQDIVQALVAPLQQELNLDPTPVAHRTHGLNPGNLIKYDARIAAIDYTLAHD

DGISLRNLDQAQVILLGVSRCGKTPTSLYLAMQYGIRAANYPFIADDMDNLVLPASLKPLQHKMFGLTIN

PERLAAIREERRENSRYASLRQCRMEVTEVEALYRKNKIPCLNSTNYSVEEIATKIMDIMGLNRRMY

>lcl|NZ\_FO834906.1\_prot\_WP\_004180369.1\_3329 [gene=aroH] [locus\_tag=BN49\_RS18260] [protein=3-deoxy-7-phosphoheptulonate synthase AroH] [protein\_id=WP\_004180369.1] [location=3387126..3388172] [gbkey=CDS]

MNKTDELRTARIESLVTPAELAQRHPVTADVAAHVSASRRRIEKILNGEDRRLLVIIGPCSIHDTDAALE

YARRLQGMRERYQPQLEIVMRTYFEKPRTVVGWKGLISDPDLNGSYRVNHGIELARRLLLQVNELGVPTA

TEFLDMVTGQFIADLISWGAIGARTTESQIHREMASALSCPVGFKNGTDGNTRIAVDAIRASRASHMFLS

PDKQGQMTIYQTSGNPYGHIIMRGGKRPNYHAEDIAAAGEALREFDLPEQLVVDFSHGNCQKQHRRQLEV

CADICQQIRAGSTAIAGIMAESFLQEGTQKVVPGQPLTWGQSITDPCLSWEDSERLLSELAAATATRL

>lcl|NZ\_FO834906.1\_prot\_WP\_004898888.1\_3330 [gene=hemP] [locus\_tag=BN49\_RS18265] [protein=hemin uptake protein HemP] [protein\_id=WP\_004898888.1] [location=3388319..3388507] [gbkey=CDS]

MTRMDNTATAEKPKDNAPYPVATDREISSRVLLGSEGRVVIEHGGQRYLLRQTHAGKLILTK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530559.1\_3331 [locus\_tag=BN49\_RS18270] [protein=protein adenylyltransferase SelO] [protein\_id=WP\_016530559.1] [location=complement(3388537..3389979)] [gbkey=CDS]

MTLSFTTHWRDELPDFYTSLSPTPLDNARLIWRNAPLAQQLEVPDALFAPESGAGVWGGEALLPGMSPLA

QVYSGHQFGAWAGQLGDGRGILLGEQQLADGRRYDWHLKGAGLTPYSRMGDGRAVLRSTIRESLASEAMH

ALGIPTTRALAMVTSDTPVYRERVEPGAMLMRVSESHVRFGHFEHFYYRREPQKVQQLADYVIRHHWPQL

QDEADKYLLWFRDIVMRTAQTIASWQTVGFAHGVMNTDNMSILGLTIDYGPYGFLDDFQPDFICNHSDYQ

GRYSFENQPAVGLWNLQRLAQSLSPFISAEALNAALDEYQHALLTAYGQRMRDKLGLFSQQKGDNDLLDG

LFALMIREKSDYTRTFRLLSHSEQLSAASPLRDEFIDRAAFDSWFAGYRARLRDEQVDDAQRQQRMQGVN

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>lcl|NZ\_FO834906.1\_prot\_WP\_002909082.1\_3332 [locus\_tag=BN49\_RS18275] [protein=NlpC/P60 family protein] [protein\_id=WP\_002909082.1] [location=complement(3390093..3390557)] [gbkey=CDS]

MRFWFMLAAALILAGCSSHRAPPPNPRLADSITVVANLNEQLRSWRGAPYRYGGMTPRGVDCSGFVVRTF

RDKFALQLPRETREQAEIGTRIDKRDLLPGDLVFFKTGSGESGLHVGIYDTDNQFIHASTSQGVTRSSLD

NVYWNKKFWQARRI

>lcl|NZ\_FO834906.1\_prot\_WP\_002909083.1\_3333 [gene=btuD] [locus\_tag=BN49\_RS18280] [protein=vitamin B12 ABC transporter ATP-binding protein BtuD] [protein\_id=WP\_002909083.1] [location=complement(3390639..3391388)] [gbkey=CDS]

MSFLMQLQDVEAAGRLAPFSAAFRAGEIVHLVGPNGAGKSTLLTRMAGLSDGPGTVHFNGRLLDEWPARE

LARRRGYLSQHQTPPFAMPVWHYLALHMQQQGDSARLSDIAARLGLDNKLGRPVNQLSGGEWQRVRLAAV

ILQIDPLSNSAGQLLLLDEPMNSLDVAQQAALDRLLHELSAAGIAVVMSSHDLNHTLRHAGQSWLLCQGE

AIACGETAEVLNEENLTAAYAIPFQRVEVAGHIMLIASQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004180371.1\_3334 [locus\_tag=BN49\_RS18285] [protein=glutathione peroxidase] [protein\_id=WP\_004180371.1] [location=complement(3391388..3391939)] [gbkey=CDS]

MQHDILNTEVTTIDGEKTTLASFAGKVLLIVNVASKCGLTPQYEQLEDLQKQFAAEGFSVLGFPCNQFLG

QEPGSEEEIKTFCSTTYGVTFPLFSKIDVNGEHRAPLYQKLIAAAPKAVAPEGSGFYERMASKGRAPLYV

DDILWNFEKFLIDRQGNVIQRFSPDMTPDDPQLVAAIKGALAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043516.1\_3335 [locus\_tag=BN49\_RS18290] [protein=MetQ/NlpA family lipoprotein] [protein\_id=WP\_046043516.1] [location=3392176..3392976] [gbkey=CDS]

MKKLFSLALIATSVALLSACSPDEDNKVKVAINTGPDEAIWKVVEQVAKDKYHLDVEVVSFNDYVLPNEA

LNNKDVDANAFQTLPYLEAQSKERGYKFAVVGKTFVFPIAAYSHRIKNISELPEGATVTISNETTTLGRS

LLLLQAQGLLKLKPGVGYLPTTLDIIDNPKQLKIVEVDTPQLTRTLDDPNVSLSIINTNFSAQVGLSAAR

DGLFMEGPDSPYVNAIVAREDNKDSKKIQELKAAFQTSEVAEKAKEVYKGDAIKGW

>lcl|NZ\_FO834906.1\_prot\_WP\_004184567.1\_3336 [gene=btuC] [locus\_tag=BN49\_RS18295] [protein=vitamin B12 ABC transporter permease BtuC] [protein\_id=WP\_004184567.1] [location=complement(3393013..3393999)] [gbkey=CDS]

MLTLAHLQQRRSRRWLLGLTLLLLVTLLISLCAGEQWIPPGEWLSAKGQLFIWQIRLPRTLAVLLVGAAL

ALSGAIMQALFENPLAEPGLLGVSNGAGVGLIAAVLLGKGVLPGWALGLCAIFGALLITFILLRFARRHL

STSRLLLAGVALGIICSALMTWAVYFSTSFDLRQLMYWMMGGFGGVDWQQLWLMIALLPVLCWVCLQSQP

LNLLALGEVSARQLGLPLWLWRKLLVVATGWMVGVSVALAGAIGFIGLVIPHILRLCGLSDHRVLLPACM

LAGASALLGADIIARLALSAAELPIGVVTATLGAPVFIWLLLRSRGRG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530845.1\_3337 [locus\_tag=BN49\_RS18300] [protein=hypothetical protein] [protein\_id=WP\_016530845.1] [location=complement(3394123..3395556)] [gbkey=CDS]

MSDSTLTGNAPVRRNITRKNVIIGLLLLLFVLIALWCHGRPGSELGLLGFTPLVALAILSLIGVDIVLAV

ISSIIIAMIMTSTGLPEMGTMLAKSTGSFIATVGLIIMLGAGVGEVATRTGAAVELVKFVVHRIGLSSQT

RVKFGIVASSILICGSLGTMAGGNAIIVAVIIPVAAAVRLTPPTVAALMMTAGSVGLFTGPFTPSTVTIL

SLGGLSYPDYLLYVGLPMSAVTLLAGWVMAGRIQKMTEGKLRYDVDLAEKPQEDLSAAQQRRRKLSALAF

AATIIVMAIVGVVIKAGFSFAIIVMLLVALMTGLVGGLRPTQILQALYHGCGRLVWMFILYWLYNPILEL

MDGLHAYQGLLEYTQPLLEGISPAWLCFSIFAFNIIGHVPGAAVAQMTFTHKIFGPMLMAAGVLPQGTTA

VLLASSQVDWFGPFPSSDMFGQMGLAQSTHLKYMLYNGWAIVVANIILFALLFQILV

>lcl|NZ\_FO834906.1\_prot\_WP\_002909089.1\_3338 [locus\_tag=BN49\_RS18305] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002909089.1] [location=3395837..3396751] [gbkey=CDS]

MKLRHLEIFYAVMTCGSLSRAAEALNISQPAASKALKSAEMKLGFTLFQRVRGKLLPTSEAITLFEKAQS

IYQDLDNLRLLADNLARDPRAKITLGCLPSLGLSLVPELVTDFYQQNSNLVMTLTTEHTETLVKKLDLRE

IDLALTLQPVQQGEILTTLIAEVPLVYIDRHYRQGAVEIDQIDQQRWISPGPHSLSAAIATRRDFSTTRL

NVQTYYMATEFVKRGMGCSITDIFSAQHNLAPEMIHPITPPMAINLCLLRRADVSLSPMAQKFVDFLCQR

LRQQLKEINLRLYPDHKKSIAPLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004180373.1\_3339 [locus\_tag=BN49\_RS18310] [protein=D-amino acid dehydrogenase] [protein\_id=WP\_004180373.1] [location=3396801..3398054] [gbkey=CDS]

MNKRIVIIGGGVVGLATAWELIKRGHQVQLLERNAEPGSATSFANGGQLSYRYVAPLADSGVPLQGMKWM

GKADSPLNMRLRMSLQQWRWLLQFLRACNNQTNKMNGDHILRLSLLSRQVMQAWRDEDNLADFHWRRSGK

LIIHRREYDFNKAAKGIDPQYQQALNAEACLQLEPALKHISPSLQGGIYSPGDETADCHQFCLALLDKLN

ASSDFSLLTQCEVRRLHKRGGRISSLETSQGTLTGDEYVVAAGNGSGSLLGHLGVRVPLCALKGYSLTLP

YPEKAGIAPDISVTDYGHKIVYARLGQQLRIAAMVDIGYDGDELRESRIQALKNIVARSFPELEGLDEAE

VWTGMRPSTPAGPPMLGRAGYPNLWMNLGQGSLGFTLAAGSAVVLGALIDNQMPDISLEGLTWKQTA

>lcl|NZ\_FO834906.1\_prot\_WP\_002909094.1\_3340 [locus\_tag=BN49\_RS18315] [protein=RidA family protein] [protein\_id=WP\_002909094.1] [location=3398051..3398404] [gbkey=CDS]

MTIIRNNPQPRLAASVAYGDLLFLSGQTPKSNEDDIVLQTREVLEKIDALLAAAGSDKQHILSAQIWLKN

IERDFAAFNEVWVQWMPEGYSPARAAVQAEMARPEILVEIMLTAVKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002909098.1\_3341 [gene=ihfA] [locus\_tag=BN49\_RS18320] [protein=integration host factor subunit alpha] [protein\_id=WP\_002909098.1] [location=complement(3398457..3398756)] [gbkey=CDS]

MALTKAEMSEYLFDKLGLSKRDAKELVELFFEEIRRALENGEQVKLSGFGNFDLRDKNQRPGRNPKTGED

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>lcl|NZ\_FO834906.1\_prot\_WP\_015958605.1\_3342 [gene=pheT] [locus\_tag=BN49\_RS18325] [protein=phenylalanine--tRNA ligase subunit beta] [protein\_id=WP\_015958605.1] [location=complement(3398761..3401148)] [gbkey=CDS]

MKFSELWLREWVNPAIDSEALSDQITMAGLEVDGVEPVAGSFNGVVVGEVVECGQHPNADKLRVTKVNVG

GERLLDIVCGAPNCRQGLKVAVATIGAVLPGDFKIKAAKLRGEPSEGMLCSFSELGISDDHSGIIELPAD

APIGTDIREYLKLDDNTIEISVTPNRADCLGIIGVARDVAVLNKAPLNAPEITPVAATIDDVLPIQVDAP

QACPRYLGRVVKGINVKAPTPLWMKEKLRRCGIRSIDAVVDVTNYVLLELGQPMHAFDRDRIEGGIVVRM

AKEGETLVLLDGSEAKLDSDTLVIADHNKALAMGGIFGGEHSGVNDETQNVLLECAFFSPLSITGRARRH

GLHTDASHRYERGVDPALQYKALERATRLLIDLCGGEAGPVIDVTSKENLPTRATITLRRSKLDRLIGHH

IDDAQVTDILQRLGCEVTVGEGEWQAVAPSWRFDMEIEEDLVEEVARVYGYNNIPDEPVQAGLIMGTHRE

ADLSLKRVKTLLNDKGYQEVITYSFVDPKVQQLIHAGEEALILPSPISSEMSAMRLSLWTGLLGTVVYNQ

NRQQSRVRIFESGLRFVPDTNAPLGIRQDVMLAGAICGNRYEEHWTLAKETVDFYDLKGDLEAVLDLTGK

LADIEFRAEATTALHPGQSAAIYLKGERIGFIGVVHPELERKLDLNGRTLVFELEWNKLADRVVPQARDI

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>lcl|NZ\_FO834906.1\_prot\_WP\_004184569.1\_3343 [gene=pheS] [locus\_tag=BN49\_RS18330] [protein=phenylalanine--tRNA ligase subunit alpha] [protein\_id=WP\_004184569.1] [location=complement(3401164..3402147)] [gbkey=CDS]

MSHLAELVASAKAAINEASDVAALDNVRVEYLGKKGHLTLQMTTLRELPPEERPAAGAVINEAKEQVQQA

LNARKAELEGAALNARLAAETIDVSLPGRRIENGGLHPVTRTIDRIESFFGELGFTVATGPEIEDDYHNF

DALNIPGHHPARADHDTFWFDATRLLRTQTSGVQIRTMEKQQPPIRIIAPGRVYRNDYDQTHTPMFHQME

GLIVDKNISFTNLKGTLHDFLNNFFEEDLQVRFRPSYFPFTEPSAEVDVMGKNGKWLEVLGCGMVHPNVL

RNVGIDPEVYSGFAFGMGMERLTMLRYGVTDLRAFFENDLRFLKQFK

>lcl|NZ\_FO834906.1\_prot\_WP\_001386830.1\_3344 [gene=pheM] [locus\_tag=BN49\_RS31125] [protein=pheST operon leader peptide PheM] [protein\_id=WP\_001386830.1] [location=complement(3402286..3402330)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_000124850.1\_3345 [gene=rplT] [locus\_tag=BN49\_RS18335] [protein=50S ribosomal protein L20] [protein\_id=WP\_000124850.1] [location=complement(3402454..3402810)] [gbkey=CDS]

MARVKRGVIARARHKKILKQAKGYYGARSRVYRVAFQAVIKAGQYAYRDRRQRKRQFRQLWIARINAAAR

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>lcl|NZ\_FO834906.1\_prot\_WP\_001124225.1\_3346 [gene=rpmI] [locus\_tag=BN49\_RS18340] [protein=50S ribosomal protein L35] [protein\_id=WP\_001124225.1] [location=complement(3402861..3403058)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004189469.1\_3347 [gene=infC] [locus\_tag=BN49\_RS18345] [protein=translation initiation factor IF-3] [protein\_id=WP\_004189469.1] [location=complement(3403151..3403693)] [gbkey=CDS]

MKGGKRVQTARPNRINGEIRAQEVRLTGLEGEQLGIVSLREAIEKAEEAGVDLVEISPNAEPPVCRIMDY

GKFLYEKSKSSKEQKKKQKVIQVKEIKFRPGTDEGDYQVKLRSLIRFLEDGDKAKITLRFRGREMAHQQI

GMEVLNRVKDDLVELAVVESFPTKIEGRQMIMVLAPKKKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002910026.1\_3348 [gene=thrS] [locus\_tag=BN49\_RS18350] [protein=threonine--tRNA ligase] [protein\_id=WP\_002910026.1] [location=complement(3403697..3405625)] [gbkey=CDS]

MPVITLPDGSQRHFDHAVSPMDVALDIGPGLAKATIAGRVNGELVDACDPIESDSTLSIITAKDEEGLEI

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WHEARETFVKRGESYKVSILDENIAHDDKPGLYHHEEYIDMCRGPHVPNMRFCHHFKLMKTAGAYWRGDS

NNKMLQRIYGTAWADKKALNAYLQRLEEAAKRDHRKIGKQLDLYHMQEEAPGMVFWHNDGWTIFRELETF

VRSKLKEYQYQEVKGPFMMDRVLWEKTGHWDNYKDAMFTTSSENREYCIKPMNCPGHVQIFNQGLKSYRD

LPLRMAEFGSCHRNEPSGALHGLMRVRGFTQDDAHIFCTEDQVRDEVNACIRMVYDMYSTFGFEKIVVKL

STRPEKRIGSDETWDRAEADLAVALEENNIPFEYQLGEGAFYGPKIEFTLYDCLDRAWQCGTVQLDFSLP

QRLSASYVGENNERQVPVMIHRAILGSLERFIGILTEEFAGFFPTWIAPVQVVVMNITDSQAEYVNELTR

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EIRSRSLQQLEE

>lcl|NZ\_FO834906.1\_prot\_WP\_015958606.1\_3349 [locus\_tag=BN49\_RS18355] [protein=hypothetical protein] [protein\_id=WP\_015958606.1] [location=complement(3406057..3406290)] [gbkey=CDS]

MKNNRYTIAALALCVLSFGASAATPVPPSGHQDHTQVGIAKATDVEAGSNIAPGAPTTGKSMNDAFNVHT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002910030.1\_3350 [locus\_tag=BN49\_RS18360] [protein=YdiY family protein] [protein\_id=WP\_002910030.1] [location=complement(3406562..3407320)] [gbkey=CDS]

MKLLKTVPAAVMLAGGLFASVGAMADDSVFTVMDDPSAAKKPFEGVVNAGYLAQSGNTKSSSMTADSTLT

WYGNTTAWSLWGNASNTSSNDERSSEKYAVGGRSRYNLTDMNYVFGQGSWLTDRYNGYQQRDVVTAGYGR

QILNGPVHSLRFEFGPGVRYDEYTDGDTDTQPLGYASGTWAWQMTDNAKFSQGVSVFGAEDTTVNSESAL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004145382.1\_3351 [gene=pfkB] [locus\_tag=BN49\_RS18365] [protein=6-phosphofructokinase II] [protein\_id=WP\_004145382.1] [location=3407677..3408609] [gbkey=CDS]

MTKIYTLTLAPSLDSATQTPQIYPEGKLRCSAPVFEPGGGGINVARAVTFLGGKATAIFPVGGATGEHLA

ALLADEQVPVETVETRDWTRQNLHVHVAASGEQYRFVMPGAALTDDEFRRLEEKVLTIEPGSLLVVSGSL

PPGISVDNLMQLVKNAQQQGLRCIIDSSGDALAAALDVGNIELVKPNQKELSALVQRDLSQPDDVRLAAQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_002910033.1\_3352 [gene=ghoS] [locus\_tag=BN49\_RS18370] [protein=type V toxin-antitoxin system endoribonuclease antitoxin GhoS] [protein\_id=WP\_002910033.1] [location=3408704..3408988] [gbkey=CDS]

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LAEAALGRPAEIAVATFAEWLKAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002910036.1\_3353 [locus\_tag=BN49\_RS18375] [protein=fructosamine kinase family protein] [protein\_id=WP\_002910036.1] [location=3409094..3409966] [gbkey=CDS]

MWQAISTLLRDWHTEDAEIELKTELPGGEIHSAWHLRFGGKDYFVKCDERELLPIFTAESDQLELLSRSK

TVRVPQVFAVGSDRDYSFVVMEYLPPRPLDAHNAFLLGQQLAHLHQWSDQPQFGLDFDNDLSTTPQPNAW

QRRWSVFFAEQRIGWQLELAAEKGLHFGDIDTLVDMVQQRLANHQPQPSLLHGDLWSGNCALGPDGPYIF

DPACYWGDRECDLAMLPMHPEQPPQIYDGYQSVSPLPSGFLDRQPIYQLYTLLNRAILFGGQHLVTAQQA

LDDVLMEKMR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145385.1\_3354 [gene=tonB] [locus\_tag=BN49\_RS18380] [protein=TonB system transport protein TonB] [protein\_id=WP\_004145385.1] [location=complement(3410010..3410756)] [gbkey=CDS]

MSAMTLDLPRRFPWPTLLSVAIHGAVVAGLLYTSVHQVIEQPSPTQPIEITMVAPADLEPPPAAQPVVEP

VVEPEPEPEPEVVPEPPKEAPVVIHKPEPKPKPKPKPKPKPEKKVEQPKREVKPAAEPRPASPFENNNTA

PARTAPSTSTAAAKPTVTAPSGPRAISRVQPSYPARAQALRIEGTVRVKFDVSPDGRIDNLQILSAQPAN

MFEREVKSAMRRWRYQQGRPGTGVTMTIKFRLNGVEIN

>lcl|NZ\_FO834906.1\_prot\_WP\_002910042.1\_3355 [locus\_tag=BN49\_RS18385] [protein=YciI family protein] [protein\_id=WP\_002910042.1] [location=3410967..3411263] [gbkey=CDS]

MLYVIYAEDIADSLEKRLSVRPAHLARLQLLHDEGRLLTAGPMPAVDSNEPGAAGFSGSTVIAEFESLEA

AQAWANDDPYIAAGVYRQVSVKPYKKVF

>lcl|NZ\_FO834906.1\_prot\_WP\_032103891.1\_3356 [locus\_tag=BN49\_RS31130] [protein=hypothetical protein] [protein\_id=WP\_032103891.1] [location=3411376..3411516] [gbkey=CDS]

MTVIRLRSLEDEHAPSPATPSSTIASLFSAIENADKTSTPRVIVNY

>lcl|NZ\_FO834906.1\_prot\_WP\_171819479.1\_3357 [locus\_tag=BN49\_RS18395] [protein=YceI family protein] [protein\_id=WP\_171819479.1] [location=3411944..3412591] [gbkey=CDS]

MFSISPVFFWANIYVPADFEDYCVNTLKKTALLSVLALYIPVSQAAAKEYSLDPQHTSVVISWNHFGFSN

PTAYISDVSGKLAFDKENPEKSSVNVTLPVKTIDAHVKALTDEFLGKEYFDVKTFPNATFQSTKVESKGD

NKYDVEGNLTIKGITKPVVLHAVLNKQDMHPMVKKEAIGFDATGVIKRSDFKLDKYVSAVSDNVTITLST

EAYAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004194006.1\_3358 [locus\_tag=BN49\_RS30495] [protein=YciY family protein] [protein\_id=WP\_004194006.1] [location=complement(3413095..3413268)] [gbkey=CDS]

MKRSRTEVGRWRMLRQVNRRKARWLEAQSRRNMRILAIRKGLVKRQRHALLFIFPDS

>lcl|NZ\_FO834906.1\_prot\_WP\_002910077.1\_3359 [gene=cls] [locus\_tag=BN49\_RS18410] [protein=cardiolipin synthase] [protein\_id=WP\_002910077.1] [location=3413412..3414872] [gbkey=CDS]

MTTFYTVVNWLVILGYWLLIAGVTLRILMKRRAVPSAMAWLLIIYILPLVGIIAYLSFGELHLGKRRAER

ARAMWPSTAKWLNDLKACKHIFAEDNSPVAESLFKLCERRQGIGGVKGNQLQLLTESDDVMQALIRDIQL

ARHNIEMVFYIWQPGGMADSVAESLMAAARRGVHCRLMLDSAGSVAFFRSPWAAMMRNAGIEVVEALKVN

LMRVFLRRMDLRQHRKMVMIDNYIAYTGSMNMVDPRYFKQDSGVGQWIDLMARMEGPVATSMGIVYSCDW

EIETGKRILPPPPDVNIMPFEEASGHTIHTIASGPGFPEDLIHQALLTAAYAAKEHLIMTTPYFVPSDDL

LHAICTAAQRGVDVSIILPRKNDSLLVGWASRAFFTELLAAGVKIYQFEGGLLHTKSVLVDGELSLVGTV

NLDMRSLWLNFEITLVIDDAGFGSDLAAVQDDYISRSRLLDARLWLKRPLWQRIAERLFYFFSPLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002910079.1\_3360 [locus\_tag=BN49\_RS18415] [protein=HI1450 family dsDNA-mimic protein] [protein\_id=WP\_002910079.1] [location=3414907..3415236] [gbkey=CDS]

MDMDLNNRLTEDETLEQAYDIFLELAADNLDPADIILFNLQFEERGGAELFDPSADWEEHVDYDLNPDFF

AEVVIGLADTDGGEINDIFARVLLCREKDHKLCHILWRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910080.1\_3361 [locus\_tag=BN49\_RS18420] [protein=ion transporter] [protein\_id=WP\_002910080.1] [location=complement(3415300..3416127)] [gbkey=CDS]

MLSAARLRLYHLLFDQNRRSGRRFEGLCGLFALLSVLVIFIESGLGTQYHLTLDEWHIFVWLELLVTAVF

TLEYLLRIATWPNPLHYIFSFWGLIDLATILPLYVMWLWPEISLNYVFAWRAMRAIRALRILKLLRFMPS

LNVFWRAIVSARHQLILFYSFIAIVMVIFGSLMYLIEGPEYGFTTLNASVYWAIVTITTVGYGDITPHTP

LGRILASILILIGYSIIAIPTGLITTHMTSALNRRRQQRLCPQCQQGDHDDNARFCHACGHALPK

>lcl|NZ\_FO834906.1\_prot\_WP\_002910083.1\_3362 [gene=oppF] [locus\_tag=BN49\_RS18425] [protein=murein tripeptide/oligopeptide ABC transporter ATP-binding protein OppF] [protein\_id=WP\_002910083.1] [location=complement(3416183..3417187)] [gbkey=CDS]

MNAVTEQRKVLLEIADLKVHFDIKDGKQWFWQPSKTLKAVDGVTLRLYEGETLGVVGESGCGKSTFARAI

IGLVKATDGKVAWLGKDLLGMKQEEWRDVRSDIQMIFQDPLASLNPRMTIGEIIAEPLRTYHPKMPRQEV

RDRVKAMMMKVGLLPNLINRYPHEFSGGQCQRIGIARALILEPKLIICDEPVSALDVSIQAQVVNLLQQL

QREMGLSLIFIAHDLAVVKHISDRVLVMYLGHAVELGTYDEVYHNPLHPYTKALMSAVPIPDPDLEKTKT

IQLLEGELPSPINPPSGCVFRTRCPLAGPECAKTRPVLEGSFRHAVSCLKVDPL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151853.1\_3363 [locus\_tag=BN49\_RS18430] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004151853.1] [location=complement(3417184..3418197)] [gbkey=CDS]

MTMIETAKAPQAQSHSGLLLDVKDLRVTFKTPDGDVTAVNDLNFTLQAGETLGIVGESGSGKSQTAFALM

GLLAANGRIGGSATFNGRQILNLPERELNKLRAEQISMIFQDPMTSLNPYMRVGEQLMEVLMLHKGLSKA

EAFEESVKMLDAVKMPEARKRMKMFPHEFSGGMRQRVMIAMALLCRPRLLIADEPTTALDVTVQAQIMTL

LNELKREFNTAIIMITHDLGVVAGICDKVLVMYAGRTMEYGQARDVFYQPSHPYSIGLLNAVPRLDAEGD

ALLTIPGNPPNLLRLPKGCPFQPRCPHAMEQCSSAPPLESFAPGRLRACFKPVGDLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004145396.1\_3364 [gene=oppC] [locus\_tag=BN49\_RS18435] [protein=oligopeptide ABC transporter permease OppC] [protein\_id=WP\_004145396.1] [location=complement(3418209..3419117)] [gbkey=CDS]

MMLSKKNSEALENFSEKLEVEGRSLWQDARRRFMHNRAAVTSLIMLVLIALFVTFAPMVSSFSYFDTDWG

MMSNAPDMASGHYFGTDSSGRDLLVRVAIGGRISLMVGVAAALVAVILGTLYGSLSGYLGGKVDSVMMRL

LEILNSFPFMFFVILLVTFFGQNILLIFVAIGMVSWLDMARIVRGQTLSLKRKEFIEAAQVGGVSTASIV

LRHIVPNVLGVVVVYASLLVPSMILFESFLSFLGLGTQEPLSSWGALLSDGANSMEVSPWLLLFPAGFLV

VTLFCFNFIGDGLRDALDPKDR

>lcl|NZ\_FO834906.1\_prot\_WP\_002910089.1\_3365 [gene=oppB] [locus\_tag=BN49\_RS18440] [protein=oligopeptide ABC transporter permease OppB] [protein\_id=WP\_002910089.1] [location=complement(3419132..3420052)] [gbkey=CDS]

MLKFILRRCLEAIPTLFILITISFFMMRLAPGSPFTGERTLPPEVMANIEAKYHLNDPIMTQYFNYLKQL

AHGDFGPSFKYKDYSVNDLVAASFPVSAKLGFAAFLLAVVIGVAAGVIAALKQNTRWDYAVMGVAMTGVV

IPSFVVAPLLVMIFAITLHWLPGGGWNGGALKFMILPMVALSLAYIASIARITRGSMIEVLHSNFIRTAR

AKGLPMRRIILRHALKPALLPVLSYMGPAFVGIITGSMVIETIYGLPGIGQLFVNGALNRDYSLVLSLTI

LVGALTILFNAIVDVLYAVIDPKIRY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529471.1\_3366 [gene=oppA] [locus\_tag=BN49\_RS18445] [protein=oligopeptide ABC transporter substrate-binding protein OppA] [protein\_id=WP\_016529471.1] [location=complement(3420138..3421772)] [gbkey=CDS]

MTIITKKRLIAAGVLSALIAGNMAMAADVPAGVQLAEKQTLVRNSGAEPQSLDPNKIEGVPEANISRDLF

EGLLNTSPKDGHPIPGVAESWDNKDFKVWTFHLRKDAKWSNGEPVTAQDFVYSWQRLVDPKTASPYASYP

QYSHIVNVDEIIDGKKAPSELGVKAIDDHTLEVTLSEPVPYFYKLLVNPAMSPVYKPAIEKFGDKWTQPG

NIVTNGAYTLKDWVVNERIVMERNPHYWDNAKTVINTVTWLPTSSEVTYVNRYRSGELDMTYNQLPIELF

QKLKKEIPNELHVDPYLCTYYYEINNQKAPFTDVRVRTALKLGLDRDIIANKVKGQGDLPAYGYTPPYTD

GAKLSEPEWFTWSQEKRNEEAKKLLAEAGYSADKPLTFNLLYNTSDLHKKLAIAAASLWRKNLGIDVKLV

NQEWKTFLDTRHQGTYDVARAGWCADYNEPTSFLNTMLSDSSMNTAHYKSPAFDKIMAESVKASDEAQRT

AAYAKAEQQLDKDSAIVPVYYYVNARLVKPWVGGYTGKDPMDNVYTKDLYVIKH

>lcl|NZ\_FO834906.1\_prot\_WP\_002910095.1\_3367 [locus\_tag=BN49\_RS18455] [protein=YchE family NAAT transporter] [protein\_id=WP\_002910095.1] [location=complement(3422510..3423157)] [gbkey=CDS]

MTQSLFDFSAYFKFFIGLFALVNPVGIIPVFISMTSYQPAAVRNKTNLTANLSVAIILLTSLFLGDGILQ

IFGISIDSFRIAGGILVVTIAMSMISGKLGEDKQNKQEKSETAVRESIGVVPLALPLMAGPGAISSTIVW

GTRYHSWVHLVGFSLAIAVFALCCWGIFRMAPWLVRLLGQTGINVITRIMGLLLMALGIEFIVTGIKALF

PGLLS

>lcl|NZ\_FO834906.1\_prot\_WP\_032103886.1\_3368 [locus\_tag=BN49\_RS18460] [protein=hypothetical protein] [protein\_id=WP\_032103886.1] [location=complement(3423371..3423556)] [gbkey=CDS]

MHVNVYVEKSGRCFTDLLKKLYLFRFQVLLPSTLLVSSRLLTSEYKLRDLDQVLSLLIPFS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529470.1\_3369 [gene=adhE] [locus\_tag=BN49\_RS18465] [protein=bifunctional acetaldehyde-CoA/alcohol dehydrogenase] [protein\_id=WP\_016529470.1] [location=3423634..3426309] [gbkey=CDS]

MAVTNIAELNALVERVKKAQREYASFTQEQVDKIFRAAALAAADARIPLAKMAVAESGMGIVEDKVIKNH

FASEYIYNAYKDEKTCGVLSEDDTFGTITIAEPIGIICGIVPTTNPTSTAIFKSLISLKTRNAIIFSPHP

RAKEATNKAADIVLQAAIAAGAPKDLIGWIDQPSVELSNALMHHPDINLILATGGPGMVKAAYSSGKPAI

GVGAGNTPVVIDETADIKRAVASVLMSKTFDNGVICASEQSVVVVDSVYDAVRERFASHGGYLLQGKELK

AVQDIILKNGALNAAIVGQPAAKIAELAGFTVPATTKILIGEVTNVDESEPFAHEKLSPTLAMYRAKDFE

DAVAKAEKLVAMGGIGHTSCLYTDQDNQPARVAYFGQMMKTARILINTPASQGGIGDLYNFKLAPSLTLG

CGSWGGNSISENVGPKHLINKKTVAKRAENMLWHKLPKSIYFRRGSLPIALDEVITDGHKRALIVTDRFL

FNNGYADQITSVLKAAGVETEVFFEVEADPTLTIVRKGADLANSFKPDVIIALGGGSPMDAAKIMWVMYE

HPETHFEELALRFMDIRKRIYKFPKMGVKAKMVAITTTSGTGSEVTPFAVVTDDATGQKYPLADYALTPD

MAIVDANLVMDMPKSLCAFGGLDAVTHALEAYVSVLASEFSDGQALQALKLLKEYLPASYHEGSKNPVAR

ERVHSAATIAGIAFANAFLGVCHSMAHKLGSQFHIPHGLANALLICNVIRYNANDNPTKQTAFSQYDRPQ

ARRRYAEIADHLGLSAPGDRTAAKIEKLLAWLESIKAELGIPKSIREAGVQEADFLAQVDKLSEDAFDDQ

CTGANPRYPLISELKQILLDTYYGREFVEGEAGAKAEVAPVKAEKKAKKSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529469.1\_3370 [gene=tdk] [locus\_tag=BN49\_RS18470] [protein=thymidine kinase] [protein\_id=WP\_016529469.1] [location=complement(3426457..3427074)] [gbkey=CDS]

MAQLYFYYSAMNAGKSTALLQSSYNYQERGMRTVVYTAEIDDRFGAGKVSSRIGLSSPARLYNPQTSLFD

DIAAEHQLKPIHCVLVDESQFLTREQVHELSEVVDTLDIPVLCYGLRTDFRGELFTGSQYLLAWSDKLVE

LKTICFCGRKASMVLRLDQEGCPYNEGEQVVIGGNERYVSVCRKHYKEALSVGSLTKVQNQHRPC

>lcl|NZ\_FO834906.1\_prot\_WP\_004145401.1\_3371 [locus\_tag=BN49\_RS31135] [protein=hypothetical protein] [protein\_id=WP\_004145401.1] [location=3427082..3427213] [gbkey=CDS]

MTPIKVFYRGDDCTIFYAHSRAFSRGIVAKLKGLQTERIKKMN

>lcl|NZ\_FO834906.1\_prot\_WP\_002910103.1\_3372 [gene=hns] [locus\_tag=BN49\_RS18480] [protein=DNA-binding transcriptional regulator H-NS] [protein\_id=WP\_002910103.1] [location=3427636..3428043] [gbkey=CDS]

MSEALKILNNIRTLRAQARECTLETLEEMLEKLEVVVNERREEENAAAAEIEERTRKLQQYREMLIADGI

DPNELLSTMAAVKAGTKTKRAARPAKYSYVDENGETKTWTGQGRTPAVIKKAMDEQGKSLDDFLI

>lcl|NZ\_FO834906.1\_prot\_WP\_002910105.1\_3373 [gene=galU] [locus\_tag=BN49\_RS18485] [protein=UTP--glucose-1-phosphate uridylyltransferase GalU] [protein\_id=WP\_002910105.1] [location=complement(3428165..3429067)] [gbkey=CDS]

MAALNSKVRKAVIPVAGLGTRMLPATKAIPKEMLPLVDKPLIQYVVNECIAAGITEIVLVTHSSKNSIEN

HFDTSFELEAMLEKRVKRQLLEEVQSICPPHVTIMQVRQGLAKGLGHAVLCAHPVVGDEPVAVILPDVIL

DEYESDLSRDNLAEMISRFDETGASQIMVEPVEDVTAYGVVDCKGESLKPGESVPMVGVVEKPKADVAPS

NLAVVGRYVLSADIWPLLAKTPPGAGDEIQLTDAIDMLIEKETVEAYHMKGKSHDCGNKLGYMQAFVEYG

IRHKTLGDDFKAWLETAVAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004175574.1\_3374 [gene=rssB] [locus\_tag=BN49\_RS18490] [protein=two-component system response regulator RssB] [protein\_id=WP\_004175574.1] [location=complement(3429265..3430278)] [gbkey=CDS]

MTQPLAGKQILIVEDEPVFRSLLHGWLTSLGATTFQAEDGKDALHKMTEVHPDLMICDISMPRMNGLELV

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EDWDALVSNPIAASRLLQELQPPVQQEMSHCRVHYRQLVSADKPGLVLDIAPLSENDLAFYCLDVTRAGD

NGVLAALLLRALFNGLLQEQLAHQGQRLPEMGSLLKQVNQLLRQANLPGQFPLLVGYYHSGLKNLILVSA

GLNGTLNTGEHQIQISNGVPLGTLGDAYLNQISQRCTSWQCQIWGAGGRLRLMLSAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910108.1\_3375 [gene=rssA] [locus\_tag=BN49\_RS18495] [protein=patatin-like phospholipase RssA] [protein\_id=WP\_002910108.1] [location=complement(3430368..3431270)] [gbkey=CDS]

MRKLKIGLALGAGAARGWSHIGVINALQRAGIEIDIVAGCSIGSLVGAAYACNRLPALESWVCSFSNWDV

LKLMDLSWRRGGLLRGEKVFNHYRRIMPVTEIERCERRFAAVATNLSTGRELWFTEGDLHLAIRASCSMP

GLMSPVRHNGYWLVDGAVVNPVPVSLTRAMGADIVIAVDLQHDAHLMQQDLFSLETPRQEAEEKEGPWHT

RLRARLTRMSSRRTAVTPTAMEIMTTSIQVLENRLKRNRMAGDPPDILLQPYCPQVSTLDFHRAGEAIAA

GQLAVEKKMDELLPLVRTAV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043529.1\_3376 [locus\_tag=BN49\_RS18500] [protein=YchJ family protein] [protein\_id=WP\_046043529.1] [location=3431383..3431841] [gbkey=CDS]

MSQLCPCGSALEYSSCCQRYLSGAELAPGPSQLMRSRYSAFVMKDADYLIKTWPPSCQAQQFRAELEKGF

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GSGKKFKKCCGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016531673.1\_3377 [gene=purU] [locus\_tag=BN49\_RS18505] [protein=formyltetrahydrofolate deformylase] [protein\_id=WP\_016531673.1] [location=3431884..3432726] [gbkey=CDS]

MHSLQRKVLRTICPDQKGLIARITNICYKHELNIVQNNEFVYHRTGRFFMRTELEGIFNDATLLADLDSA

LPEGSIRELNPAGRRRVVILVTKEAHCLGDLLMKANYGGLDVDIAAVIGNHDTLRSLVERFGIPFELVSH

EGLSREEHDQRMGDAIAAHEPDYVVLAKYMRVLTPEFVARFPNKIINIHHSFLPAFIGARPYHQAYERGV

KIIGATAHYVNDNLDEGPIIMQDVIHVDHTYTAEDMMRAGRDVEKNVLSRALYQVLAQRVFVYGNRTIIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004152249.1\_3378 [locus\_tag=BN49\_RS18520] [protein=Lrp/AsnC family transcriptional regulator] [protein\_id=WP\_004152249.1] [location=complement(3433909..3434352)] [gbkey=CDS]

MNDVLDEIDRAILTCLTQDARVSLKVLSARVGLTSPSTAERVKRLEERGVIQGYGARVNLAALGYSLQAL

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KRRLPPL

>lcl|NZ\_FO834906.1\_prot\_WP\_004189450.1\_3379 [locus\_tag=BN49\_RS18525] [protein=DMT family transporter] [protein\_id=WP\_004189450.1] [location=3434460..3435356] [gbkey=CDS]

MQLTRGVWQMSLAMIISGSIGAFVLLSGLPVTDVVFWRCLIGALTLLVFIVLSRQPFSRLTRFTLALAVI

GGAALVVNWLLLFAAYSRISIGMATVVYNTQPFMLVLMGMVLGERVSAVKWGWLLLAFGGVVILLSSELM

PAHEEGLTTGVLLALGAAFFYALTAIIARKLHPLPAQHIAFIQVLVGVVMLLPLVHAPELTASFPWRYLL

ILGIVHTGIMYQLLYSAIQKLPTPVTGSLSFIYPLVAMVVDYLVFHHALSAVQLLGGMLILFAAAGNNLG

WGEKKPRRGGVSEQSRAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002910189.1\_3380 [gene=narI] [locus\_tag=BN49\_RS18530] [protein=respiratory nitrate reductase subunit gamma] [protein\_id=WP\_002910189.1] [location=complement(3435353..3436030)] [gbkey=CDS]

MHFLNMFFFDIYPYIAGSVFLIGSWLRYDYGQYTWRAASSQMLDRKGMNLASNLFHIGILGIFAGHFLGM

LTPHWMYESFLPIDVKQKMAMIAGGACGVMTLVGGLLLLKRRLLSPRVRATTTGADILILSLLMVQCALG

LLTIPFSAQHMDGSEMMKLVGWAQSVVTFHGGASQHLDGVAFIFRVHLVLGMTLFLLFPFSRLVHIWSAP

VEYLTRKYQIVRARR

>lcl|NZ\_FO834906.1\_prot\_WP\_002910191.1\_3381 [gene=narJ] [locus\_tag=BN49\_RS18535] [protein=nitrate reductase molybdenum cofactor assembly chaperone] [protein\_id=WP\_002910191.1] [location=complement(3436030..3436740)] [gbkey=CDS]

MIELVIVSRLLEYPDAALWQHQQEMFEALASSEKLSKEDAHALGVFLRDLVAQDPLDAQAAYSELFDRGR

ATSLLLFEHVHGESRDRGQAMVDLMAQYERHGLLLDSHELPDHLPLYLEYLAQLPEEEALGGLRDVAPIL

GLLSARLQQRESRYAVLFELLLKLANTQVDSQKVAEKIADEARDDTPQALDAVWEEEQVKFFADQGCGES

EISAHQRRFAGAVAPQYLNISNGGQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002910193.1\_3382 [gene=narH] [locus\_tag=BN49\_RS18540] [protein=nitrate reductase subunit beta] [protein\_id=WP\_002910193.1] [location=complement(3436737..3438272)] [gbkey=CDS]

MKIRSQVGMVLNLDKCIGCHTCSVTCKNVWTSREGMEYAWFNNVESKPGVGFPNDWENQEKWKGGWIRKI

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PNWEEILGGEFEKRAKDQNFDNMQKAMYGQFENTFMMYLPRLCEHCLNPACVATCPSGAIYKREEDGIVL

IDQDKCRGWRMCITGCPYKKIYFNWKSGKSEKCIFCYPRIESGMPTVCSETCVGRIRYLGVLLYDADAIE

NAASTENEKDLYQRQLDVFLDPNDPKVIEQALKDGVPQGVIEAAQQSPVYKMAMDWKLALPLHPEYRTLP

MVWYVPPLSPIQSAADAGELGSNGILPDVESLRIPVQYLANLLTAGDTQPVLLALKRMLAMRHYKRAETV

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NLFNSRRIDAIDVTSKTEPHA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043531.1\_3383 [locus\_tag=BN49\_RS18545] [protein=nitrate reductase subunit alpha] [protein\_id=WP\_046043531.1] [location=complement(3438269..3442012)] [gbkey=CDS]

MSKFLDRFRYFKQKGETFADGHGQLLNTNRDWEDGYRQRWQHDKIVRSTHGVNCTGSCSWKIYVKNGLVT

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EDADKAKSFKQARGRGGFVRSSWQEVNELIAASNVYTVKTYGPDRVAGFSPIPAMSMVSYASGARYLSLI

GGTCLSFYDWYCDLPPASPMTWGEQTDVPESADWYNSSYIIAWGSNVPQTRTPDAHFFTEVRYKGTKTVA

ITPDYAEIAKLCDLWLAPKQGTDAAMALAMGHVMLREFHLDKPSQYFTDYVRRYTDMPMLVMLEERDGYY

AAGRTLRASDLVDSLGQENNPEWKTVAFDEKGDMTVPNGSLGFRWGDKGKWNLEQRDGKTGEEIELRLSL

LGSHDEVANVGFPYFGGEGSEHFNKVDLENILLHKLPAKRLQLADGSTALVTTVYDLTMANYGLERGLND

DNCAAGYDEVKAYTPAWAEKITGVSRAHIIRTAREFADNADKTHGRSMIIVGAGLNHWFHLDMNYRGLIN

MLIFCGCVGQRGGGWAHYVGQEKLRPQTGWQPLAFALDWQRPARHMNSTSYFYNHSSQWRYETVTAQELL

SPMADKSRYSGHLIDFNVRAERMGWLPSAPQLGVNPLRIADEAKKAGMTPVDYTVKSLKEGSIRFAAEQP

ENGKNHPRNLFIWRSNLLGSSGKGHEYMLKYLLGTENGIQGKDLGKQGGVKPEEVEWRDNGLDGKLDLVV

TLDFRLSSTCLYSDIVLPTATWYEKDDMNTSDMHPFIHPLSAAVDPAWESKSDWEIYKGIAKKFSEVCVG

HLGKETDVVTLPIQHDSAAEMAQPLDVKDWKKGECDLIPGKTAPHIIPVERDYPATYERFTSIGPLLETI

GNGGKGIAWNTQSEMDLLRKLNYTKAEGPAKGQPKLETAIDAAEMILTLAPETNGQVAVKAWQALSEITG

REHTHLALNKEDEKIRFRDIQAQPRKIISSPTWSGLEDEHVSYNAGYTNVHELIPWRTLSGRQSLYQDHQ

WMRDFGESLLVYRPPIDTRSVKAVMGEKSNGNPEKALNFLTPHQKWGIHSTYSDNLLMLTLSRGGPIVWM

SEADAKDLGIEDNDWIEVFNANGALTARAVVSQRVPAGMTMMYHAQERIVNLPGSEITGQRGGIHNSVTR

ITPKPTHMIGGYGHLAYGFNYYGTVGSNRDEFVVVRKMKNINWLDGEGNDQVQESVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004218943.1\_3384 [locus\_tag=BN49\_RS31140] [protein=hypothetical protein] [protein\_id=WP\_004218943.1] [location=complement(3442179..3442292)] [gbkey=CDS]

MGLPVKWLYPLIPPLLTNPGEAPLFEVKTIKKQQVKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004175568.1\_3385 [locus\_tag=BN49\_RS18555] [protein=NarK family nitrate/nitrite MFS transporter] [protein\_id=WP\_004175568.1] [location=complement(3442418..3443806)] [gbkey=CDS]

MSQSSLPEKANRSVITDWRPEDPEFWQQRGHRVASRNLWISVPCLLLAFCVWMLFSAVAVNLNKVGFQFT

TDQLFMLTALPALSGALLRVPYAFMVPLFGGRRWTAFSTGIMIVPCVWLGFAVQDTSTPFSIFVIISLLC

GFAGANFASSMANISFFFPKAKQGGALGVNGGLGNMGVSVMQLVAPLVVSISIFAVFGGNGSEQPDGSML

YLENAAWIWVPFLIIFTLAAWFFMNDLSASKASLSEQLPVLKRLHLWIMALLYLATFGSFIGFSAGFAML

SKTQFPDVQILHYAFFGPFIGALARSMGGAISDRLGGTRVTLVNFVVMAVFCALLFLTLPTNGQGGNFIA

FFAVFMVLFLTAGLGSASTFQMISVIFRKLTMDRVKAQGGSEAQAMREAATDTAAALGFISAIGAIGGFF

IPKAFGISLDLTGSPAGAMKVFLVFYIACVVITWAVYGRKRQ

>lcl|NZ\_FO834906.1\_prot\_WP\_023280254.1\_3386 [gene=narX] [locus\_tag=BN49\_RS18560] [protein=nitrate/nitrite two-component system sensor histidine kinase NarX] [protein\_id=WP\_023280254.1] [location=3444118..3445896] [gbkey=CDS]

MLKRLFTPLTLVNQLALIVLLATVIGVAGMAISARLVNGVQGSAHAINKAGSLRMQSYRLLAAIPLNEND

QKLVADMTATVFSPELQNSARRDGQEIQLKALQQYWQLALAPGMQRAVNQAEVAQDVADFVDRIDQLVTA

FDHTTEQRIERVVWIHRILAIGMALLLIFTIIWLRARLLRPWKQLLSMARAVSQRDFTQRAHISGRNEMA

TLGMALNNMSEELAESYAVLERRVQEKTAGLEQKNEILAFLWQANRRLHSSAPLCERISPVLNGLQGLTL

LRDIEVRVYDLEDEDNHQEFTCHSDDDCDDKGCYLCPRNLPPLPDGGTTLKWRLSDAHSQYGILLATLPV

GRHLSHDQQQLVDTLVEQLTSTLALDRHQEKQQQLIVMEERATIARELHDSIAQSLSCMKMQVSCLQMQG

DALPTESRQLLGQIRNELNTSWAQLRELLTTFRLQLTEPGLRPALEASCQEYSAHFGFTVQLDYQLPPRF

VPSHQAIHLLQIAREALSNALKHASATEVTVTVSQRDNQVRLVVADNGRGVPDHAERSNHYGLIIMRDRA

QSLRGDCQVRRRETGGTEVIVTFIPEKTFSIQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002910198.1\_3387 [gene=narL] [locus\_tag=BN49\_RS18565] [protein=two-component system response regulator NarL] [protein\_id=WP\_002910198.1] [location=3445907..3446557] [gbkey=CDS]

MSQQERATILLIDDHPMLRTGVKQLISMAPDIQVIGEASNGAQGIELAESLDPDLILLDLNMPGMNGLET

LDKLREKSLSGRVVVFSVSNHEEDVVTALKRGADGYLLKDMEPEDLLKALQQAAAGEMVLSEALTPVLAA

SLRANRATSDRDISQLTPRERDILKLIAQGLPNKMIARRLDITESTVKVHVKHMLKKMKLKSRVEAAVWV

HQERIF

>lcl|NZ\_FO834906.1\_prot\_WP\_002910201.1\_3388 [locus\_tag=BN49\_RS18570] [protein=YchO/YchP family invasin] [protein\_id=WP\_002910201.1] [location=complement(3446554..3447936)] [gbkey=CDS]

MPVSFRLLPTLTFLLLLPGVPVWALTASDTTRPAQAQDPLPDMGIAPQVDDDARHFAEVAKKFGEASMSD

NGLTAGEQAQLFAISKIGNEVSHQLESWLSPWGNANVDLLVDKEGKFTGSKGSWFVPLQDNDRYLTWNQY

SVTRREHDLVGNIGLGQRWRVGGWLLGYNSFYDKVLSESLARGSVGAEAWGEYLRLSANYYHPLGDWQLR

DNQTQEQRMAAGYDVTAQARLPFYQHINTSVSVEQYFGDSVDLFHSGTGYHNPVAVSVGLNYTPVPLVTV

TAKHKQGENGVSQNNVGLKLNYRFGVPLKQQLAADEVAISNSLRGSRFDSPERDNLPVVEYRQRKNLTVY

LATPPWDLQSGETVQLKLQIHSLHGIKALHWQGDTQALSLTPPVDASSPDGWSIIMPVWNSEPGAANRWR

LSVVVEDKQGQRVSSNEIALALTEPLVKFTTPGVSWTDSP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043534.1\_3389 [locus\_tag=BN49\_RS18575] [protein=nitrate reductase] [protein\_id=WP\_046043534.1] [location=complement(3448088..3450688)] [gbkey=CDS]

MNIIRTTCPYCGVGCGVLASVDDAGQVSVRGDDQHPANLGRLCVKGAALGETTGLAGRLLTPEVDGQQVA

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AFGADVVPCSYDDVENSDLVVLVGSNAAWAHPVLFQRLAQAKRDNPRLRIVAIDPRRTATCEIADRHLAL

APGSDGGLFVGLLNALAEAGACVDGFRDGPQALAAARGWDVARVAAFCGLPADEVAGFYREFIAAPRAIT

LYTMGINQSASGSDKCNAIINVHLASGKYGRRGCGPFSLTGQPNAMGGREVGGLATMLAAHMDFVPDDLQ

RLARFWGTERLAQTPGLTAVELFAAIGRGEVKAVWIMGTNPVVSLPDSHAVSQALAACPLVIVSDVAAQT

DTGRFAHIRFPALAWGEKNGTVTNSERRISRQRSFLPPPGEAKADWWIIARVGQALGYREAFAWQHPHDV

FREHAALSGFENDGQRAFDIGALADLSREAWDAMPPVRWPVSRSEAAWDITRGWHGDGRLRMVPVTPQPT

RATTDAFYPLILNSGRIRDQWHTMTRTGAVPRLMQHIAEPMVEVAPQDAVRYQLPADGLARIWSRHGVMV

AKVAISEGQRPGSLFVPMHWNNQFARQGRVNNLLAAVTDPYSGQPESKQAAVAIAAWQPAWHSELFCREP

LPFPATWHWRWRAAPGVLHYSLAGEASARQWLSAWCARRGWQLQVADGGAVWNLLAWHQGRLMLGWWSDA

REPAVDCAWISAAFAAPPSDAVQRHALLSGRPGAAVAPRGRIVCSCFGVGEWSINEAIASGCASVGALGG

KLKCGTNCGSCVPELNALLAAQRTRA

>lcl|NZ\_FO834906.1\_prot\_WP\_077260998.1\_3390 [gene=nirB] [locus\_tag=BN49\_RS18580] [protein=nitrite reductase large subunit NirB] [protein\_id=WP\_077260998.1] [location=complement(3450688..3454755)] [gbkey=CDS]

MTRRLVVIGNGMAATRLVQRLVERDPARFAITVVGDEPHPAYNRIQLSPLLAGEKTAAQIPLLPAEWYTR

HGVCLRSGEAVDEVDIQQRRLRIAETWLPWDELVFATGSRPFIPPLPGIDRPQVMPFRTLADVERILAIP

GPAVVIGGGVLGVEAAAALRRHGGEVTLLHRGSGLMAPLTDAFAADELRQQLEARGIRCVLECSIAAIDA

DGVRLADGRVFRAARVVLATGVQPDSRLAAQSGVLCQRGIVVDRQMASSLPGISAIGECCEIDGQTWGLV

APCLRQAEVLADRLCGAPGEGFVWQDAGTRLKVTGIEFFCAGEQQAGEQDDIYTSWDPIDRHYRRLLLRD

GRLRGVLLMGDCTAAAALTARLESDEPATVDWLFDPSSTQPQAAGIMTMTKPVLVLVGHGMVGHHFLEQC

VSRNLHQQYRIVVFGEERYPAYDRVHLSEYFAGRSAESLSLAAGDFFIEHGIELRLGEAVATIDREARLV

RDAEGHEIHWDKLVLATGSYPFVPPIPGNDLAGCFVYRTLDDLDRIAAHAAAAKSGVVIGGGLLGLEAAN

ALKQLGLETQVVEFAPNLMAVQLDNGGAAMLREKIVALGVGVHTSKATTAIVREADGLRLNFADGGALRT

DMVVFSAGIRPQDALARGCALQVGERGGIHIDGQCRTSDPDVLAIGECALWDNKIYGLVAPGYQMARIAA

ATLAGEDACFSGADMSTKLKLLGVDVASFGDAQGRTPGCQSYQWTDGPQQIYKKIVVSQDGKALLGGVLV

GDASDYATLLQMMLNGMALPPRPESLILPALEGAAPKALGVAALPDSAPICSCHNVSKGDICQAVNNGAG

DMSAIKSCTRAATGCGGCSALVKQVMEYQLAEQGVEVKKDVCEHFPWSRQEIYHLVRVNHIHTFEQLISR

YGQGHGCDVCKPLVASVLASCWNEYLLKPAHLPLQDTNDRYFANIQKDGSYSVVPRMAAGEVTPDGLIAI

GQIAKRYQLYSKVTGGQRIDLFGARLEQLPAIWRELADAGFETGHAYGKSLRTVKSCVGSTWCRYGVQDS

TGLAVRLEHRYKGLRAPHKIKMAVSGCTRECAEAQGKDIGVIATDKGWNLYVCGNGGMKPRHADLFASDL

DEATLIRSIDRLLMFYIRTADRLQRTSTWMDNLEGGVAYLRQVVLEDSLGIGEELEQEMARIVDSYQCEW

QTTLNDPQRLALFRSFVNSDQPDEAVQRRDLRGQPQPLLTETLPEGELPSRPWQAVCDLDAIPAQAGIGA

RLGERQIALFRFGERVYALDNREPGSAANVLSRGLLGDVGGEPVVISPLYKQRIRLRDGWPCDGDEQAVR

AWPVKVENGKVWVGNQQLLARAEAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004200289.1\_3391 [locus\_tag=BN49\_RS18585] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004200289.1] [location=complement(3454766..3455554)] [gbkey=CDS]

MKPLIQVQAVSQRFNTASGEFLALQNVSFDIVEGETISLIGHSGCGKSTLLNLIAGITTPTEGGLLCDNR

EIAGPGPERAVVFQNHSLLPWLSCFDNVALAVDQVFRRTMSKSERREWIEHNLARVQMGHALHKRPGEIS

GGMKQRVGIARALAMKPKVLLLDEPFGALDALTRAHLQDTVMHIQQELNTTIVMITHDVDEAVLLSDRVL

MMTNGPAATVGEILSVDLPRPRHRVQLADDSRYHHLRQQILHFLYEKQPKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004152255.1\_3392 [gene=ntrB] [locus\_tag=BN49\_RS18590] [protein=nitrate ABC transporter permease] [protein\_id=WP\_004152255.1] [location=complement(3455564..3456448)] [gbkey=CDS]

MKQAQRKQPVVSVDNAPGEVIILPPVQVRRTTPTVTRWLRELTQRLLPPLLGLGVLLLAWQLAAMHSKGF

PTPLSTLDSALTLFADPFYQDGPNDMGIGWNVLASLQRVAVGFGLAALAGIPLGFLIGRSLFFARMFNPL

IALLRPVSPLAWLPIGLLLFQKAEPASSWTIFICSIWPMVINTAEGVRRIPQDYLNVARVLQLSEWTVMR

KILFPAVLPAVLTGVRLSIGIAWLVIVAAEMLTGGLGIGFWIWNEWNNLNVENIIIAIVIIGVVGLLLEQ

GLMLLARRFSWQEK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530676.1\_3393 [locus\_tag=BN49\_RS18595] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016530676.1] [location=complement(3456450..3457706)] [gbkey=CDS]

MGDKFSISRRRLLQAGAALGGAMLLPGVMQAAWAGGSDKPEQTRVRVGFIPLTDCAPLAIAAAKGFDQKY

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GVTDLGGLKRLIDRSAPGSYTFAHTFPTGTHAMWLYYWLASAGIDPFNDVRTVVVPPPQMVMNMRIGNMS

GFCVGEPWNARAINDRIGFTAATSQDIWPEHPEKVLGTRRDWVERNPNTARALVAALMEAQRWIAASPEN

TRETARLLARRGWLNTKEQYLTGRMLGEYDNGLGRRWQDAHPMRFWAGGEVSFPWLSDGMWFLTQFRRWG

LLKQAPDYLAVASRINRIDVWQAAAQAVGGISAPAARMRSSTLMDGTVWNGSDPEGYARHFSIQRKGA

>lcl|NZ\_FO834906.1\_prot\_WP\_021313032.1\_3394 [gene=nasR] [locus\_tag=BN49\_RS18605] [protein=nitrate regulatory protein NasR] [protein\_id=WP\_021313032.1] [location=complement(3457950..3459131)] [gbkey=CDS]

MNNTTGHAHDATAWLQLARRLQKQQLQQFSQLGELASQLSALVHMLQCERGASNIYLCSGGLLYTAECRA

GGALVDERLALFYASLERARAVAGSALCWRIARAVDELAQLPALRAQIGRRQIAAEAATEQFSRVIRHLL

NIAPQLNDSIDDPPVAGRMVALYSFMQGKELVGQERALGALGFTRGEFSDSLRQQLVDRIDGQQPCFDSF

QALGSPATVQLFRTQCHAGLDIEQLRRIACTRQPAADGGETALRWFGLQTQRLEQLREVEEQLIDDLLDA

TDALLADDAPGWQAGEEDDSVTPRLDKQLLPLVRQQAYELQQLSSQLASLKDALEERKLIEKAKSLLMTH

QGMQEEQAWQTLRKMAMDKNQRMVEIARALLMVKAIWPLTPKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910380.1\_3395 [locus\_tag=BN49\_RS18610] [protein=DsrE/DsrF/TusD sulfur relay family protein] [protein\_id=WP\_002910380.1] [location=3459199..3459552] [gbkey=CDS]

MQRIVIIANGAAYGSESLFNSLRLAIALREQQSDLDLKLFLMSDAVTAGLRGQKPAEGYNVQQMLEILTA

QQVPVKLCKTCADGRGVSALPLVDGVEVGTLVELAQWTLAADKVLTF

>lcl|NZ\_FO834906.1\_prot\_WP\_002910387.1\_3396 [locus\_tag=BN49\_RS18615] [protein=DUF1883 domain-containing protein] [protein\_id=WP\_002910387.1] [location=3459790..3460032] [gbkey=CDS]

MAMVKASLTLFGGDTLVVRCSERCHIHLMSAKVPGDSHADILSVQDRDSAYLTVPYSGTWNVLIDSHSQS

LEHSISYVPA

>lcl|NZ\_FO834906.1\_prot\_WP\_004152258.1\_3397 [locus\_tag=BN49\_RS18620] [protein=gamma-glutamylcyclotransferase] [protein\_id=WP\_004152258.1] [location=complement(3460250..3460930)] [gbkey=CDS]

MLTRDFLMNADCKTAFGAIEESLLWSAEQRAASLAATLACRPDDGSVWIFGYGSLIWNPALNYRESCTGT

LPGWHRAFCLRLTAGRGSACQPGRMLALKEGGRTTGVAYRLPDDTLEEELTLLWKREMITGCYLPTWCKL

ELDDGRTVNALVFIMDPRHPLFEPDTSAQVIAPLIARASGPLGTNAQYLFSLEQALRKLGMHDASLDDLV

ASVRALLGESPTPGLA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530679.1\_3398 [gene=chaB] [locus\_tag=BN49\_RS18625] [protein=putative cation transport regulator ChaB] [protein\_id=WP\_016530679.1] [location=complement(3461067..3461297)] [gbkey=CDS]

MPYRSKQELPDSVQHVLPAHAQEIYKEAFNSAWDQYKDKDERRDDASREETAYKVAWAAVKNSYEKGDDD

KWHKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002910392.1\_3399 [gene=chaA] [locus\_tag=BN49\_RS18630] [protein=sodium-potassium/proton antiporter ChaA] [protein\_id=WP\_002910392.1] [location=3461561..3462661] [gbkey=CDS]

MTHAHEAVKTRHKESSLVFPVLALAVLFFWGSSQSLPVVIAINILALVGILSSAFSVVRHADVLAHRLGE

PYGSLILSLSVVILEVSLISALMATGDAAPTLMRDTLYSIIMIVTGGLVGFSLLLGGRKFATQYMNLFGI

KQYLIALFPLAIIVLVFPMALPGANFSTGQSLLVAVISAAMYGVFLLIQTKTHQSLFVYEHEDDSDDDDP

HHGKPSAHSSGWHTAWLLVHLVAVIAVTKMNANPLETLLTSMNAPVAFTGFLVALLILSPEGLGALKAVL

NNQVQRAMNLFFGSVLATISLTVPVVTLIAFLTGNELRFGLGAPEMVVMVASLVLCHISFSTGRTNVLNG

AAHMALFAAYLMTIFA

>lcl|NZ\_FO834906.1\_prot\_WP\_002910393.1\_3400 [gene=kdsA] [locus\_tag=BN49\_RS18635] [protein=3-deoxy-8-phosphooctulonate synthase] [protein\_id=WP\_002910393.1] [location=complement(3462748..3463602)] [gbkey=CDS]

MKQKVVSIGDINVANDLPFVLFGGMNVLESRDLAMRICEHYVTVTQKLGIPYVFKASFDKANRSSIHSYR

GPGLEEGMKIFQELKQTFGVKIITDVHEASQAQPVADVVDVIQLPAFLARQTDLVEAMAKTGAVINVKKP

QFVSPGQMGNIVDKFIEGGNDKVILCDRGANFGYDNLVVDMLGFGVMKKASNNSPVIFDVTHALQCRDPF

GAASGGRRAQVSELARAGMAVGIAGLFIEAHPDPDHAKCDGPSALPLDKLEPFLKQMKAIDDLVKSFDEL

DTSK

>lcl|NZ\_FO834906.1\_prot\_WP\_002910395.1\_3401 [gene=sirB1] [locus\_tag=BN49\_RS18640] [protein=invasion regulator SirB1] [protein\_id=WP\_002910395.1] [location=complement(3463642..3464454)] [gbkey=CDS]

MGSLADFEFNKAPLCDGMVLISEQVRDDFPSRFVEEELQRLLRLAQEEIAPSWDQERQIERLLELFYDEW

GFGASQGVYRLSDALWLDKVLVNRQGSAVSLGAILLWIAQRLALPVVPVIFPTQMLLRADPETSEEMWLI

NPFNGETLDEHTLEVWLKGNIGPVAELFNEDLDEADNAEVIRKLLDTLKSALMEERQMELALRASEALLQ

FNPEDPYEIRDRGLIYAQLDCDHVALLDLSYFVEQCPEDPISEMIRAQINTISHKQITLH

>lcl|NZ\_FO834906.1\_prot\_WP\_004145428.1\_3402 [gene=sirB2] [locus\_tag=BN49\_RS18645] [protein=invasion regulator SirB2] [protein\_id=WP\_004145428.1] [location=complement(3464458..3464850)] [gbkey=CDS]

MNLFTAVLYLHIATVAVSVGLFVLRYWWMYHQSPLLNQRWVRIAPHCSDTLLFLSGAGLMAITHYLPFTE

DGAWLTEKLFGVIIYIALGFIALGRRRPRSQQSRFIAFLLALVVLFIIIQLAITRIPILG

>lcl|NZ\_FO834906.1\_prot\_WP\_032102720.1\_3403 [gene=prmC] [locus\_tag=BN49\_RS18650] [protein=peptide chain release factor N(5)-glutamine methyltransferase] [protein\_id=WP\_032102720.1] [location=complement(3464850..3465698)] [gbkey=CDS]

MTFQAWLQQAIARLAESDSPRRDAEILLGHVTGRARTWILAFGETTLSADEAARLEALLVRRQRGEPIAH

LVGQREFWSLPLFVSPATLIPRPDTECLVEQALARLPTAPCRILDLGTGTGAIALALASERPDCEVTAVD

VMPDAVALALRNAEHLSIANVTISQSDWFSALAGQRFATIVSNPPYIDAADPHLAEGDVRFEPLTALVAG

DQGLADLAHIIREGRQYLQPGGWMLLEHGWTQGEAVRALFREAGYLDVATCRDYGDNERLTLGRLPDMEN

VG

>lcl|NZ\_FO834906.1\_prot\_WP\_002910403.1\_3404 [gene=prfA] [locus\_tag=BN49\_RS18655] [protein=peptide chain release factor 1] [protein\_id=WP\_002910403.1] [location=complement(3465698..3466780)] [gbkey=CDS]

MKSSIVAKLEALYERHEEVQALLGDAATIADQDKFRALSREYAQLSDVARCYTDWRQVQEDIETAQMMLD

DPEMREMAQEELRDAKEKGDQLEQQLQVLLLPKDPDDERNAFVEVRAGTGGDEAALFAGDLFRMYTRYAE

SRRWQVEILSANEGEHGGFKEVIAKISGDGVYGRLKFESGGHRVQRVPATESQGRIHTSACTVAVMPELP

EAEMPDINPADLRIDTFRSSGAGGQHVNTTDSAIRITHLPTGIVVECQDERSQHKNKAKALSVLGARIRA

AEVAKRQQAEASTRRNLLGSGDRSDRNRTYNFPQGRVTDHRINLTLYRLDEAMEGKLDMLIEPIVQEHQA

DQLAALSEQE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531392.1\_3405 [gene=hemA] [locus\_tag=BN49\_RS18660] [protein=glutamyl-tRNA reductase] [protein\_id=WP\_016531392.1] [location=complement(3466823..3468079)] [gbkey=CDS]

MTLLALGINHKTAPVALRERVTFSPETLDKALESLLAQPMVQGGVVLSTCNRTELYLSVEEQDNLQEALI

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MFQKSFSVAKRVRTETDIGASAVSVAFAACTLARQIFESLSSVTVLLVGAGETIELVARHLREHHVRKMV

IANRTRERAQALAEEVGAEVIALSDIDERLKEADIIISSTASPLPIIGKGMVERALKARRNQPMLLVDIA

VPRDVEPEVGKLANAYLYSVDDLQNIIQHNLAQRKAAAVQAESIVEQETSEFMAWLRAQSASETIREYRS

QSEQVREELTAKALAALEQGGDAQEIMQDLARKLTNRLIHAPTKSLQQAARDGDDERLHILRNSLGLE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910405.1\_3406 [gene=lolB] [locus\_tag=BN49\_RS18665] [protein=lipoprotein insertase outer membrane protein LolB] [protein\_id=WP\_002910405.1] [location=3468350..3468961] [gbkey=CDS]

MNRLFRLLPLASLVLTACSLHTPQGPGKSPDSPQWRQHQQAVRSLNQFQTRGAFAYLSDEQKVYARFFWQ

QTGQDRYRLLLTNPLGSTELSLTAQPGSVQLIDNKGQTYTATDAEEMIGRLTGMPIPLNSLRQWIIGLPG

DATDYSLDDRYRLRELNYTQNGKTWHVTYGGYTSDTQPALPSNVELNNGAQRIKLKMDNWIVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004898981.1\_3407 [gene=ispE] [locus\_tag=BN49\_RS18670] [protein=4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase] [protein\_id=WP\_004898981.1] [location=3468961..3469809] [gbkey=CDS]

MTRWPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTLTIEPRTDGQLRLLTPVAGVPDEENLIVRAA

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VPVFVRGHAAFAEGVGEILTPVEPEEKWYLVAHPGVSIPTPIIFRDPELPRNTPRRSINTLLNCEFSNDC

ELIARKRFREVDAALSWLLEYAPSRLTGTGACVFAEFNTESAARQVLDTAPAWLNGFVARGVNLSPLKQA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002910407.1\_3408 [gene=prs] [locus\_tag=BN49\_RS18675] [protein=ribose-phosphate diphosphokinase] [protein\_id=WP\_002910407.1] [location=3469993..3470940] [gbkey=CDS]

MPDMKLFAGNATPELAQRIANRLYTSLGDAAVGRFSDGEVSVQINENVRGGDIFIIQSTCAPTNDNLMEL

VVMVDALRRASAGRITAVIPYFGYARQDRRVRSARVPITAKVVADFLSSVGVDRVLTVDLHAEQIQGFFD

VPVDNVFGSPILLEDMLQLNLDNPIVVSPDIGGVVRARAIAKLLNDTDMAIIDKRRPRANVSQVMHIIGD

VAGRDCVMVDDMIDTGGTLCKAAEALKERGAKRVFAYATHPIFSGNAIQNIKNSVIDEFVVCDTIPLAPE

IKALDKVRTLTLSGMLAEAIRRISNEESISAMFEH

>lcl|NZ\_FO834906.1\_prot\_WP\_004200291.1\_3409 [gene=dauA] [locus\_tag=BN49\_RS18680] [protein=C4-dicarboxylic acid transporter DauA] [protein\_id=WP\_004200291.1] [location=3471065..3472744] [gbkey=CDS]

MNRLFSSHVMPFRALIDACWKEKYTTARFTRDLIAGITVGIIAIPLAMALAIGSGVPPQYGLYTSAVAGI

VIALTGGSRFSVSGPTAAFVVILYPVSQQFGLAGLLVATLMSGIFLILFGLARFGRLIEYIPLSVTLGFT

SGIGITIGTMQIKDFLGLQMPHVPEHYLQKVAALAMALPTINVGDAAIGVVTLGILILWPRLGIRLPGHL

PALLGGCAVMLVVNLLGGDVATIGSQFHYQLADGTQGNGIPQLLPQLVLPWDMPGSNFTLSWASLQALLP

AAFSMAMLGAIESLLCAVVLDGMTGTKHKANSELIGQGLGNIVAPFFGGITATAAIARSAANVRAGATSP

VAAVIHALLVILALLILAPLLSWLPLSAMAALLLMVAWNMSEAHKVINLLRHAPKDDIVVMLMCMSLTVL

FDMVIAISVGIVLASLLFMRRIARMTHLAPVNVEVPDDVLVLRVIGPLFFAAAEGLFNDLETRIAGKRIV

VLKWDAVPVLDAGGLDAFQRFVNKLPEGCELRVSNLEFQPLRTLARAGVKPLPGRLSFYPDRQAALADL

>lcl|NZ\_FO834906.1\_prot\_WP\_004175547.1\_3410 [locus\_tag=BN49\_RS18685] [protein=MerR family transcriptional regulator] [protein\_id=WP\_004175547.1] [location=complement(3472745..3473791)] [gbkey=CDS]

MLIQVGELAKRAGLTVRTLHHYEQTGLLTPSARSEAGYRLYNLSAVQRLHMIKALAQAGLTLATIKDYLD

RQTLSLPELLTQQIDMLNAQLRDVGRLRDRLLVLREALASGNEPDLESWLQTLELMKMYDRWFSQQELAA

LPFAAQDEQRAQAWRELTEEVQTLMASGCPTDSPQAMRLATRWMERLEQDTAGRPEFLTRLNEMHAAEPQ

MVEQTGVTPAIIAYITEAFAESKLAIWARYLDEEEMAFTRQHYFDRLQEWPALVAKLHQACREGVAPDSA

SGQALARAWLELFQSYAGTRPQTLQKFRRAMEQEPHLMKGTWMTPAVLSWLQQATGSLMRQAQGPAAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002910437.1\_3411 [gene=ychH] [locus\_tag=BN49\_RS18690] [protein=stress-induced protein YchH] [protein\_id=WP\_002910437.1] [location=complement(3474012..3474287)] [gbkey=CDS]

MKRKNASLLGNVLMGLGLVVMVVGVGYSILNQLPQLNLPQFFAHGAILSIFVGAVLWLAGARIGGHEQVS

DRYWWVRHYDKRCRRNQHRHS

>lcl|NZ\_FO834906.1\_prot\_WP\_004180389.1\_3412 [gene=pth] [locus\_tag=BN49\_RS18695] [protein=aminoacyl-tRNA hydrolase] [protein\_id=WP\_004180389.1] [location=3474560..3475144] [gbkey=CDS]

MTIKLIVGLANPGAEYAATRHNAGAWYVDLLADRHRAPLREESKFFGYTSRINLAGEDVRLLVPTTFMNL

SGKAVAAMATFYRINPDEILVAHDELDLPPGVAKFKLGGGHGGHNGLKDIISKLGNNPNFHRLRVGIGHP

GDKNKVVGFVLGKPPASEQKLIDDAVDEAARCTEIWLKDGLTKATNRLHAFKAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002910443.1\_3413 [gene=ychF] [locus\_tag=BN49\_RS18700] [protein=redox-regulated ATPase YchF] [protein\_id=WP\_002910443.1] [location=3475262..3476353] [gbkey=CDS]

MGFKCGIVGLPNVGKSTLFNALTKAGIEAANFPFCTIEPNTGVVPMPDPRLDKLAEIVKPQRILPTTMEF

VDIAGLVKGASKGEGLGNQFLTNIRETEAIGHVVRCFENDNIIHVAGKVNPAEDIDVINTELALSDLDTC

ERAIHRVSKKAKGGDKDAKVELAALEKCLPQLENAGMLRALDLTKEEKEAIRYLSFLTLKPTMYIANVNE

DGFENNPYLDQVRAIAEQEGSVVVPVCAAVEADIAELDDEERDEFMAELGLEEPGLNRVIRAGYALLNLQ

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VKDGDVMNFLFNV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530916.1\_3414 [locus\_tag=BN49\_RS18705] [protein=DUF1869 domain-containing protein] [protein\_id=WP\_016530916.1] [location=complement(3476436..3476765)] [gbkey=CDS]

MATARSGYTLQVIKAGQQGHVEMRWGHLADVDTRAAATAIMQHIGRSSSSRGQLEISLSLTNAASGISVE

LHHPASGESATPAFIEAELKKIVQIVDGYEAAEDTHIVE

>lcl|NZ\_FO834906.1\_prot\_3415 [locus\_tag=BN49\_RS18710] [protein=substrate-binding domain-containing protein] [pseudo=true] [location=complement(3476850..3477532)] [gbkey=CDS]

MKHCKIILLVGLLASSASALAEKIGVSMAYFDQNFLTIIRQSIEKEAQARHVDVQFEDARGDTGRQADQV

QSFIASGVDAIIVDPVDSASTPQLTKMAQQAKMPLVYVNRTPGDKTLPPGVVGRATEKRLILWRRTTMRW

RLARRWRWRKARRSC\*SAGSTPPRTG\*KPWPAIRFR\*RFSRTPSVRAKRP\*R\*R\*S\*LKEKRSSLMSGSR

LS\*\*PKKTCRPMWKRVI

>lcl|NZ\_FO834906.1\_prot\_WP\_046043538.1\_3416 [locus\_tag=BN49\_RS18715] [protein=type VI secretion system ImpA family N-terminal domain-containing protein] [protein\_id=WP\_046043538.1] [location=complement(3477664..3479079)] [gbkey=CDS]

MMTTHHDRHYKAGGDPRTLADFMALRAEMNKLSHPARPDINWPYAEQLARGLLEHHGADLQTVAWYTLAR

ARLGGVAGINEGLTLMESLLVRQGKNLWPQALPAQTEIFRTLSKRLRQVIRTLNLTPEDVESLEQAERSL

QSFDAVLQRLEIAPENQLSDLRALLHSTATRFESLDPAPALPTAPPVAVSDAELPGTLVSEEDAAKVEPV

PDLKRRPKAEPLAPPSPAKRPAPVAASTPAPVPRWKPFIAGMVTMLAVTGIAVGGWLALRQSDLPPISVT

QNAGPIPGLPATTPPGPVDLPQTQRQLGELARLAPDWAVSYGDQLVHHALIRWPDQAQPLAQQWRQQLSA

GALPAENITGWSEGMQQLQRLADQLNALDEQKGKYLTVSELKTAVFAITQSFNRAVPLEEQLRQLAALPV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004175538.1\_3417 [gene=tssE] [locus\_tag=BN49\_RS18720] [protein=type VI secretion system baseplate subunit TssE] [protein\_id=WP\_004175538.1] [location=complement(3479099..3479542)] [gbkey=CDS]

MPRPSLYDILYGNFAGGLDLNTVSETDQVILSVLDNMQRILNCRAGTLAHLPDYGLPDMTAVLQGMPASA

HQLMSTLSAVLLKYEPRLQRIAVVMLDQHAPGELRYAIDAELKDIGLVRYGTEFMPEGRVLIRHLKRQQY

LDARSAL

>lcl|NZ\_FO834906.1\_prot\_WP\_077255016.1\_3418 [gene=tssJ] [locus\_tag=BN49\_RS18725] [protein=type VI secretion system lipoprotein TssJ] [protein\_id=WP\_077255016.1] [location=complement(3479545..3480081)] [gbkey=CDS]

MAITAVKPSARLLAFLMVTVLTGCGLTQTVKDGAVSVTQSIFYPQVKTLHLDLRAREGVNNNAKGASLAT

VVRIYQLKDRQAFDNTDYPSLFAGDGQALQADRVAEKDVRLRPGESVTVDMPMETSAQFVAVAAMFIDPD

LTQNSWRLVFTRDELDPARPRIIEASQNQLTLHPFKEK

>lcl|NZ\_FO834906.1\_prot\_WP\_164995970.1\_3419 [gene=tssG] [locus\_tag=BN49\_RS18730] [protein=type VI secretion system baseplate subunit TssG] [protein\_id=WP\_164995970.1] [location=complement(3480062..3481078)] [gbkey=CDS]

MNFYRFCQLLEKNHPKAPIIGSGWLVGDEPIRFRPHPGMGFPAGEIRGMDDPEPPRPPAVHVTFMGLYGV

ESPLPTHYSDDIAQRREGVEATEDFLDIFNHRLIAQYYRIWRKYSYPATFRAGGTDNISQYLLGLAGLGI

PGCAAVAASPLSRFLALLPVMMLPGRSGEGMEALVALLAPGTRATVYHHDPCRIPLSQPLTMSVRQPVSL

QHRPVMGTHATDVNGQVLLQLATEKPDEVRGWLPGGELFSDLMALLHVWLGSHLDVRLQLCVARHLLPDA

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043540.1\_3420 [gene=tssF] [locus\_tag=BN49\_RS18735] [protein=type VI secretion system baseplate subunit TssF] [protein\_id=WP\_046043540.1] [location=complement(3481108..3482871)] [gbkey=CDS]

MDDLTLRYFDAEMRYLREAAKALAQAHPDRAAMLDLDKAGTPDPYVERLFEGFAFSVGRLREKIDDDLPE

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IEEAVMTAEPDGRSALRLRFACSELADWSQTDLRRLALYLGEDAVTGSALHLWLTRRQAALYLRLPGQTE

RVSLDGYFSPGGFSEEDRLWPKGESAFSGYQLLLEYFTFREKFMFVQLNGLENITLPVGISHFTLEVVFS

EVWQSDLPVSASSLRLHCVPVINLFTLEADPLTISGLESEYLLRPKRLQDGHTEIYSVDSVTGSGRTGEA

RYVPFTRFRHQGGMMRRHAPKRYYHTRVKRGVTGMHDTWLILGGQGWEADRELARETISLRITGTNGQLP

RRALQSTLLDRCESISATPLTVRNLCKPTLPAYPPAEDRYHWRVMSHLGTRFLNMMSSAEVLRGTLSLYN

WREDELNNRRLDAILAVSHHRIQRFEQGFLLRGLDIEVTLDGSGFTGAGDVHLFGDMLNRFFALYADMNQ

FNQLTLIVQPEGKCIRWKENHSLRLPG

>lcl|NZ\_FO834906.1\_prot\_3421 [locus\_tag=BN49\_RS18740] [protein=type VI secretion protein VasK] [pseudo=true] [location=complement(3483005..3486395)] [gbkey=CDS]

MNATDSILRLGSRFGVLMLIAGAILWGIYHYGDKIGLNTLQAKLYFCLGLGILILLFRYGGRIVQFILGR

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ERFSLLGWAVPLYVWSLHPQADDQAGRIVQSVGSLFPPDCQSSQMRQLLSALPSRLLETGVQQVTGNPQH

HFLLGLADQLTRQPERISVPLSTFLEPHRALPLAGVVFSPSSPQASHSLKHHWRHDKRWDVLLESLRPSG

LKARKIGFPWRRAVSASTGALMLLWAASMTVSFIANRELVAIAQEQVRLASAEKQPLAVRLHALSALQKT

LSQLEYRSQHGAPWYLRAGLSQNDDLLAALFPRYGERAQPLLRDAAAHHLEEQLTAFVQLPPDSPLREKM

TKTAYGQLKQYLMLTRPEKMDAAWFATTLMQDWSQRSGIADAVWQGSGTSLLAFYAASLASHPQWRLPVD

DGLVSQVRTRLIRQLGQRNSESTLYQKMLAQVANQYADMRLADMTADNDASRLFSTDEVVPGMFTRQAWE

QAVQPAIEKVVAERRDEMDWVLSDTKQTAAQSTLPEALRARLAERYFADFSGAWLDFLNSLRWQRAATLS

DAIDQLTLMADVRQSPLVALMNTLSVQGRTGQTGEAIADSLVKSARQLFNRDNPPVIDQRSGARGPLDAT

FGPVLALLDNRDGGTPTSRLSLQTFLTRVTQVRLRLQQVTNATDPQAMTRLLAQTVFQGKAVDLTETRDY

GSLVAAGLGQEWIWANAVCSPDGTGLAAGADPGGGKSQRPVAQRGGGGLE\*RFWRSLPL\*KYQQ\*SLSAA

AGKIPRQRDRAHRPLSADPAERRAA\*RGEPLDGGQYQCSGADV\*PGLSAGDEYPEPSLRRRVRQRRSGIA

FCASPRHGGRRDADGAGHRQSETCLYEPDAGLAAVQLAR\*HRSAGRQSELDQYPGGHPPVWRFPGRLGLD

PSAG\*GGGQRLSRNEQQLEPELESAGWSVAELHAAYRGGGRTAGAAGAAKLYATGDDIQRARVC\*TCSAD

RRYTRRRGIL

>lcl|NZ\_FO834906.1\_prot\_WP\_227502849.1\_3422 [locus\_tag=BN49\_RS18745] [protein=hypothetical protein] [protein\_id=WP\_227502849.1] [location=complement(3486501..3487763)] [gbkey=CDS]

MPVDLKRIPPPAQRPRAPVWWVWLLFLLCWLAAGTCWAIMSNTDKLQIHTADFWQTALILPALLWLILLA

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QPSWWSDEGIRHSRLIRIGDETPEQLVRRIMSNTLNELTSVLASVPAEIPLSLIIESDSSLSVSEIQSIW

RQCLASSHIRQPVTYLEGKGLQMIDHWLDQPMTEPSLMLIVALQVAPKQVEGTAETVVSLLLASPQVAAD

LMPLALLHRPEQVKGISHEAFHYAFARAFDWAALPAEAVPAGWLVGIKMNYHQPIATGLIALSSPINIGR

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>lcl|NZ\_FO834906.1\_prot\_WP\_016532068.1\_3423 [locus\_tag=BN49\_RS18750] [protein=PAAR domain-containing protein] [protein\_id=WP\_016532068.1] [location=complement(3487766..3488029)] [gbkey=CDS]

MKGIIRTGDTHTGGGKVLRGSSNMKFGGIGVARLGDPVSCPIKGHGPTVIAEGHPTFSDHGIPVAFHGHR

CACGCILLSSLPQARVR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532069.1\_3424 [locus\_tag=BN49\_RS18755] [protein=hypothetical protein] [protein\_id=WP\_016532069.1] [location=complement(3488119..3489096)] [gbkey=CDS]

MRKFLIGFFIFFSGIATGQSNLEDFNHSPKWVDSAGQINPDPGLMKYFQNMKVVCHNASGFTPKENKSAA

KAFSELVQYTSEGDQIKGFWNSPEHKQKREGLLVTAIKAGSWKAAYVNSVWAIKYPSAETPIEVASTKLH

ELVSRGIPIAAYKYASYLFGRDYETMYYLYAEAIKRGSPQAMSAVGGTIVVRVQELHPLGKQLLECAVGQ

GYAEAYDHLGLLADMEGRRLDAYHLWEKGINEGCEGCIKKMSNLAKVRHGYSADVPMMELMPELMRIKEF

NENNFFYQLTELPDFYRRLPEELIFHLNDSELLSLLKLEKFSRAL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043542.1\_3425 [locus\_tag=BN49\_RS18760] [protein=DUF6396 domain-containing protein] [protein\_id=WP\_046043542.1] [location=complement(3489311..3490375)] [gbkey=CDS]

MKGITTWIVLGSLLLSGCDQKSIHKDVPVNPLTAINARLAFTCKHQIIPEASADTDVLFKYARWRQKNNL

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HGAAGLAQDPEMALRYYRKAADEGNPQAQAFLGEKLFPAKRAPQVAMQMFRCAALQGEGKAANSLGIMLT

IDQKYQDAVDVYQLGVAAGDSGSASFLEHGFAGPAPTDRLYYLALEKDPERARRYEQIGAVLAKYSWAHP

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VAAP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043544.1\_3426 [locus\_tag=BN49\_RS18765] [protein=sel1 repeat family protein] [protein\_id=WP\_046043544.1] [location=complement(3490413..3491693)] [gbkey=CDS]

MKGITTWIVLGSLLLSGCDQKSIHKDVPVNPLTDINARLAFTCKHQIIPEASADTDVLFKYARWRQKNNL

INRDKMVDAEIARLYRIAAENGHYKASINLQNGALRGRFSLSSTELLRLSQQLIDAKVAAGYYFIAIYLE

HGAAGLAKDPEMALRYYRKAADEGNPQAQAYVGEKLFPAKMAPQVAMQMFQCAAEQGEGKAANSLGNMLA

IYKKYPEAVEVFQLGVAAGDSTSAGFLMHGFSGPEPTDRLFYLALEKDPERARRYEQIVKVLAKYSWAHP

VVPEINDIVPLPPAPLPEWDGKLKWLEEREANIPPPEPSAALIEKLAQAKQLNPATGRPLPTSPDFEKDS

VARLQCRSGEPCPQSGYWQPAWRPREGMSEHAIRYFREGDIMPVEKVTFVRPRPWPLRDRLVVEAQETVW

RRVGEA

>lcl|NZ\_FO834906.1\_prot\_WP\_038431327.1\_3427 [locus\_tag=BN49\_RS18770] [protein=DUF6396 domain-containing protein] [protein\_id=WP\_038431327.1] [location=complement(3491731..3493002)] [gbkey=CDS]

MKRLLLLFCMVLTACDQNNTHKDAPMNPLTDIHTRLAFTCKHQIIPEASADTDVLFKYARWRQKNNLINR

DKTVDAEIARLYRIAAENGHYKASINLQNGALRGRFALSSHERLRLSQQLIDAKVAAGYYFIAIYLEHGA

AGLAQDPEMALRYYRKAADEGNPQAQAYVGDKLAPIDIAPDISRQMRRCAAEQGEREVSSDLGVNLKNNK

RFQQATEAFQLGVAAGDSTSAGFLMHGFSGPEPMDRLFYLALEKDPERARRYEQIGAVLAKYSWAHPVVP

EINDIVPLPPAPLPEWDGKLKWLEEWEANIPPPVPDAALIEKLAKAKQLNPATGRPLPTSPDFEKDSVAR

LQCRSGEPCPQSGYWQPAWRPREGMSEHAIRYFREGDIMPVEKVTFVRPRPWPLRDRLVVEAQETVWRRV

GEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043546.1\_3428 [locus\_tag=BN49\_RS18775] [protein=phospholipase] [protein\_id=WP\_046043546.1] [location=complement(3493002..3494873)] [gbkey=CDS]

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PSMYFIRDGQSLCIGELLCKIAETKKVQVRILGWEMPCNAAGVGGEANLPGKGVIRYKDRKGQSTTDERY

AYDRQWFRQYSLSGEWSDHQLKKGQAGIAEIAAAPIAQRQEKLSSLSPLFVGRGFNFLERAEIAYRAANM

ALDPDISPDTMLTLAGTVTHHQKTVLVDYELPESAVGFVMGHNMLDEYWDTDKHSALFRPGNNMDPRLGA

NGKLPRQDISSRVTGPILEHLHHNFAMAWEKETGQDLLTIRDSVSIAKKLKLRALHGTPVMAQLLRTQAQ

AGKHDIETLYLQAVNNATQFIYIENQYFRWPPLAELINQVAERQSKVGRELHLFVVTNVTDEGIGAGTVN

TQRMLEVLGRANIIPEVTKLRKIGQLSNATFGGSVGYIDPGDINKRNREMSEKIADFKKKADEIQSSEIL

PEERPGLKVHICSLVAPDSPPEEWVPVYIHSKLMIVNDVFTTHGSANINTRSMRVDSEMNIAHEWSSVTR

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>lcl|NZ\_FO834906.1\_prot\_WP\_226956969.1\_3429 [locus\_tag=BN49\_RS18780] [protein=DUF6396 domain-containing protein] [protein\_id=WP\_226956969.1] [location=complement(3495042..3496043)] [gbkey=CDS]

MEASSDTDPLSDISSSPAFTCQHETLPAPSADTDVLFKYARWLQKNNLLKQDKSVDAQTERLYRIAAENG

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EGNPQAQAYVGDKLAPVDRAPNIAHQMRRCAAEQGEGKAAAMLGINLQGKEDYQSAIEAFQLGVAAGNGS

SARFLANGFSGPEPGDRLYYLAQQKDPERARRYKQIAKILSNYSYASPTVPEINDIVPLPPALLPEWDGK

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>lcl|NZ\_FO834906.1\_prot\_WP\_226326503.1\_3430 [locus\_tag=BN49\_RS18785] [protein=DUF6396 domain-containing protein] [protein\_id=WP\_226326503.1] [location=complement(3496153..3497349)] [gbkey=CDS]

MNPLSDTHAALAFTCAHQIIPEASADTDVLFKYARWLQKNNLLKQDKSVDAQTERLYRIAAENGHYKASI

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QAYVGDKLAPVDRAPDIAHQMRRCAAEQGEGKAAVMLGVNLQGKGYYRRAIEAFQLGVAAGDTSSALALS

HGFDGPESSDELYYLAQQKDPERARRYKLITKILSNYSYASPTVPEINDIVPLPPAPLPEWDGKLKWLEE

WEANIPPPAPDAALIEKLAQAKQLNPATGRPLPTSPDFEKDSVARLQCRSGEPCPQSGYWQPAWRPREGM

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530477.1\_3431 [locus\_tag=BN49\_RS31510] [protein=phospholipase D/transphosphatidylase] [protein\_id=WP\_016530477.1] [location=complement(3497427..3497990)] [gbkey=CDS]

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YKPLVNGEEAFAAVYRAIEKAQKSVDIICWGVQPSMYFIRDGQALRIGELL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043552.1\_3433 [gene=vgrG] [locus\_tag=BN49\_RS18800] [protein=type VI secretion system tip protein VgrG] [protein\_id=WP\_046043552.1] [location=complement(3498991..3501690)] [gbkey=CDS]

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VNSPSGMSDSGAESIWGLSITHNVVEANVTTRDYNPRDAQSVLQSATADMTRGNGEGITYGEVYHYKLRH

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GFTASRREALRVSLLAVPYSETLCWRPPLLPRPKVTGTMTARVTSAKANDIYAWQDASGLYRVKFDADRD

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KSETE

>lcl|NZ\_FO834906.1\_prot\_WP\_004891113.1\_3436 [gene=tssL] [locus\_tag=BN49\_RS18810] [protein=type VI secretion system protein TssL, short form] [protein\_id=WP\_004891113.1] [location=complement(3503850..3504503)] [gbkey=CDS]

MNTSESDLINKTFYPGWLMVSQLRCGQPVTDGEALYRQACRWVTEAREALTAGGVSEASAEQMLYAYCAL

LDESVLNRASQDDGYRRWRKDPLQARFFSTLNAGEELWERIRQLLREPTADAAVLTCFFRTLQLGFVGQY

RAEDDERREDVAQALGARVPPFSLTQEAPVVVRASRLRSGRRMYWCGWAAGIVALAALWLTCSAMLSQMV

AQIAGQG

>lcl|NZ\_FO834906.1\_prot\_WP\_032102706.1\_3437 [gene=tssK] [locus\_tag=BN49\_RS18815] [protein=type VI secretion system baseplate subunit TssK] [protein\_id=WP\_032102706.1] [location=complement(3504500..3505840)] [gbkey=CDS]

MKIFRPLWRDGAFLVPQQFQQQARWDAYVADTVSRMALAHPWGVLRAEFDASALTLSRLNATRLIVRFAD

GTLIDTELADILPPVRDVSDVMQDSVEVLLALPLLSASGGNLDDGQESARPRRWRAEQVTVQELAGHERS

ELAVLRHALTLRLSTEENAAFLTCPVARLVRDAQGQWIVDPEFIPPLLSLAASPTLVSELGELLHRLQAR

RRRLMAMRRESNARMADFAVADVSLFWLLNALNSAEPVLSELHLDPSRHPELLYRELARLAGSLLTFSLE

HHLEAIPRYRHASPEQVFPPLFALLDTLLEVSLPSRVIAIVLEQGADREIWRGRLHDARLREGADFYLSV

RSSLPPHQLQSRFPQLCKAGSHDDVAEVVNIALSGIAIKPLSHVPAAIPLRLENQYFALDLSTDAARAML

EAGNCTFYTPESLGDVKLELFAVLRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002910650.1\_3438 [locus\_tag=BN49\_RS18825] [protein=gamma-glutamylcyclotransferase] [protein\_id=WP\_002910650.1] [location=3506409..3506738] [gbkey=CDS]

MKPLFVYGTLCPGRSNAHILEAIGGEWRPGYVTGTFYARGWGAAADFPGIVLDAHGPRVNGYLFLSDRLA

AHWPMLDDFEEGYDRVPVEVTTDDGQQISAWIYQLQPRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002910652.1\_3439 [locus\_tag=BN49\_RS18830] [protein=DUF2058 domain-containing protein] [protein\_id=WP\_002910652.1] [location=3506853..3507392] [gbkey=CDS]

MTKLTLQEQMLKAGLVSSKKMAKVQRTAKKSRVQAREAREAVEENKKAQLERDKQLSEQQKQAVLAKEYK

AQVKQLIEMNRITVARGDIGFNFTDNNLIKKIMVDKPTQTQLINGRLAIARLAVDNKPEGEYAIIPAVVA

EKIAQRDASSIVLHSALSQDEQDEDDPYADFKVPDDLMW

>lcl|NZ\_FO834906.1\_prot\_WP\_016530143.1\_3440 [locus\_tag=BN49\_RS18835] [protein=RluA family pseudouridine synthase] [protein\_id=WP\_016530143.1] [location=complement(3507418..3508116)] [gbkey=CDS]

MSTIIDTFVAPPCREQITLLYQDEHLVLINKPAGLLSLSGKDPRNLDSVHHRLVQRFPGCTLVHRLDFGT

SGLMVIARNKGINALLCQQFSQRTVGKVYTALLCGHLAEDEGIVEAAIAKDPAHFPRMALCARHGKPARS

RYRVIDRLYQAREGERALALTRVTLTPETGRTHQLRIHCQLLGYPILGCDLYGGRELPGTECAPRLMLHA

SELRFVHPVSHEPMHIQQASPF

>lcl|NZ\_FO834906.1\_prot\_WP\_002910657.1\_3441 [locus\_tag=BN49\_RS18840] [protein=cold shock domain-containing protein] [protein\_id=WP\_002910657.1] [location=3508307..3508789] [gbkey=CDS]

MAMNGTITTWFKDKGFGFIKDENGENRYFHVIKVANPDLIKKDAAVTFEPTTNNKGLSAYAVKVIPESKY

IYIAGERLKLTSIKSYVVYREEEPVETRVDKENAVLSVGLLMNSIRPKATVQPGEMRSVKKLAITTFQGT

TLIFSEDEIDIDATVKLLKV

>lcl|NZ\_FO834906.1\_prot\_WP\_004152315.1\_3442 [locus\_tag=BN49\_RS18845] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004152315.1] [location=3508899..3509798] [gbkey=CDS]

MPVNFDFNDLYAFRALMEYGSFRLAAESICLSQSALSRRIEKLETALGNRLFDRTTRRVTLTLYGQNFAE

RSEQLLAHVETVLADISQVSKARTGLVTVATVPSAAYYFMPEIIRSFQARYPQVRIRLIDSSVGNVIEAV

SSGQADFGLCFAKNLPASIEFTPLADDRYVAACRHDHPLARKTHLSWQAYFEQDYIGLDRVSGNRTLLDR

ELAHLTPARPSICETRHVTTMLGMVEAGIGIAAVPAMSMPAGEHSVLRAVPLTDPVVTRTVGLIRLSGRI

QSYVAAELEKLIIEQYPSG

>lcl|NZ\_FO834906.1\_prot\_WP\_004899032.1\_3443 [locus\_tag=BN49\_RS18850] [protein=substrate-binding domain-containing protein] [protein\_id=WP\_004899032.1] [location=complement(3509773..3510582)] [gbkey=CDS]

MMRKTTGTLLATLLLAATGGSALSAEVTVMISGGFKAALEKLAPAWEKQTGNHLVVIPGPSMGKTPQAIP

NRLARGEHADVVIMVGDALTSLEKAGRTQPDSRRELADSPIGVVVKAGAPLPAIHSADQLRATLLAAPSV

AYSDSASGRYVSSTLFHTLGIDDAMQSKAQMVERIPVASEVAKGRYAIGFQQVSELLPVPGVTFVGELPD

NLQYITRFAGAVTISADHPQEGKALLTYLASPAAQETIHATGMRSVAAAAPVSQKDTVQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004152313.1\_3444 [locus\_tag=BN49\_RS18855] [protein=MFS transporter] [protein\_id=WP\_004152313.1] [location=complement(3510594..3511889)] [gbkey=CDS]

MHSTTSQMSTRDRIGAILRVTSGNFLEQFDFFLFGFYATYIAHTFFPASSEFASLMMTFAVFGAGFLMRP

IGAIVLGAYIDKVGRRKGLIVTLSIMATGTFLIVLIPSYQTIGLWAPLLVLIGRLLQGFSAGAELGGVSV

YLAEIATSGRKGFYTSWQSGSQQVAIMVAAAMGFALNAVLEPSAISDWGWRIPFLFGCLIVPFIFILRRK

LEETQEFTARRHHLAMRQVFATLLANWQVVIAGMMMVAMTTTAFYLITVYAPTFGKKVLMLSASDSLLVT

LLVAISNFFWLPVGGALSDRFGRRSVLIAMTLLALATAWPALTMLANAPSFLMMLSVLLWLSFIYGMYNG

AMIPALTEIMPAEVRVAGFSLAYSLATAVFGGFTPVISTALIEYTGDKASPGYWMSFAAICGLLATCYLY

RRSAVALQTAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002910715.1\_3445 [locus\_tag=BN49\_RS18860] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002910715.1] [location=complement(3512193..3513119)] [gbkey=CDS]

MNIMHPVLRRIDLNLLPVFDAVYRSRSVRLAAEELAMSTSALSHALSRLRSALNDPLFYREGHRMCPSVY

ASQLAPSIASALKFLNQELTPPAAFVPAASTDCMQIAITDFTAFCVFPTLMHHLQREAPGLRFELRYLPH

SPALTELLAGEVDLALGFNTPDEPAHPDLEEINWLRDEYVVISQANRTALTLDAYLAARHLVVTPWNERQ

GVLDCELERQGYSRQVAMKTPSMLSAPFIIEQSDLLMALPRRAAETMARAARLTIFPLPFPVPPFDVKIY

AHQRSGKREATRWLISLLQTLVGESTAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002910717.1\_3446 [locus\_tag=BN49\_RS18865] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002910717.1] [location=3513218..3513694] [gbkey=CDS]

MSITIRQATPDDATAIYDMIYELAVYEKAPEEVVTTPEEIRETLFASGSKTEALICEVAGKAVGYAVFFT

SYSTWLGRNGIYMEDLYVTPDYRGIGAGKALLKTIAQYAVQRQCGRLEWSVLDWNQPAIDFYLSIGAQPQ

DEWVRYRLTGDALRAFAE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043555.1\_3447 [gene=pckA] [locus\_tag=BN49\_RS18870] [protein=phosphoenolpyruvate carboxykinase (ATP)] [protein\_id=WP\_046043555.1] [location=complement(3513744..3515387)] [gbkey=CDS]

MSQQIESVKMALQELGINASGEFFYNPDYDLLIAHETSPELTGAARGVMTDSGAVAVDTGIFTGRSPRDK

YIVRDEQTRDTVWWADSGLGRNDNKPLSPDVWRSLKSLVAGQLSGKKLYVIDAWCGASPDTRLGVRFVTE

VAWQAHFVKNMFIVPSADELASFTPDFVVLNGAGCTNANWQAQGMNSENFVAFNLSERIQLIGGTWYGGE

MKKGLFSVMNYLLPQKGIASMHCSANRGEAGDVALFFGLSGTGKTTLSTDPHRQLIGDDEHGWDDDGVFN

FEGGCYAKTINLDPQAEPEIYGAIRRNALLENVVVRADGSVDYADGSKTENTRVSYPLSHIDNIVKPVSR

AGHPSKVIFLAADAFGVLPPVSRLTTEQMQYHFLSGFTSKLAGTERGITQPTPTFSACYGAAFLLLHPTQ

YASVLAAKMAQSGAEAWLVNTGWNGEGKRLSLRDTRSIISAILNGTTGPLREETIPVFGLAIPQSIPGVD

SAVLDPRNGWSSADKWQEKAESLAQLFMDNFKQYSDTEAGARLALAGPQLQKSAVEA

>lcl|NZ\_FO834906.1\_prot\_WP\_002910720.1\_3448 [locus\_tag=BN49\_RS18875] [protein=LysR substrate-binding domain-containing protein] [protein\_id=WP\_002910720.1] [location=3515671..3516564] [gbkey=CDS]

MLANLEVKWLYDVIALEESRSFTLAAKARNISQSSFSRRIQSLEASLGFSIFDRSANPLQLTNRGKIFVG

YARNMLDDMDFQISRIKGLNNTTQKIRIDAAPSLSVLLLPEIIAGYTDRKNKTFHVESINVNDAVFNLKE

GKSDFILSFYNEELMNYPFINHKIFDSYLHLVSPCDEHGRPLFHLHRGVLPLMKYANDSYMGRQVNQVID

RTPEITFSLTFVSSMSELLKRMILNGDGVGWLPQYSIQRELDEGRLTILDESLSLPIGAWLYRSGSRLNQ

AAERFWQHIKTRNEPRE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530335.1\_3449 [locus\_tag=BN49\_RS18880] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016530335.1] [location=complement(3516570..3517289)] [gbkey=CDS]

MSQPLLAFNEVDVFYGPIQALKQVSLTVNEGETVALIGANGAGKSTLLMSVFGQPRIAGGEIFYRGEAIS

RKSTHFIASNGIAQAPEGRRIFPDMTVEENLLMGTIAIGNRCQAEDKARMYQLFPRLEERRGQRAMTLSG

GEQQMLAIARALMSRPRLLLLDEPSLGLAPLVVKQIFQILRELTAQGMTLFLVEQNARHALNLSDRAYVM

VNGQIRLSGSGQTLLNDPEVRKAYLGISG

>lcl|NZ\_FO834906.1\_prot\_WP\_004189332.1\_3450 [locus\_tag=BN49\_RS18885] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_004189332.1] [location=complement(3517286..3518161)] [gbkey=CDS]

MTDSILRVEHLMMHFGGIKALNDVNLEVERGSITALIGPNGAGKTTVFNCLTGFYRATGGSIVLRAREKV

TDVIQVLGQKLHPDDFLHPAQLGRRIYYKMFGGTHLVNRAGMARTFQNIRLFREMSVIENLLVAQHTQVN

RHLLAGILNTRGYRQAENQALDRAFYWLEVVEMVDCANRLAGTLSYGQQRRLEIARAMCTRPEMICLDEP

AAGLNPVETQALSRIIRFLRQQHGITVLLIEHDMGMVMEISDHIIVLDHGDVIARGAPQAIQANASVIAA

YLGAEEEETRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004148804.1\_3451 [gene=livM] [locus\_tag=BN49\_RS18890] [protein=high-affinity branched-chain amino acid ABC transporter permease LivM] [protein\_id=WP\_004148804.1] [location=complement(3518158..3519444)] [gbkey=CDS]

MGEITRQPARAIQNALIDSVLAGLCALIVFGPIVGVVLKGYGFTLAPARVAILVAVVMAGRLALSLLLQS

HRGKAFIARFEGADDGVYVRPPGYRSRLRWIIPLLVGLAIVFPFLATKYLLTVAILGLIYVLLGLGLNIV

VGLAGLLDLGYVAFYAIGAYGLALGYQYLGLGFWAMLPLGAVMAALAGALLGFPVLRMHGDYLAIVTLGF

GEIIRLVLNNWVSFTGGPNGVPVPSPTLFGLEFTRRAKDGGIPIHEFFHVSYNPNLKFIFLYAVLCLVVM

LVLLVKHRLTRMPIGRAWEALREDEIACRAMGLNHVLVKLSAFMLGASTAGIAGVFFASYQGFVNPTSFT

FFESALILAIVVLGGMGSTLGVVLAAFVLTVTPELLRGFDEYRVLLFGVLMVMMMIWRPRGLVRTSRSGV

ALRKGVAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004175489.1\_3452 [locus\_tag=BN49\_RS18895] [protein=branched-chain amino acid ABC transporter permease] [protein\_id=WP\_004175489.1] [location=complement(3519454..3520368)] [gbkey=CDS]

MTAFFLQQLINGLTLGAVYGLIAIGYTMVYGIIGMINFAHGEVYMVSAYLCAIGLALLSFFGIHSFPLLI

FATLVFTIVVTGVYGWAIERIAYRPLRNSTRLAPLISAIGMSLILQNYVQLSQGPNQQGIPTLLSGALRM

TVGDGVVQITWTKVFILVAALVGMLILTWIIQYTRLGRICRATQQDRRMAAILGINTDRVISLVFVIGAA

MAGLAGVLVTMNYGTFDFYIGFIIGIKAFTAAVLGGIGSLPGAMLGGLLLGVAEAQFAGLVNSDYKDVFS

FALLVAILIFRPQGLLGRPLVAKV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530773.1\_3453 [locus\_tag=BN49\_RS18900] [protein=branched-chain amino acid ABC transporter substrate-binding protein] [protein\_id=WP\_016530773.1] [location=complement(3520478..3521536)] [gbkey=CDS]

MAFYAQADVKIGVAGPFTGPNATYGAQYWKGASQAVADINAAGGIKGEKIVLVQGDDACEPKQAVAVANR

LVDEAKVSAVVGHFCSSSTMPASEVYDEAGILTITPGSTNPQITERGMKDLFRMCGRDDQQGAIAANYML

DVLKAKKIAVIHDKDTYGQGLADATRAALAKRGTKEVLYEGLSRGEKDFNALVTKIGVLKPDVVYFGGCH

PEAGPLVRQMREQGVQAKFFSGDCIVTEELVTAAGGPQFTNGVLMTFGQDPRTLPDGKAVIEKFRASGFE

PEGYTLYAYASIQAIAAAWNAVGTDNAKASDWLKSHDVETVMGKKAWDGKGDLKVSDYVVYQWDDKGKYH

QL

>lcl|NZ\_FO834906.1\_prot\_WP\_004225356.1\_3454 [locus\_tag=BN49\_RS31150] [protein=hypothetical protein] [protein\_id=WP\_004225356.1] [location=3521825..3521971] [gbkey=CDS]

MPSRGEPDNAVSVPARELNIDAVSGRCAPAWCKNANMINSGDYFVAVM

>lcl|NZ\_FO834906.1\_prot\_WP\_016530774.1\_3455 [gene=pflB] [locus\_tag=BN49\_RS18910] [protein=formate C-acetyltransferase] [protein\_id=WP\_016530774.1] [location=complement(3522023..3524317)] [gbkey=CDS]

MKVDIDTQDVRYADAWLGFRGTAWQTQIDVRDFIQHNYTPYEGDESFLADATPATTALWEQVMAGIRVEN

ATHAPVDFDTNVATSITAHAAGYINQPLEKIVGLQTDQPLKRALHPFGGIKMIKSAFEAYGREMDPDFEY

QFTALRKTHNQGVFDVYSPDMLRCRKSGVLTGLPDGYGRGRIIGDYRRVALYGIRYLVRERELQFADLQP

ALERGEALEATLRLREELAEQRRALLQMQEMAARYGCDIAHPARTAREAVQWLYFAYLAAVKSQNGGAMS

LGRTATFLDIYIERDLRAGLLNEEQAQELIDHFIMKIRMVRFLRTPEFDSLFSGDPIWATEVLGGMGLDG

RTLVSKTTFRYLHTLHTMGPAPEPNLTVLWSQALPAAFKKYAARVSIATSSLQYENDDLMRSDFHSDDYA

IACCVSPMVIGKQMQFFGARANLAKTLLYAINGGVDEKLKIQVGPKTAPLRDEVLDYGTVMASLDHFMDW

LAVQYISALNIIHCMHDKYSYEAALMALHDRDVYRTMACGIAGLSVAADSLSAIKYARVKPVRDHHGLAV

DFVIEGDYPQYGNNDDRVDAIACDLVERFMRKIQALPTWRQAVPTQSILTITSNVVYGQKTGNTPDGRRA

GTPFAPGANPMHGRDRKGAVASLTSVAKLPFTYAKDGISYTFSIVPAALGKAPSAQENNLVGLLDGYFHH

EETVEGGQHLNVNVLNREKLLDAIEHPEQYPNLTIRVSGYAVRFNALTHEQQQDVISRTFTSQL

>lcl|NZ\_FO834906.1\_prot\_WP\_004175486.1\_3456 [gene=tdcD] [locus\_tag=BN49\_RS18915] [protein=propionate kinase] [protein\_id=WP\_004175486.1] [location=complement(3524346..3525554)] [gbkey=CDS]

MTEFPVVLVINCGSSSIKFSVLDAASCDCLLNGVAEGINAERASLSLNGGEPVALAQRGYEGALQAIAGA

LAQRDLIDSVALIGHRVAHGGDLFTESVIISEEVINNIRQVSSLAPLHNYASLSGIASAQRLFPEVMQVA

VFDTSFHQTLAPEAFLYGLPWEYYQNLGVRRYGFHGTSHRYVSQRALALLGLPEQESGLVIAHLGNGASI

CAVRNGRSVDTSMGMTPLEGLMMGTRSGDVDFGAMAWIAGETRQTLSDLERVANTASGLLGISGLSSDLR

VLEQAWHEGHARARLAIKTFVHRIARHIAGHAAALQRLDGIIFTGGIGENSVLIRRLVSERLTVFGLAMD

AARNQQPNSAGERLISADGSRVRCAVIPTNEERMIALDAIRLGRIHTAAALA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145486.1\_3457 [gene=tdcC] [locus\_tag=BN49\_RS18920] [protein=threonine/serine transporter TdcC] [protein\_id=WP\_004145486.1] [location=complement(3525582..3526913)] [gbkey=CDS]

MSTTESIASSQTSLSSWRKSDTTWTLGLFGTAIGAGVLFFPIRAGFGGLIPILVMLVLAYPIAFYCHRAL

ARLCLSGANPSGNITETVEEHFGKTGGVVITFLYFFAICPLLWIYGVTITNTFMTFWENQLQMPALNRGV

VALLLLLLMAFVIWFGKDLMVKVMSYLVWPFIASLVVISLSLIPYWNSAVIDQVNLSDIALTGHDGILVT

VWLGISIMVFSFNFSPIVSSFVVSKREEYEAQFGREYTERKCSQIISRASMLMVAVVMFFAFSCLFTLSP

QNMADAKAQNIPVLSYLANHFASMSGTKSTFATLLEYGASIIALVAIFKSFFGHYLGTLEGLNGLILRFG

YKGDKTRVSSGKLNTLSMVFIMGSTWVVAYANPNILDLIEAMGAPIIASLLCLLPMYAIRKAPSLAKYRG

RLDNLFVTAIGLLTILNIAYKLF

>lcl|NZ\_FO834906.1\_prot\_WP\_016531140.1\_3458 [gene=tdcB] [locus\_tag=BN49\_RS18925] [protein=bifunctional threonine ammonia-lyase/L-serine ammonia-lyase TdcB] [protein\_id=WP\_016531140.1] [location=complement(3526939..3527928)] [gbkey=CDS]

MHITYDLPVSIDDILEAKQRLAGKIYKTGMPRSNYFSERCQGEIFLKFENMQRTGSFKIRGAFNKLCGLT

AAEKRKGVVACSAGNHAQGVSLSCAMLGIDGKVVMPKGAPKSKVAATCDYSAEVVLHGDNFNDTLAKASD

IVELEGRIFIPPYDDPQVIAGQGTIGLEILEDLYDVDNVIVPIGGGGLIAGIAIAIKSINPTIRIIGVQS

ENVHGMAASWYAGEITSHRHAGTLADGCDVARPGKLTYQIARQLVDDIVLVSEDDIRQSMVALIQRNKVI

TEGAGALACAALLSGKLDSYIQNRKTVSLISGGNIDLSRVSQITGFVDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002910764.1\_3459 [gene=tdcA] [locus\_tag=BN49\_RS18930] [protein=transcriptional regulator TdcA] [protein\_id=WP\_002910764.1] [location=complement(3528022..3528963)] [gbkey=CDS]

MNTFSLPKTQHLVVFQEVIRSGSIGAGAKALGLTQPAVSKIIGDMESYFGSELIVRRNTGVSLTEAGQVF

LNWSEAITREMKNMVNEMNALTNSAVVDVSFGFPSLVGFTFMSEMVHQFKMTFPKARVSMYEAQLSAFLP

AIRDGRLDFAIGTLSDEMKLQDLHVEPLFESEFVLVANRARIGNGTVRLASLQHEQWVLPETNMGYYSEL

LTTLQRSGIRRENIVNTDSVVTIYNLVLNADFLTVIPCDMTTPFGSSQFVTIPIKEALPVARYAAVWSKN

YRLKTAAASLVEMAKHYSSGQGNRHWQPLQIIA

>lcl|NZ\_FO834906.1\_prot\_WP\_004219597.1\_3460 [locus\_tag=BN49\_RS31155] [protein=hypothetical protein] [protein\_id=WP\_004219597.1] [location=3529140..3529283] [gbkey=CDS]

MPWPNAGIKIIDGDNIDGEMAIKNTPFVRYSTRAIRVRRKPKIKLML

>lcl|NZ\_FO834906.1\_prot\_WP\_004145488.1\_3461 [locus\_tag=BN49\_RS18940] [protein=nitrilotriacetate monooxygenase] [protein\_id=WP\_004145488.1] [location=3529581..3529703] [gbkey=CDS]

MIPRLRQQLNEQLMSDQLAVDLLSSYLRMDLSAQPWDQPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531139.1\_3462 [locus\_tag=BN49\_RS18945] [protein=PhnD/SsuA/transferrin family substrate-binding protein] [protein\_id=WP\_016531139.1] [location=complement(3529741..3530541)] [gbkey=CDS]

MAERMTFPMYAIHRQQTQALWQAVQSLLAERGVMVAGDPPAADPGDLLAHWRQPTLLLSQTCGYPLVTQL

PEVQTVGCFHYAAPGCEGRRYRSLLVVREADSHRMLGDFLGRRAVCNAEHSQSGYNVLRKMVAPLSREGR

FFSAVMFSGSHRQSLRELQQENADIAAIDCVTYALLQRYQPQALAGLVAIGWSPAAPGLPLITAGVTPAA

TLNSLREALQQLVSDDRYRSLCDALLICGYSDMSREAYAPLLAWRDEAAALGVSQL

>lcl|NZ\_FO834906.1\_prot\_WP\_171819481.1\_3463 [locus\_tag=BN49\_RS18950] [protein=fatty acid desaturase] [protein\_id=WP\_171819481.1] [location=complement(3530534..3531520)] [gbkey=CDS]

MTEKKTAVYVDDQQRILIRQLARSWLWRSELPTWLLIVTVYGGWFACVAGWRTLGLFPATLLLIWFTAWY

MSLQHELIHGHPTRLAWFNQLLGTLPLAVWYPYGVYRDSHLAHHRNHLLTHPEDDPESYYVTVESWQRFS

AWQRRLIHLRNTFWGRLLLAPMMDIIHTLNSALWAFHEGDRRAIAMWSLHLLLLTGLLTWMAAQGFSPLW

FVLAVSYPALALTKVRSFLEHRAADDPLARSVINEAGLPWRALFLNLNYHAVHHDLPGVPWYALRQLYLH

RQAAYLQRNQGFLVRGYGEWRRHFSRRAVAVNAHPGFGEQAQAGGEHG

>lcl|NZ\_FO834906.1\_prot\_WP\_002910830.1\_3464 [locus\_tag=BN49\_RS18955] [protein=proteasome-type protease] [protein\_id=WP\_002910830.1] [location=complement(3531959..3532705)] [gbkey=CDS]

MTYCVAMCLADGLVFASDSRTNAGVDHIATFKKLHVFHQEGERVLVLQSAGNLATTQSVISLLSARIRTQ

QEPNLMQVTSLYDAAMLIGKTLLEVIQRDSSNQQTCSNTNFNCNLLLGGQIAGETHRLFHIYPEGNFIEA

TRDTPYFQIGESKYGKPIIDRVLTIDTPLEQAMCCALISIDSTLRSNLSVGLPLDTLLYRSGSFSSAGQH

RITDSDPYFNRIRKAWSEGLLHTFQTLPTWTPAEREEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910832.1\_3465 [locus\_tag=BN49\_RS18960] [protein=transglutaminase family protein] [protein\_id=WP\_002910832.1] [location=complement(3532722..3533537)] [gbkey=CDS]

MKLVIDHLTRYGYDEEVKFSTQYLRLTPRSTARQTITAWTLTLPDGAAVTTTDGWGNVLHVLTLDNPHKE

ITIRASGIVDIADEGEETRDEEAELLSPLVFLRCTPLTRADTAIREFAQRLYRPDAAEESLNQLMADLLL

RMPYSPGATQVQDSAADAFARAKGVCQDHTHVFLACCRALEIPARYVSGYVYSDNAQHVAMHAWAEVWLD

GRWLSFDITNNTRRLNQHLRLATGLDYLDACPVRGTRLGGGGEIMLTNAEVREHSQQAQQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004184646.1\_3466 [locus\_tag=BN49\_RS18965] [protein=alpha-E domain-containing protein] [protein\_id=WP\_004184646.1] [location=complement(3533534..3534463)] [gbkey=CDS]

MLSRTASELFWMARYLERAESYARVLDVTWKLSMIPRHSQQSRDLALPLNLSMTHELFQARHARFTMSNL

LNFFALDGNNPCSIYSCVEMAWNNAHAVRGSLSAEVWESINATRIELRSLRQQGLGELGSDGFFEWVKER

VHLFRGAVIGTLLRNDALSFIGIGTLIERAFATTQLLLIKDQQLTNDPDPVREYYRLDTLLNAVSAREAY

NSLYRQPVSRETVMELLILRNDIPRSLRASIADLVGELEKIANDRSYQPLRLAHQLNVDLRFSTRDDLAQ

ADLQTTLNGLLARINALSDSIRQTYLEAL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043559.1\_3467 [locus\_tag=BN49\_RS18970] [protein=circularly permuted type 2 ATP-grasp protein] [protein\_id=WP\_046043559.1] [location=complement(3534457..3535896)] [gbkey=CDS]

MIKITLPDGHYYDEMLTAQGEQRPHYNAWWQWFRNTDQFSIRQKKAQAELLFHRIGITFNVYGEDEGTER

LIPFDSVPRIIPAGEWQRIDRGIRQRVKALNAFLYDIYHEQNILRAGLIPAEQVLANEQYQPCMQGINLP

NNTYAHITGVDMVRNNDGQYYVLEDNLRTPSGVSYMLENRKMMMRLYPEMFEQHHIAPVERYPSYLLQTL

RESSLVDDPCVVVMTPGRFNSAYFEHSFLAQQMGVELVESADLFIKNGAVYMRTTEGPRRVDVIYRRIDD

AWLDPLAFRADSMLGVPGLLSVYRAGGVVLANAIGTGVADDKSIYPYVPEMIRFYLGEQPILSNIPTWQC

RKAEDLRYVLSNLELMVVKEVHGAGGYGMLVGPRSTKEEREAFRQRLLANPANYIAQDTLALSTCPTFVE

EGLSPRHIDLRPYVLSGQEMRLVPGGLTRVSLTEGSLVVNSSQGGGTKDTWVMEDDASC

>lcl|NZ\_FO834906.1\_prot\_WP\_042940402.1\_3468 [locus\_tag=BN49\_RS18975] [protein=carbohydrate porin] [protein\_id=WP\_042940402.1] [location=complement(3536182..3537567)] [gbkey=CDS]

MEIQGASLSGLFSSGLWAAANNHPTDIEKRLAQLEQRVINAEQRAADAEAKIQTLTRQQNVVAKSTPTVK

VESAEPVAPGAEPTTLTLSGYGDIKFYGDVEFNMDGASSSGSLTSVKTTANKDWAPGNNERWDINGRLLL

GFDGMRKMDNGRFAGFSVQPLADLNGKMNLDDAVFFFGQENDWKVKVGRFEAYDMFPLNQDTFVEYSGNT

ANDLYSDGYGYIYMMKEGRGRSNSGGNFLMSKTLDNWYFELNTLLENGSTLFQDQQYHGTALENEKNVAY

LRPVIAWNSGRFSTAIAMESNVVNNAYGYHDAKGRWVDQSSRTGYGYTMTWNGQKTDPQDGVVTNLNVAY

MDAEDETDFTAGVNSLWHGFELGYIYAHNKIDSFNTADFIANCDDNCWIADPGNYDIHTIHASYLFPNVM

NMKNFNIYLGAYASWIESNPNNGDGQEDSRYGGRLRFKYFF

>lcl|NZ\_FO834906.1\_prot\_WP\_115217266.1\_3469 [locus\_tag=BN49\_RS18985] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_115217266.1] [location=join(3537635..3537950,3537950..3538863)] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_WP\_016532291.1\_3470 [locus\_tag=BN49\_RS18990] [protein=glycoside-pentoside-hexuronide (GPH):cation symporter] [protein\_id=WP\_016532291.1] [location=complement(3539010..3540368)] [gbkey=CDS]

MSAGEKISVREKIGYSLGDAASHIVFDSSVAILAYFYTDIYGLPPAVMGTMFLLVRLLDAITDPIMGAIA

DATSTRWGRFRPWLLAICVPFAVSCVLVYSIPSFSDSGKIAYAVAAYIFMTLMYTAINIPYCSLGAALTS

DPRESLSLQSWRFAITPIGGALGTAFILPLADFLYPGDRATGIQVSMALFGVIGCLMFITCFATTKERVQ

PIKEQNLNIARDVKILFRNDQWRILSVYNFMMLVAVVIRGGAVVYYVNSVLHKGADVITIFMLGGMFASM

LGSVLAKPFGTRFCKVRFSFWINLLTAALGVVCFIVPVQYWIAVLGVHILISIIQGGNGALQWSMITDVN

NYGEWKTQRRITGMNVAANIFVIKLGVAVGGAILGWILAYFHYAANTTVQSASAVQGVVLLFTLVPSVFY

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>lcl|NZ\_FO834906.1\_prot\_WP\_016532292.1\_3471 [locus\_tag=BN49\_RS18995] [protein=alpha,alpha-trehalase] [protein\_id=WP\_016532292.1] [location=3540881..3542623] [gbkey=CDS]

MTSPFSRRPATLPYALRLVLGGAFIALATLTAEAEETRPIPQSPDILLGPLFNDVQSAKLFSDQKTFADA

IPNSDPLMILADYRMQKNQASFDLRHFVELNFTLPKENDTYVPPKGQTLRQHIDGLWPVLTRSTVEVEKW

DSLLPLPKPYVVPGGRFREVYYWDSYFTMLGLAESGHWDKVEDMVANFAAEIDAWGHIPNGNRTYYLSRS

QPPFFSFMVSLLATHDGDQVLKTYQPQLEKEYRYWMAGADALAPGSADKRAVRMADGALLNRYWDDNDTP

RPESWLDDVKTAKSNPNRPATEIYRDLRSAAASGWDFSSRWMDNPQQLATIRTTSIVPVDLNALMFHLEK

TLARASKASGDSAGATQYDALANARQQAIEKYLWNDKEGWYADYDLKTHKVRNQLTAAALFPLYVNAASR

ERATKVAAAAESRLLKPGGLTTTTVNSGQQWDAPNGWAPLQWVAVEGLQNYGQQKIAMEVTWRFLTNVQH

TYDSKQKLVEKYDVSSTGTGGGGGEYPLQDGFGWTNGVTLKMLDLICPQEKPCDALPATRPATTPSPQDK

PVAAPAANDPAPAEPQKTGS

>lcl|NZ\_FO834906.1\_prot\_WP\_014343229.1\_3472 [locus\_tag=BN49\_RS19000] [protein=TonB-dependent siderophore receptor] [protein\_id=WP\_014343229.1] [location=3542875..3544995] [gbkey=CDS]

MNVAISRKRPGLLYALAVTLPFTAQAEETVVVTATPPASASAPTEGYSASTSLGATKTDQPLITTAQSVS

VVTRQQMADQGANTISQALEYTPGVYSSFGGGATRFDAISLRGYHGGDVDNLFLDGMRLMSDGGSHNVLQ

IDPWFIERVDVIRGPSSALYGQSVPGGVVNLTSKRPQFSQQGHIRLTGGTQNTKGAAFDYTDAINDQWAW

RLIGMTRSSDTQYDHTREERYAISPSLLWQPDSDTSLLLRAYLQKDPSGGYHGSLPLDGTRYAHNGRKLS

PSTNEGDPGDGYQRRQQIYSYEFDHQFTDVWSVYSAGSYTHTNVSLDQVYQVGWIDDSDMLARGYSGSRG

SLDGWSTDNRLRADFNTGDLAHTLILGAEYHRFRNDLWTGAGGAAPLNPFSGYTAQTGHTVTYSDDNNRR

YYQTGLYLQDEMVWNRWHVDVSARYDRIVSQQVSDTQGTSNRRSDDHISGRASLLYALDNGLSPYLSYSQ

AITPAMLPGADGKPLKPTTAEQVEAGLKFQPPGSSDLYSIAIYDLTQKDVATRDPNIATATYIPAGKVHS

QGVELEAHHQITPQLSTIASYTWNRLRFQDTQDGTDNNTPQLTPDQMASFWARYQFPAGISVGAGVRYIG

KQWADDANTARLPSVTLMDAMMRADLGVWSPTLKGAYVQVNANNIGDREYISGCYGTGNCYWGAERSVIA

TVGYDF

>lcl|NZ\_FO834906.1\_prot\_WP\_002910846.1\_3473 [gene=emtA] [locus\_tag=BN49\_RS19005] [protein=membrane-bound lytic murein transglycosylase EmtA] [protein\_id=WP\_002910846.1] [location=complement(3545037..3545648)] [gbkey=CDS]

MKLRWLLILVVFLAGCSSKHDYTNPPWNPEVPVKRAMQWMPISEKAGAAWGVDPQLITAIIAIESGGNPA

VVSKSGAVGLMQLKPSTSGRDVYRRMGWRGEPSVSELKNPERNISMGAAYLSILENGPLAGIKDPQVMRY

AVVVSYANGAGALLRTFSSNRQDAIEEINDLDADEFFEHVVKKHPAPQAPRYIWKLQKALDAM

>lcl|NZ\_FO834906.1\_prot\_WP\_046043561.1\_3474 [gene=ldcA] [locus\_tag=BN49\_RS19010] [protein=muramoyltetrapeptide carboxypeptidase] [protein\_id=WP\_046043561.1] [location=3545824..3546738] [gbkey=CDS]

MSQFYLVAPSGYCINQQAAARGVERLQQAGHEVAHQQVIPRRQQRFAGTEHERLADINQLAQLPGRNRIV

LAVRGGYGASRLLPHIDWQGLVARQQRDPLLICGHSDFTAIQSGLQAMGNVITFSGPMLAGNFGAETLDP

FTEHHFWQALRQPEFTLEWPGEGPNCRVEGTLWGGNLAMLTSLIGTPWLPAIRDGILVVEDINEHPFRVE

RMLLQLLHSGVLAAQKAVIFGSFTGSAPNDYDAGYDLPQVFDYLRQQLPLPLISGLEFGHEQRTVTLPLG

ARARLVNQAAATTLTIGGHPVLTE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910885.1\_3475 [locus\_tag=BN49\_RS19015] [protein=potassium/proton antiporter] [protein\_id=WP\_002910885.1] [location=3546831..3548564] [gbkey=CDS]

MDAAAVISLFILGSVLVTCSILLSSFSSRLGIPILVIFLAIGMLAGIDGIGGIPFDNYPFAYMVSNLALA

VILLDGGMRTQASSFRVALWPALSLATVGVLITSALTGMMAAWLFKLDLIEGLLIGAIVGSTDAAAVFSL

LGGKGLNERVGSTLEIESGSNDPMAVFLTITLIEMIQQHQTGLSWMFAVHIIQQFGLGIAIGLGGGYLLL

QMINRIVLPAGLYPLLALSGGIMIFAVTTSLDGSGILAVYLCGFLLGNRPIRNRHGILQNFDGLAWLAQI

AMFLVLGLLVTPSDLLPIAIPALLLSMWMIFIARPLSVFAGLLPFRGFNLRERVFISWVGLRGAVPIILA

VFPMMAGLDNARLFFNVAFFVVLVSLLLQGTSLSWAAKKAKVVVPPISWPISRVGLDIHPENPWEQFVYQ

LGADKWCIGAALRDLHMPPETRIAALFRNNVLLHPTGSTRLREGDILCVIGREHDLPALGKMFSQSPPVA

LDQRFFGDFILDAEARFADVAQIYGLDGGEEFREHQQSLGEVVQQLLGAAPVVGDQVEFAGMVWTVAEKE

NDHVLKVGVRVAEDEAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910887.1\_3476 [gene=dadX] [locus\_tag=BN49\_RS19020] [protein=catabolic alanine racemase DadX] [protein\_id=WP\_002910887.1] [location=complement(3548581..3549651)] [gbkey=CDS]

MTRPVVASIDLLALRQNLQIVRRAAPGSRLWAVVKANAYGHGVARVWSALSAADGFALLNLEEAILLREQ

GWKGPILLLEGFFHADELAVLDQYRLTTSVHSNWQIKALQQAKLRAPLDIYLKVNSGMNRLGFMPERVHT

VWQQLRAISNVGEMTLMSHFAEAENPQGIVEPMRRIEQAAEGLDCPRSLANSAATLWHPEAHFDWVRPGI

VLYGASPSGQWQDIANTGLKPVMTLRSEIIGVQNLRPGEAIGYGGLYRTTQEQRIGIVACGYADGYPRVA

PSGTPVLVDGVRTTTVGRVSMDMLAVDLTPCPQAGIGAPVELWGKEIKIDDVAASSGTVGYELMCALAPR

VPVVTL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530395.1\_3477 [locus\_tag=BN49\_RS19025] [protein=D-amino acid dehydrogenase] [protein\_id=WP\_016530395.1] [location=complement(3549661..3550959)] [gbkey=CDS]

MRVVILGSGVVGVASAWYLSQAGHDVTVIDRQPGPAEETSAANAGQISPGYAAPWAAPGVPLKAIKWMFQ

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FRTAKQYENATRDIAVLEDAGVPYQLLEAKRLAEVEPALAEVSHKLTGGLRLPNDETGDCQLFTTRLASM

AEQAGVTFRFNTAVDALLHEGDRIAGVKCGDEIIKGDAYVMAFGSYSTAMLKGLVDIPVYPLKGYSLTIP

IAQEDGAPVSTILDETYKIAITRFDQRIRVGGMAEIVGFNKALLQPRRETLEMVVRDLFPRGGHVEQATF

WTGLRPMTPDGTPVVGRTAYKNLWLNTGHGTLGWTMACGSGQLISDLISGRTPAIPYDDLAVARYSPGFT

PARPQHLHGAHN

>lcl|NZ\_FO834906.1\_prot\_WP\_004145506.1\_3478 [locus\_tag=BN49\_RS31160] [protein=hypothetical protein] [protein\_id=WP\_004145506.1] [location=complement(3551058..3551204)] [gbkey=CDS]

MLYANRFSSRFPHLKAVFLPCLQNLMLGKNKAQHEIVNLTAQGWCGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002910889.1\_3479 [locus\_tag=BN49\_RS19035] [protein=SpoVR family protein] [protein\_id=WP\_002910889.1] [location=3551281..3552813] [gbkey=CDS]

MATIDSMNRDTTRLSDGPDWTFELLETYLAEVDRVAKLYRLDTYPHQIEVITSEQMMDAYSSVGMPINYP

HWSFGKKFIETEQAYKHGQQGLAYEIVINSNPCIAYLMEENTITMQALVMAHACYGHNSFFKNNYLFRSW

TDASSIIDYLIFARKYITECEERYGVDEVEKLLDSCHALMNYGVDRYKRPQKISLQEEKARQKSREEYLQ

SQVNMLWRTLPKREEEKAIESARRYPSEPQENLLYFMEKNAPLLEPWQREILRIVRKVSQYFYPQKQTQV

MNEGWATFWHYTILNHLYDEGKVTERFMLEFLHSHTNVVFQPPYNSPWYSGINPYALGFAMFQDIKRICQ

SPTEEDKYWFPDIAGSDWLETLHFAMRDFKDESFISQFLSPKIMRDFRFFTVLDDDHNNYLEISAIHNEE

GYREIRNKLSAQYNLSNLEPNIQVWNVDLRGDRSLTLRYVPHNRVPLDKGRREVLKHVHRLWGFDVLLEQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_002910890.1\_3480 [gene=fadR] [locus\_tag=BN49\_RS19040] [protein=fatty acid metabolism transcriptional regulator FadR] [protein\_id=WP\_002910890.1] [location=complement(3552888..3553607)] [gbkey=CDS]

MVIKAQSPAGFAEEYIIESIWNNRFPPGSILPAERELSELIGVTRTTLREVLQRLARDGWLTIQHGKPTK

VNNFWETSGLNILETLARLDHDSVPQLIDNLLSVRTNISTIFIRTAFRQHPDKALAVLDSAREVEDHADA

FAELDYNIFRGLAFASGNPIYGLILNGMKGLYTRIGRHYFSSPEARSLALGFYHQLAKVCEAGLHDQVYE

LVRRYGHDSGEIWHRMQKSLPGDLAMNMR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530394.1\_3481 [gene=nhaB] [locus\_tag=BN49\_RS19045] [protein=sodium/proton antiporter NhaB] [protein\_id=WP\_016530394.1] [location=3553856..3555406] [gbkey=CDS]

MEISYGRALWRNFLGQSPDWYKLALIIFLIVNPLVFAVAPFVAGWLLVVEFIFTLAMALKCYPLLPGGLL

AIEALLIGMTSPAHVRDEIAGNLEVLLLLMFMVAGIYFMKQLLLFVFTRLLLGIRSKMLLSLAFCLAAAF

LSAFLDALTVVAVVISVAVGFYGIYHRVASARPDDSDLLDDSHIEQHYREVLEQFRGFLRSLMMHAGVGT

ALGGVMTMVGEPQNLIIAKAAGWHFGEFFLRMAPVTLPVMVCGLLTCLLVEKYRLFGYGEPLPPTVRKVL

QEFDDRSRAQRSRQERLRLIAQALIGVWLIVALAFHLAEVGLIGLSVIILATTFTGVTDEHAIGKAFTEA

LPFTALLTVFFSIVAVIIDQQLFTPVIEFVLQASPHAQLSLFYLFNGLLSSISDNVFVGTVYINEAKAAL

EHGAISLPQFEMLAVAINTGTNLPSVATPNGQAAFLFLLTSALAPLIRLSYGRMVWMALPYTIVLTLVGL

LCVEFTLMPVTDWLLSHGWLVTPSLP

>lcl|NZ\_FO834906.1\_prot\_WP\_002910894.1\_3482 [gene=dsbB] [locus\_tag=BN49\_RS19050] [protein=disulfide bond formation protein DsbB] [protein\_id=WP\_002910894.1] [location=3555535..3556065] [gbkey=CDS]

MLQYLNQCSRGRGAWLLMALTAFILELVALWFQHVMLLQPCVMCIYERCALFGIMGAGLVGAIAPKTPLR

YVAMAIWLYSAIRGLQLAWEHTMIQLHPSPFQTCDFAARFPTWLPLDKWLPQVFVASGDCSVRQWQFLSL

EMPQWLVGIFAAYLLVAILVIVAQPFKAKKRDLFGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002910895.1\_3483 [locus\_tag=BN49\_RS19055] [protein=DUF1971 domain-containing protein] [protein\_id=WP\_002910895.1] [location=3556216..3556560] [gbkey=CDS]

MSSLLIPADWKVKRSTPFFTKENVPAALLSHHNTAAGVFGQLCVMEGTVTYYGFANEQATEPEKKVVIHA

GQFATSPPQYWHRVELSDDARFNIHFWVAEETDGENGLFHAKKA

>lcl|NZ\_FO834906.1\_prot\_3484 [locus\_tag=BN49\_RS31520] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=complement(3556567..>3556635)] [gbkey=CDS]

AVPESTVVDWQDHILNLPDRAR

>lcl|NZ\_FO834906.1\_prot\_3485 [locus\_tag=BN49\_RS30510] [protein=cytoplasmic protein] [pseudo=true] [partial=5'] [location=<3556630..3556731] [gbkey=CDS]

HRVELSDDARFNIHFWVAEETDGENGLFHAKKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043564.1\_3486 [locus\_tag=BN49\_RS19060] [protein=YcgN family cysteine cluster protein] [protein\_id=WP\_046043564.1] [location=complement(3556738..3557184)] [gbkey=CDS]

MSEQPFWQQKTLDDMSDAEWESLCDGCGQCCLHKLMDEDTDEIYFTNVACRQLNIKTCQCRNYARRFEYE

PDCIKLTRENLPTFEWLPPTCAYRLLAEGKPLPAWHPLLTGSKAAMHGERISVRLIAVPESTVVDWQDHI

LNLPDRAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180422.1\_3487 [locus\_tag=BN49\_RS19065] [protein=fumarylacetoacetate hydrolase family protein] [protein\_id=WP\_004180422.1] [location=complement(3557279..3557938)] [gbkey=CDS]

MYQHHNWQGALLDYPVSKVVCVGSNYAKHIKEMGSATPEEPVLFIKPETALCDLRQPLVLPEGLGSVHHE

VELAVLIGSTLRQATEEHVLKGIAGYGVALDLTLRDLQAKMKKAGQPWEKAKGFDNACPISGFIPAAEFH

GDPQNTSLSLKINGEVRQQGTTADMIHRIVPLIAYMSRFFTLKAGDVILTGTPEGVGPLHSGDELEVGFN

GLALTTRVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002910898.1\_3488 [locus\_tag=BN49\_RS19070] [protein=YcgL domain-containing protein] [protein\_id=WP\_002910898.1] [location=complement(3557955..3558236)] [gbkey=CDS]

MFCVIYRSTKREQTYLYVEKKDDFSRVPDELMRSFGTPQMAMLLPLDGRKKLVNADLEKVKQALSEQGYY

LQLPPPSENLLKKHLAEQGKQSD

>lcl|NZ\_FO834906.1\_prot\_WP\_004180423.1\_3489 [gene=minC] [locus\_tag=BN49\_RS19080] [protein=septum site-determining protein MinC] [protein\_id=WP\_004180423.1] [location=3558363..3559061] [gbkey=CDS]

MSNTPIELKGSSFTLSVVHLHDANPEVIRQALEDKIAQAPAFLRHAPVVVNIASIEEEVEWRAINEAIAA

TGLRIMGVSGCKIPRLKTEIDRAGIPLLTEGKEKASRPAPSDPTPPPPVASQITKTRLIDQPVRSGQRIY

APHCDLIVTNHVSAGAELIADGNIHVYGMMRGRALAGAGGDRDAQIFCTHLAAELVSIAGEYWLSDNIPA

EFYGKAARLRLGESALAIQPLN

>lcl|NZ\_FO834906.1\_prot\_WP\_002910900.1\_3490 [gene=minD] [locus\_tag=BN49\_RS19085] [protein=septum site-determining protein MinD] [protein\_id=WP\_002910900.1] [location=3559085..3559897] [gbkey=CDS]

MARIIVVTSGKGGVGKTTSSAAIATGLAQKGKKTVVIDFDIGLRNLDLIMGCERRVVYDFVNVIQGDATL

NQALIKDKRTENLYILPASQTRDKDALTREGVDKVLEELKKMEFDFIVCDSPAGIETGALMALYFADEAI

ITTNPEVSSVRDSDRILGILASKSRRAENGEEPIKEHLLLTRYNPGRVNKGDMLSMEDVLEILRINLVGV

IPEDQSVLRASNQGEPVILDAASDAGKAYADTVERLLGEERPFRFIEEEKKGFLKRLFGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002910902.1\_3491 [gene=minE] [locus\_tag=BN49\_RS19090] [protein=cell division topological specificity factor MinE] [protein\_id=WP\_002910902.1] [location=3559901..3560170] [gbkey=CDS]

MALLDFFLSRKKNTANIAKERLQIIVAERRRGDAEPHYLPQLRKDILEVICKYVQIDPEMVSVQLEQRDG

DISILELNVTLPETEESKS

>lcl|NZ\_FO834906.1\_prot\_WP\_004148826.1\_3492 [gene=rnd] [locus\_tag=BN49\_RS19095] [protein=ribonuclease D] [protein\_id=WP\_004148826.1] [location=complement(3560248..3561363)] [gbkey=CDS]

MITTDDGLRAVCEAASAASAVALDTEFVRTRTYYPQLGLLQLFDGQQVSLIDPLTINDWAPMRDLLLNQD

VTKYLHAGSEDLEVFLNAFNLMPQPLIDTQILAAFCGRPMSWGFASMVEEYSGVALDKSESRTDWLARPL

TERQCEYAAADVWYLLPIASQLMAETDRAGWLPAALDECRVMQQRRQEVVDPAEAWRDIGNAWQLRTRQL

GCLQLLAEWRLRKARERDLAVNFVVREEHLWSVARYMPTSLGELDSLGLSGSEIRFHGKTLISLVEKAQA

LPESALPAPLQNLIDMPGYRKAFKDIKALVQEVSTEKGVSAELLASRRQINQLLNWHWQLKTQAGEPELI

SGWRGELMAERLKRLLNDYPR

>lcl|NZ\_FO834906.1\_prot\_WP\_002910904.1\_3493 [gene=fadD] [locus\_tag=BN49\_RS19100] [protein=long-chain-fatty-acid--CoA ligase FadD] [protein\_id=WP\_002910904.1] [location=complement(3561445..3563130)] [gbkey=CDS]

MKKVWLNRYPADVPAEINPDRYQSLVELFEHATTRYADQPAFINMGEVMTYRKLEERSRAFAAYLQEGLG

LQKGDRVALMMPNLLQYPVALFGILRAGMIVVNVNPLYTPRELEHQLNDSGAAAIVIVSNFAHTLEKVVA

KTQVQHVILTRMGDQLSTAKGTLVNFVVKYIKRLVPKYHLPDAISFRSALQHGYRMQYVKPEIVAEDLAF

LQYTGGTTGVAKGAMLTHRNMLANLEQVNATYGPLLHRGKEFVVTALPLYHIFALTMNCLLFIELGGQNL

LITNPRDIPGLVKELAKYPFTAMTGVNTLFNALLNNKEFQQLDFSSLHLSAGGGMPVQQAVAERWVKLTG

QYLLEGYGLTECSPLVSVNPHDIDYHSGSIGLPVPSTEAKLVDDDDNEVAPGQPGELCIKGPQVMLGYWQ

RPDATDEIIKDGWLHTGDIAVMDEEGFLRIVDRKKDMILVSGFNVYPNEIEDVVMQHSGVLEVAAIGVPS

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>lcl|NZ\_FO834906.1\_prot\_WP\_002910905.1\_3494 [locus\_tag=BN49\_RS19105] [protein=Slp family lipoprotein] [protein\_id=WP\_002910905.1] [location=complement(3563336..3563917)] [gbkey=CDS]

MAGQKQGVRWLLAAAVAVALSGCVSVPDAIKGTSPTPQQDLVRVMNAPQLYVGQEARFGGKVVNVQNQQG

KTRLEIATVPLDSGARPVLGEPSRGRIFADVNGFLDPVDFRGQLVTVVGPIAGVVDGKVGSTPYKFMLMN

ATGYKRWNVVQQVVMPPQPIDPWMLGPRPWGYGYGGWGWYNPGPAEVRNVVTE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151443.1\_3495 [gene=tsaB] [locus\_tag=BN49\_RS19110] [protein=tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex dimerization subunit type 1 TsaB] [protein\_id=WP\_004151443.1] [location=complement(3563956..3564651)] [gbkey=CDS]

MRILAIDTATEACSAALWNDGTLSAHFEICPREHTQRILPLVQEVLTESGTTLSELDALAFGRGPGSFTG

VRIGIGIAQGLALGAELPMIGVSTLATMAQGAWRKTGATRVLAAIDARMGEVYWAEYQRDEQGVWHGEET

EAVLKPDAVAERLAQLSGEWATVGTGWQAWPDLAKASGLTLSSGEIELPAAEDMLPLACYLLAAGKTVAV

EKAEPVYLRNEVAWKKLPGRE

>lcl|NZ\_FO834906.1\_prot\_WP\_004175456.1\_3496 [locus\_tag=BN49\_RS19115] [protein=ATP-dependent DNA helicase] [protein\_id=WP\_004175456.1] [location=complement(3564797..3566707)] [gbkey=CDS]

MIDDFAADGQLAKAIPGFKPREPQRQMAVAVSEAIEASRPLVVEAGTGTGKTYAYLAPALRAKKKVIIST

GSKALQDQLYSRDLPTVAKALKFTGKLALLKGRSNYLCLERLEQQALAGGDLPVQTLSDVILLRSWSNQT

QDGDISTCASVAEDSQAWPLVTSTNDNCLGSDCPLYKDCFVVKARKKAMDADVVVVNHHLFLADMVVKES

GFAELIPEAEVMIFDEAHQLPDIASQYFGQSLSSRQLLDLAKDITIAYRTELKDTQQLQKCADRLAQSAQ

DFRLQLGDPGYRGNLRELLADSHIQRALLLLDDALELCYDVAKLSLGRSALLDAAFERATLYRGRLKRLK

EINQPGYSYWYECTSRHFTLALTPLTVAEKFKEVMAQKSGSWIFTSATLSVNDDLHHFTARLGIDEAQTL

LLPSPFDYQHQALLCVPRNLPLPNQPGAARHLAAMLKPLIEANDGRCFMLCTSHAMMRDLAEQFRATMTL

PVLLQGETSKGQLLQQFVSAGNALLVATSSFWEGVDVRGDALSLVIIDKLPFTSPDDPLLKARMEDCRLR

GGDPFDEVQLPDAVITLKQGVGRLIRDIDDRGVLVICDNRLVMRPYGAVFLASLPPAPRTRDIRRAVRFL

AVPPAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002910910.1\_3497 [locus\_tag=BN49\_RS19120] [protein=RidA family protein] [protein\_id=WP\_002910910.1] [location=3566839..3567183] [gbkey=CDS]

MTITRIDAEARWSDVVIHNQTLYYTGVPANLDADAFEQTANTLAQIDAVLEKQGSDKSRILDATIFLADK

SDFAAMNKAWDAWVVAGHAPVRCTVEATLMNPQYKVEIKIIAAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004145519.1\_3498 [locus\_tag=BN49\_RS19125] [protein=YoaH family protein] [protein\_id=WP\_004145519.1] [location=complement(3567184..3567369)] [gbkey=CDS]

MFAGLPSLSHEQQQKAVERIHELMAQGISSGQAIALVAEELRATHTGEQIVARFEDEDEDE

>lcl|NZ\_FO834906.1\_prot\_WP\_004145520.1\_3499 [gene=pabB] [locus\_tag=BN49\_RS19130] [protein=aminodeoxychorismate synthase component 1] [protein\_id=WP\_004145520.1] [location=3567458..3568813] [gbkey=CDS]

MLSPAIITLPWRPDAAEHYFAPLSALPWAMLLHSGFADHPHNRFDILVAAPRATLLTRGEQTWVDDGETV

VVSAEDPLQLLQQQLDRQPFTPQPHDDLPFLGGALGLFGYDLGRRFERLPSHAQADIALADMAVGIYDWA

LIVDHQRQQISLLSYDDPQQRLQWLEAQTPTPGETFALTSAWQSNMSRQQYGEKFRQVQAYLHSGDCYQV

NLAQRFQASYVGDEWQAFRQLNAVNRAPFSAFIRLDEGAILSLSPERFIQLRQGEIQTRPIKGTLPRLDS

PLADAQQAEKLANSPKDRAENLMIVDLMRNDIGRVAVPGSVRVPELFVVEPFPAVHHLVSTITARLPMTL

HASDLLRAAFPGGSITGAPKVRAMEIIDELEPQRRNAWCGSIGYLSYCGNMDTSITIRTLTAWQGQLYCS

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>lcl|NZ\_FO834906.1\_prot\_WP\_004180429.1\_3500 [locus\_tag=BN49\_RS19135] [protein=CoA pyrophosphatase] [protein\_id=WP\_004180429.1] [location=3568817..3569395] [gbkey=CDS]

MADRALNLDDFLSRFQLLRPQPSRHALNQRQAAVLVPIVRRPQPGLLLTQRSPLLRKHAGQVAFPGGAVD

NTDATLIAAALREAQEEVAIPPEAVEVIGVLPPVDSVTGFQVTPVVGIIPPDLHYHASQDEVSAVFEMPL

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043568.1\_3501 [gene=sdaA] [locus\_tag=BN49\_RS19140] [protein=L-serine ammonia-lyase] [protein\_id=WP\_046043568.1] [location=3569558..3570922] [gbkey=CDS]

MISLFDMFKVGIGPSSSHTVGPMKAGKQFVDDLVEKGLLNAVTRVAVDVYGSLSLTGKGHHTDIAIIMGL

AGNQPDTVDIDAIPAFIRDVEARGRLLLANGQHEVDFPADDGMRFRSDNLPLHENGMTIHAWAGEKEIYC

KTYYSIGGGFIVDEEHFGKENANELQVPYPFKSAQEMLAYCKETGLSLSGMVMQNELALHSKKEIEDYFA

NVWQTMRACIDRGMNTEGVLPGPLRVPRRASALRRLLVASDKLSSDPMNVVDWVNMFALAVNEENAAGGR

VVTAPTNGACGIVPAVLAYYDHFIESVSPENYIRYFMACGAIGALYKMNASISGAEVGCQGEVGVACSMA

AAGLAELLGASPEQVCVAAEIGMEHNLGLTCDPVAGQVQVPCIERNAIASVKAINAARMAMRRTSEPRVS

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528868.1\_3502 [locus\_tag=BN49\_RS19150] [protein=EAL domain-containing protein] [protein\_id=WP\_016528868.1] [location=3571105..3572682] [gbkey=CDS]

MQTAQKVITAYRHKRIIVCLLVALATLGATLAIRFISQRSVNEDYIRTAASQRVAALNDILRPLSAQRAT

LLPLVGKPCPDIHLTLRKMAASLQTIRSVALVTSGIVYCSSIFGPRQADLHRLQPALPAPRPLLLFSNDS

SLLKGSPVLIQWYPAAESGLDGVMLVVNIELLGTLILNEKSALISNVSLQVGDRYFSSRHGLLEKAHVPQ

GTVIYRQRSTEFPFTVNINGPGASAIALEELPGELPLALIFSLLMTGIAWLATAGRMSFSREISLGISAR

EFALWCQPLQDARSGRCCGVEILLRWNNPRRGTISPEVFIPIAEGNNLIIPLTRYVIAETARRLDAFPRD

RHFHIAINVAARHFANGLLLRDLHNYWFSVDPVQQLVVELTERDVLQDGDQHMAEHLHFKGVQLAIDDFG

TGNTSLSWLEKLRPDVLKIDRSFTSSVGIDSVNATVTDIIIALANRLHIVTVAEGVETLEQENYLRSHGV

DVLQGFYYARPMPVEAFPAWLASREESVGESETTE

>lcl|NZ\_FO834906.1\_prot\_WP\_016528869.1\_3503 [gene=yoaE] [locus\_tag=BN49\_RS19155] [protein=CNNM family cation transport protein YoaE] [protein\_id=WP\_016528869.1] [location=complement(3572716..3574275)] [gbkey=CDS]

MELLMDPSIWAGLLTLIVLEIVLGIDNLVFIAILADKLPPKQRDKARLIGLSLALVMRLGLLSVISWMVT

LTKPLITIADFSFSGRDLIMLLGGIFLLFKATTELHERLENRQHDAGHGKGYASFWVVVLQIVVLDAVFS

LDAVITAVGMVNHLPVMMAAVVIAMILMLLASKPLTRFVNQHPTVVVLCLSFLLMIGLSLVAEGFGFHIP

KGYLYAAIGFSIIIEFFNQVARRNFVRHQSTLPLRARTADAILRLMGGRKQASVSHDADSPAAVPVPEGA

FAEEERYMINGVLTLAQRSLRSIMTPRGEISWVDAEQSEDEIRRQLLSSPHSLFPVCRGELDEIIGIVRA

KEMLVALESGENVAALASASPAIVVPETLDPINLLGVLRRARGSFVIVTNEFGVVQGLVTPLDVLEAIAG

EFPDADETPEIVIDGDGWLIKGSTDLHALQQALGLDPLINDDEDIATVAGLVISANGHIPRIGDVVSLPP

LHFTVVEANDYRVDLVRAVVTRPPSDVEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002910917.1\_3504 [gene=manX] [locus\_tag=BN49\_RS19160] [protein=PTS mannose transporter subunit IIAB] [protein\_id=WP\_002910917.1] [location=3574722..3575693] [gbkey=CDS]

MTIAIVIGTHGWAAEQLLKTAEMLLGEQENVGWIDFVPGENAETLIEKYNAQLAKLDTSKGVLFLVDTWG

GSPFNAASRIVVDKEHYEVIAGVNIPMLVETFMARDDDPSFDELVALAVETGSEGVKALKAKPVEKAAPA

PAPAAAPKAAAPAKPMGPNDYMVIGLARIDDRLIHGQVATRWTKETNVTRIIVVSDEVAADTVRKTLLTQ

VAPPGVTAHVVDVAKMIRVYNNPKYAGQRVMLLFTNPTDVERIVEGGVKITSVNIGGMAFRQGKTQVNNA

ISVDAKDIEAFKKLNARGIELEARKVSTDPKLKMMDLIAKVDK

>lcl|NZ\_FO834906.1\_prot\_WP\_002910918.1\_3505 [locus\_tag=BN49\_RS19165] [protein=PTS mannose/fructose/sorbose transporter subunit IIC] [protein\_id=WP\_002910918.1] [location=3575750..3576550] [gbkey=CDS]

MEITLLQIVLVFIVACIAGMESVLDEFQFHRPLIACTLIGAVLGDMKTGIIIGGTLEMIALGWMNIGAAV

APDAALASIISTVLVIAGHQSIGAGIALAIPLAAAGQVLTIIVRTITVAFQHAADKAAENGNLTALSWLH

VSSLFLQAMRIAIPAVIVAISVGTSEVQGLLNAIPEVVTSGLNIAGGMIVVVGYAMVINMMRAGYLMPFF

YLGFVTAAFTNFNLVALGVIGAVMAILYIQLSPKYNRVAGAPAQAAGNNDLDNELD

>lcl|NZ\_FO834906.1\_prot\_WP\_004145526.1\_3506 [locus\_tag=BN49\_RS19170] [protein=PTS mannose transporter subunit IID] [protein\_id=WP\_004145526.1] [location=3576563..3577414] [gbkey=CDS]

MVDMTKNTTEKKLTQSDIRGVFIRSNLFQGSWNFERMQALGFCFSMVPAIRRLYPENNDARKQAIKRHLE

FFNTHPYVAAPVLGVTLAMEEQRANGAEIDDGAINGIKVGLMGPLAGVGDPIFWGTVRPVFAALGAGIAM

SGSLLGPLLFFILFNAVRLLTRYYGVAYGYRKGVDIVKDMGGGFLQKLTEGASILGLFVMGALVNKWTHV

NIPMVVSKITGSDGQVHVTTVQTILDQLMPGLVPLLLTFACMWLLRKKVNPLWIIVGFFVIGIAGYAVGL

LGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002910920.1\_3507 [locus\_tag=BN49\_RS19175] [protein=DUF986 family protein] [protein\_id=WP\_002910920.1] [location=3577477..3577935] [gbkey=CDS]

MTFTDLVIILFILALLAYAIYDQFIMPRRNGPVLLAIPLLRRSRVDGMIFVGLTAILIYNNITQHGTAIT

TWLLSALALMGLYLFWIRTPKIIFKPRGFFFANVWIEYQRIKEMNLSEDGVLVMQLEQRRLLIRVRNIDD

LEKIYKLLITTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002910921.1\_3508 [gene=mntP] [locus\_tag=BN49\_RS19180] [protein=manganese efflux pump MntP] [protein\_id=WP\_002910921.1] [location=3578354..3578920] [gbkey=CDS]

MNLSATILLAFGMSMDAFAASIGKGATLHKPKFSEAVRTGLIFGAIETLTPLVGWGLGMLASQFILEWNH

WIAFILLVFLGGRMIVEGFRGDSDEACEAPHRHGFWLLVTTAFATSLDAMAVGVGLAFLQVSIVTTALAI

GCATFIMSTLGMMVGRFIGPLLGKRAEILGGIVLIGIGSEILWSHFAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016528870.1\_3509 [gene=rlmA] [locus\_tag=BN49\_RS19185] [protein=23S rRNA (guanine(745)-N(1))-methyltransferase] [protein\_id=WP\_016528870.1] [location=complement(3578924..3579718)] [gbkey=CDS]

MSYSCPLCHAPLSRSDNHYSCPQRHQFDLAKEGYVNLLPVQFKRSRDPGDSAEMMQARRAFLDAGHYRPL

RDAIAERLRHYAPTDLLDIGCGEGYYTHAFAAIASRSWGLDVSKPAIRAAAKRYPQVNFCVTSSQRLPFS

DASFDAVVRIYAPCNAEELARVVRPGGWVITATPGPRHLLELKGLIYDEVRLHELKTEAMPGFRLEAQQQ

LAYPMILTGSEAQALLQMTPFAWRAKAEVHAALRQQPTFGCQTDFMIHCWQREA

>lcl|NZ\_FO834906.1\_prot\_WP\_032102661.1\_3510 [gene=ftsI] [locus\_tag=BN49\_RS19190] [protein=peptidoglycan glycosyltransferase FtsI] [protein\_id=WP\_032102661.1] [location=complement(3579780..3581528)] [gbkey=CDS]

MVLKKKTKSAASFTPIRFGLLCVAILGCLGLLLVRVGWLQIISPDNLVKQEDMRSLREEPVAVERGMISD

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QAEWIDKLHLPGVYLRDESRRFYPAGHVAANLLGFTNVDNQGIEGVEKSFNAQLTGKPGRRLVRKDKHGN

VIENITEVPPVPAHNLQLSIDERLQTVTEDALDNAVRWNKAESGAAVLIKIDTGEILAMASYPDFNPNNR

DSATLDDFRNRAISDTFEPGSTVKPLVIMTALQQGIVQPDSVVDTHPFVLDGHRIRDVGYYPELSLTGIL

QKSSDTGVSHLSLAMPVQHLIDTYKAFGFGEPTGLGLTGESAGLMPHRRYWGQLDRATFAFGYGLMVTPL

QLAHVYATIGGFGIARPLSITRIDPPVMGTRVMPESIVHSVEHMMESVALPGGGGTKAAVRDYRVAVKTG

TAKKIGPDGKYIDKYVAYTAGVAPASRPQFALVVVMNDPSNGSYYGGAVSAPVFSQIMGDVLRLENVMPD

GMPQGAENLIVMHDSHLQGPAL

>lcl|NZ\_FO834906.1\_prot\_WP\_001062678.1\_3511 [gene=cspE] [locus\_tag=BN49\_RS19195] [protein=transcription antiterminator/RNA stability regulator CspE] [protein\_id=WP\_001062678.1] [location=complement(3581716..3581925)] [gbkey=CDS]

MAKIKGQVKWFNESKGFGFITPADGSKDVFVHFSAIQGNGFKTLAEGQNVEFEIQDGQKGPAAVNVTAI

>lcl|NZ\_FO834906.1\_prot\_3512 [locus\_tag=BN49\_RS29265] [protein=YobF family protein] [pseudo=true] [partial=3'] [location=complement(<3582011..3582082)] [gbkey=CDS]

MCGIFSKEVLSKHVVVEYRFSAEP

>lcl|NZ\_FO834906.1\_prot\_WP\_002911374.1\_3513 [locus\_tag=BN49\_RS19205] [protein=YebO family protein] [protein\_id=WP\_002911374.1] [location=complement(3582673..3582963)] [gbkey=CDS]

MSELLNPGILNLASLAVSVALLLVGLLLWFFVNRASSRANEQIELLQALLDQQKRQNALLRRLCEANAPE

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>lcl|NZ\_FO834906.1\_prot\_WP\_002911375.1\_3514 [gene=mgrB] [locus\_tag=BN49\_RS29275] [protein=PhoP/PhoQ regulator MgrB] [protein\_id=WP\_002911375.1] [location=complement(3583038..3583181)] [gbkey=CDS]

MKKLRWVLLIVIIAGCLLLWTQMLNVMCDQDVQFFSGICTINKFIPW

>lcl|NZ\_FO834906.1\_prot\_WP\_004145533.1\_3515 [locus\_tag=BN49\_RS19215] [protein=YobH family protein] [protein\_id=WP\_004145533.1] [location=3583341..3583580] [gbkey=CDS]

MRLIIRTIILVAILWIGVLLSGYGVLFHSEENVGGLGLKCQYLTARGVSTALYVHSDSGVIGVSSCPLLR

KSTTVVDNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002911378.1\_3516 [gene=kdgR] [locus\_tag=BN49\_RS19220] [protein=DNA-binding transcriptional regulator KdgR] [protein\_id=WP\_002911378.1] [location=complement(3583638..3584429)] [gbkey=CDS]

MAGADLDKQPDSVSSVLKVFGILQALGEEREIGITELSQRVMMSKSTVYRFLQTMKSLGYVAQEGESEKY

SLTLKLFELGARALQNVDLVRSADIQMRELSRLTKETIHLGALDEDSIVYIHKIDSMYNLRMYSRIGRRN

PLYSTAIGKVLLAWRDRSEVEQILDGVEYKRSTERTITSTEELLKVLDGVREQGYGEDNEEQEEGLRCIG

VPVFDRFGVVIAGLSISFPTLRFSEERLHEYVAMLHQAARKISEQMGYNDYPF

>lcl|NZ\_FO834906.1\_prot\_WP\_002911379.1\_3517 [locus\_tag=BN49\_RS19225] [protein=MFS transporter] [protein\_id=WP\_002911379.1] [location=3584607..3585977] [gbkey=CDS]

MDKNSSDGVPLPQRYGAILTIVLGLTMAVLDGAIANVALPTIASDLNASPAASIWIVNAYQIAIVIALLP

LSFLGDMVGYRRIYKIGLVVFIFTSLACALSRSLEMLTFARVAQGLGGAALMSVNTALIRLIYPQRFLGR

GMGINSFVVAVSSAAGPTIAAAILSLASWQWLFLINVPLGIVAFVLAMRFLPPNSARSKIIRFDLPSAIM

NALTFGLLITALSGFAQGQSTQLVLAEVAAMLVVGFFFVRRQLTMPVPLLPVDLLRIPLFSLSICTSICS

FCAQMLAMVSLPFFLQSMMGRSEVETGLLLTPWPLATMVMAPLAGYLIEKCHAGLLGAIGLLIMACGLFG

LALLPSSPSDLDIIWRMALCGAGFGLFQSPNNHTIVASAPSHRSGGASGMLGTARLLGQSTGAALVALLF

NLLGNNGTHTALLLAGTLAIVAALISGLRVTQPRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002911381.1\_3518 [gene=htpX] [locus\_tag=BN49\_RS19230] [protein=protease HtpX] [protein\_id=WP\_002911381.1] [location=complement(3586043..3586927)] [gbkey=CDS]

MMRIALFLLTNLAVMVVFGLVLSLTGIQSSSMTGLLIMALLFGFGGSIVSLMMSKWMALKSVGGEVIEQP

RNETERWLMNTVAQQAQQVGIAMPQVAIYHAPDINAFATGARRDASLVAVSTGLLQNMSRDEAEAVIAHE

ISHIANGDMVTMTLIQGVVNTFVIFISRVIAQIAAGFLGGNREDEGESSNGNPLIYFAVATVLELVFGIL

ASIITMWFSRYREFHADAGSARLVGREKMIAALQRLKTSYEPQEASSMMAFCINGKAKSMSELFMTHPPL

DKRIEALRSGEYLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004145536.1\_3519 [gene=prc] [locus\_tag=BN49\_RS19235] [protein=carboxy terminal-processing peptidase] [protein\_id=WP\_004145536.1] [location=complement(3587163..3589211)] [gbkey=CDS]

MNTFFKITALAGLLAIAGHAFAVDDITRADQIPVLKEEPQHATVSERVTSRFTRSHYRQFDLDNAFSAKI

FDRYLNLLDYSHNVLLASDVAKFAAKKDQIGDELRSGKLDVFYDLYNLGQQRRFERYQYALKVLERPMDF

TGNDNFNLDRSKAPWPKDEAELNKLWDAKVKFDQLSLKLAGKDDKEIRDTLTRRYKFAIRRLAQTNSEDV

FSLAMTAFAREIDPHTNYLSPRNTEQFNTEMSLSLEGIGAVLQMDDDYTVINSLVAGGPAAKSKAISVGD

RIVGVGQTGKSMVDVIGWRLDDVVALIKGPKGSKVRLEILPAGKGAKTRIVTLTRERIRLEDRAVKMSVK

TVGKEKVGVLDIPGFYVGLTDDVKVQLQKLEKQNVSSIIIDLRSNGGGALTEAVSLSGLFIPSGPVVQVR

DNNGKVREDSDNDGVVYYKGPLVVLVDRFSASASEIFAAAMQDYGRALIVGEPTFGKGTVQQYRSLNRIY

DQMLRPEWPALGSVQYTIQKFYRINGGSTQRKGVTPDIMMPTGNEDRETGEQYEDNALPWDSINAATYVK

SGDLTPFGPELLKRHDERIAQDPEFQYIMKDIARYNAMKDKRNIVSLNYAQREKENEEDDAIRLARINDR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002911385.1\_3520 [gene=proQ] [locus\_tag=BN49\_RS19240] [protein=RNA chaperone ProQ] [protein\_id=WP\_002911385.1] [location=complement(3589231..3589908)] [gbkey=CDS]

MENQPKLNSSKEVIAFLAERFPQCFSAEGEARPLKIGIFQDLVERVGGEMNLSKTQLRAALRLYTSSWRY

LYGVKAGAIRVDLDGNPCGELEEQHIAHARQQLEEAKARVQAQRAAQQAKKREAAAAAGQQDEGVRRERK

PRPQQPRRKEGAEQRKPRPVAAKAPREERLTPVSDVSVLTVGQALKVKAGNNAMDATVLEITKDGVRVQL

TSGMSMIVRAEHLVF

>lcl|NZ\_FO834906.1\_prot\_3521 [locus\_tag=BN49\_RS19245] [protein=GAF domain-containing protein] [pseudo=true] [location=complement(3589990..3590503)] [gbkey=CDS]

MSKTEFYADLNRDFQALMAGETSFLAMIANTSALLFERLSEVNWAGFYLLEGDTLVLGPFQGKLACVRIP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002911387.1\_3522 [gene=yebS] [locus\_tag=BN49\_RS19250] [protein=membrane integrity lipid transport subunit YebS] [protein\_id=WP\_002911387.1] [location=3590636..3591919] [gbkey=CDS]

MPIKTPTLKPAKKMVVHTVSTPLPYAHYQRCTQCDMLFRLPVLKRNQSAWCPRCNAKVRDGRDWSLTRLG

SMALAMLLLMPFAWSEPLLRLHLLGVRIDANVLQGIWQMTAQGDPITAAMVLFCAVVAPVLLVVSISYLW

LGNVLGMNLRPVLLMLGKLKEWVMLDIYLVGIGVASIKVQDYAFLQPGIGLVAFISLTLLSILTLIHMNV

EELWERFYPERPATRADNNLQVCTGCHYTGYRDARGRCRRCHTPLHHRRPQSLQRSWAALIASLVFLFPA

NLLPISIIYVNGARQDDTILSGIISLASSNIAIAGVVFIASILVPFTKVIVLFTLLLSIQFKCEQGLRTR

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GNARFAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002911388.1\_3523 [locus\_tag=BN49\_RS19255] [protein=PqiB family protein] [protein\_id=WP\_002911388.1] [location=3591888..3594521] [gbkey=CDS]

MSQETPASQTEARIKTKRRISPFWLLPVIALLIAAWLIWTSFDDRGSTITIDFQSANGIVPGRTPIRYQG

VEVGTVQDISLSKDLSKIEVSASIKRDMKDALRKETQFWLVTPKASLAGVSGLDALVGGNYIGMMPGKGE

PEDHFVALDTQPKYRINNGELMIHLQAPDLGSLNSGSLVYFRKIPVGRVYDYSLNANNQGVTIDVLIERR

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DNPSISTLLTGNTFELVPGEGEPRNHFSVMPADKALLDEPNVATVTLSAPESYGIDGGQPLVLHGVKVGQ

VLERKLTAKGVTFQVAIDPEYRDLIHGDSKFVVNSRLDVKVGLDGVQVLGASASEWVNGGIRVIPGEKGK

MQSSYPLYANLEKAQENSLSEVPTTTLSLSAETLPDVQAGSVVLYRKFAVGEIIAVKPRKDAFDIDLHIK

PEYRYLLTNNSVFWAEGGAKVKLDGNGLTVQASPLARAIKGAISFDNLNGSSAGARLNNKRILYASETAA

RAVGGQITLHAYDAGKMAAGMPIRYLGIDIGQIQSLELITAKNEVQAKAVLYPEYVGTFARAGTRFSVIT

PQISAAGVEHLDTLFQAYINVEPGRGPARRDFEIQDTTISDSRYIDGLNIVVEAPEAGSLGIGTPVLFRG

LEVGTVTGLSLGSMSDRVMVKLRISKRYQYLVRNNSVFWLASGYSLDFGLIGGVVKTGTFNQFIRGGIAF

ATPPGTPLAPKAQDGKHFLLQESEPKEWREWGTALPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529029.1\_3524 [gene=rsmF] [locus\_tag=BN49\_RS19260] [protein=16S rRNA (cytosine(1407)-C(5))-methyltransferase RsmF] [protein\_id=WP\_016529029.1] [location=3594645..3596078] [gbkey=CDS]

MAENTVYFPEAFLAQMRAAMPAHLSFDDFIAACQRPLRRSIRVNTLKISVDDFLSLVAPYGWQLAPVPWC

AEGFWIEREDDDALPLGSTAEHLSGLFYIQEASSMLPVAALFADNRQPERVMDVAAAPGSKTTQIAARMG

NAGGILANEFSASRVKVLHANISRCGISNVALTHFDGRVFGAALPETFDAILLDAPCSGEGVVRKDTDAL

KNWSPDSNLDIAATQRELIDSAFHALRPGGTLVYSTCTLNREENQSVIEWLLSRYPQAVEILPLGELFPG

AADALTAEGFLHVFPQIYDCEGFFVARLRKTAAIDPLPAPGYKVGKFPFTPLKDREAAAVTAAARAVGLE

WDAGHTLWQRDKELWLFPLALEPLFGKVRFSRIGVRLAELHNKGYRWQHEAVIAFAAPQRAFELSQEEAE

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>lcl|NZ\_FO834906.1\_prot\_WP\_002911393.1\_3525 [locus\_tag=BN49\_RS19265] [protein=YebV family protein] [protein\_id=WP\_002911393.1] [location=3596194..3596433] [gbkey=CDS]

MSKTNVRIGAFEIDDAELHGEHQGERTLSIPCKSDPDLCMQLDAWDADTSVPAILNGEHSVLYRKHYDRQ

SDAWVMRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002911395.1\_3526 [locus\_tag=BN49\_RS19270] [protein=YebW family protein] [protein\_id=WP\_002911395.1] [location=3596531..3596722] [gbkey=CDS]

MFALVLFICYLDGGCEDIVVDVYREETQCLVAMEDQRIRHGGCYPIEDFIDGFWQPASEYSDF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529030.1\_3527 [gene=pphA] [locus\_tag=BN49\_RS19275] [protein=protein-serine/threonine phosphatase] [protein\_id=WP\_016529030.1] [location=complement(3596719..3597372)] [gbkey=CDS]

MYQRINGSDWRNIWLMGDLHGCFALLMNRLRQLRFDPWADLLISVGDLIDRGPQSADCLGLLRCRWFRAV

RGNHEQMALEALESGDMRLWQMNGGDWYVKGDARQRADVDRLLAHCRRLPLIIEVQCGKARHVIAHADYP

APVYRWQQPVDPQRVLWSRYRLSEHLAGRHGAIAGADHFWFGHTPLQARYDHDNQHYIDTGAVFGGTLTL

VALQSAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151446.1\_3528 [locus\_tag=BN49\_RS19280] [protein=VirK/YbjX family protein] [protein\_id=WP\_004151446.1] [location=3597529..3598497] [gbkey=CDS]

MFIVTDNSLHSSGVLAPRSHLIADLVMGRLTPAPIWRQKNYRFKFLLRTALFYNATRAMLEALSARDDFN

QLLAAQATLPGKVHRQYLTRDLNAWQRAVAVINHYRYIDTLRGSRLAHAMTAVSEVPLLTLNGKEDRRFT

LYASSAGKAEREGETTLWLRDSDHTLLASATFSVTRDHDAWQLVIGGLQGPRRHVSHEVIKQATRACYGL

FPKRLLLEFIWQLAARSQIAAIYGVSDNGHVFRALRYRLSKGRHFHASYDEFWQSIDGQPESPWRWRLPL

CLERKSLESIASKKRAEYRRRFQLLDQLTEQVAILTQRHAGD

>lcl|NZ\_FO834906.1\_prot\_WP\_002911398.1\_3529 [locus\_tag=BN49\_RS30735] [protein=Ecr family regulatory small membrane protein] [protein\_id=WP\_002911398.1] [location=3598602..3598745] [gbkey=CDS]

MSKTEIFLLIILAVILLGSIWFIFSDEIWLLLCYLESQIYPTFSVPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529031.1\_3530 [locus\_tag=BN49\_RS19290] [protein=YebY family protein] [protein\_id=WP\_016529031.1] [location=complement(3599381..3599719)] [gbkey=CDS]

MKKIVLTMLLLASSGAALAAPQIITVSRFEVGKESWAFNREEVMLTCRPGNALYAINPSTLVQYPLNEVA

EQQVKAGKTTAQPISVIQIDDPQHPGQKMSLAPFIERAKKLC

>lcl|NZ\_FO834906.1\_prot\_WP\_004184661.1\_3531 [gene=copD] [locus\_tag=BN49\_RS19295] [protein=copper homeostasis membrane protein CopD] [protein\_id=WP\_004184661.1] [location=complement(3599736..3600605)] [gbkey=CDS]

MLTGLYITLRFGHFISLMLAFGCVLYGAWWAPVPLRRVLMLRFYPLLRPLLLIGAISTLALYLLQGGMMG

EGWTDVWRPAVWQAVAGTRFGGVWIWQILLAWIALAVVWIRPRHGARQLVALLAAQLLLSAGVGHAAMHD

GITGVLQRTNHAVHLFCVASWFGGLLPFIYCLRLAQGRWRPAAVYTMARFSRYGHLAVAGTIASGALNAL

LIQGGLIGASPWGRMLLIKCALVAGMVVIALVNRYVLVPRMSASGSQAESLILRTTQAEIGLGALALLAV

SLFATWEPY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529032.1\_3532 [gene=yobA] [locus\_tag=BN49\_RS19300] [protein=CopC domain-containing protein YobA] [protein\_id=WP\_016529032.1] [location=complement(3600609..3600983)] [gbkey=CDS]

MRLLAGRALRLSVALAGMLTAAGAFAHAHLQQQIPTAGAQLSASPQTLTLSFSEGIEPAFSGVTVTGPQQ

HAVATGKLTRSADNPAEVTLPLAEVLPPGEYTVAWHVVSVDGHKTKGQYTFSVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002911406.1\_3533 [locus\_tag=BN49\_RS19305] [protein=DNA polymerase III subunit theta] [protein\_id=WP\_002911406.1] [location=3601096..3601326] [gbkey=CDS]

MERNLAKISQDEMDKVNVDLAAAGVAFKERYNMPVVADLVEREQPAHLRDWFRERLIAHRLASVSLSRLP

WEPKQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002911407.1\_3534 [gene=exoX] [locus\_tag=BN49\_RS19310] [protein=exodeoxyribonuclease X] [protein\_id=WP\_002911407.1] [location=3601405..3602064] [gbkey=CDS]

MLRVIDTETCGLQGGIVEIASVDIVDGQITNPMSHLVRPDRPISPQAMAIHRITEEMVADKPWIEEIIPH

YHGSPWYVAHNASFDRRVLPEMHGEWICTMKLARRLWPGIKYSNMGLYKSRKLNVTTPPGLHHHRALYDC

YITAALLLDIINVSGWTPDEMADITGRPALLTTFTFGKYRGKAVAEIAENDPGYLRWLFNNLDRMSPELR

LTLRHYLGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004148850.1\_3535 [gene=ptrB] [locus\_tag=BN49\_RS19315] [protein=oligopeptidase B] [protein\_id=WP\_004148850.1] [location=complement(3602068..3604128)] [gbkey=CDS]

MPPKAKRIPHAMTLHGDTRIDNYYWLRDDERARPDVLEYLHAENAYGKQVMDSQLSLQERLLKEIIDRIP

QREVSAPYSKNGFRYRQVYEPGCEYAIYQRQSVLKEEWDEWEILLDANQRAAKSEFYTLGGLGIAPNNQL

MAVAEDYLSRRQYGLRFCDLSNGEWYPEILENVTSGFAWSNDSRFVWYVRKHPTTLLPYQVWRHTVGTPA

QSDALVYEEKDETFYVSVHKTTSQQFVVIYLSSATTSEVLLLNAELPDAEPVCFLPRRKDHEYSLDHYQH

AFYLRSNREGKNFGLYRTVLRDEEQWTTLIPPRHDVMLEGFTLFTDWLVVEERQRGLTSLRQINRKTREV

VGIAFDDPAYVTWLAYNPEPETSRLRYGYSSMTTPDTLFELDMDTGERRVIKQQEVKGLDTSCYQSEHLW

VTARDGVEVPVSLVYHREHFRQGSNPLLVYGYGSYGESIDADFSASRLSLLNRGFVYAIAHVRGGGELGQ

QWYEDGKFLCKKNTFNDYLDVCDALLAQGYGDPRLCYGMGGSAGGMLMGVAVNERPELFHGVIAQVPFVD

VVTTMLDETIPLTTGEFEEWGNPQDETYYHYMKSYSPYDGVRAQAYPHMLVTTGLHDSQVQYWEPAKWVA

KLRELKTDDNLLLLCTDMDSGHGGKSGRFKSYEGVALEYAFFIALAQGTLPGKAAV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043573.1\_3536 [locus\_tag=BN49\_RS19320] [protein=tellurite resistance TerB family protein] [protein\_id=WP\_046043573.1] [location=complement(3604249..3604908)] [gbkey=CDS]

MANWLHQLQSLLGQQGASPSGESSKGSGLLPGAIGGLAGLLVASKSSRKLLAKYGTSALLAGGGAVAGTV

LWNKYQQKMRAQNTSAQAPETAAVPTDVDPRSVRLITALVFAAKSDGHIDDHERANIETQLRAANIDVQA

RVLIDQALAQPLDPQRLAEGIIDPQEALEIYYVSCAVIDIDHFMERSYLNALGDALALPKDVRADIEQDI

QSQKQALSV

>lcl|NZ\_FO834906.1\_prot\_WP\_004184662.1\_3537 [locus\_tag=BN49\_RS19325] [protein=YebG family protein] [protein\_id=WP\_004184662.1] [location=complement(3605048..3605395)] [gbkey=CDS]

MAVEIKYVVIREGEEKMSFASKKEADAYDKMLDLAEVLNDWLVTSPLEMDDVQRDTMAMWLAERKEALQH

ILRVGRLPEQETPAQDASAPSATAETSPAGDDAVPAAKARKAKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151450.1\_3538 [gene=purT] [locus\_tag=BN49\_RS19330] [protein=formate-dependent phosphoribosylglycinamide formyltransferase] [protein\_id=WP\_004151450.1] [location=3605540..3606718] [gbkey=CDS]

MTVLGTALRPAATKVMLLGSGELGKEVAIECQRLGIETIAVDRYPDAPAMQVAHRAHVINMLHGESLRAL

IEQEKPDYIVPEIEAIATDTLVELEQAGQKVVPTARAAKLTMNREGIRRLAAEELQLPTSRYRFADSEEG

FRAAVTEIGLPCIVKPVMSSSGKGQSFIRSADQLSEAWRYAQQGGRAGAGRVIVEGVVNFDFEITLLTVS

AVDGVHFCAPVGHRQEDGDYRESWQPQQMSDLALERAQTIARKVVLALGGYGLFGVELFVCGDEVIFSEV

SPRPHDTGMVTLISQDLSEFALHVRAFLGLPVGAIRQYGPAASAVILPQLSSQNVSFGQLQSAVGAGLQL

RLFGKPEIDGTRRLGVTLAVADSVEEAVARAKAAAAAVIVEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002911423.1\_3539 [locus\_tag=BN49\_RS19335] [protein=bifunctional 4-hydroxy-2-oxoglutarate aldolase/2-dehydro-3-deoxy-phosphogluconate aldolase] [protein\_id=WP\_002911423.1] [location=complement(3606776..3607417)] [gbkey=CDS]

MKNWKTTAEAILTSGPVVPVIVVKKLEHAVPMAKALVAGGVRVLEVTLRTECALEAIRAIAKEVPDAIVG

AGTVTNVEQLKAVTEAGAQFAISPGLTESLLKAATEDGTIPLIPGISTVSELMLGMQYGLKEFKFFPAEA

NGGVKALQAIAGPFGHIRFCPTGGISPANYRDYLALNSVLCIGGSWLVPADALEAGDYDRITTLAREAVE

GAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002911425.1\_3540 [gene=edd] [locus\_tag=BN49\_RS19340] [protein=phosphogluconate dehydratase] [protein\_id=WP\_002911425.1] [location=complement(3607456..3609267)] [gbkey=CDS]

MNSTMLRVTNRIIERSRDTRAAYLARINQAKTDTVHRAQLACGNLAHGFAACQADDKASLKSMLRNNIAI

ITSYNDMLSAHQPYEHYPEIIRKALHSANAVGQVAGGVPAMCDGVTQGQDGMELSLLSREVIAMSAAIGL

SHNMFDGALYLGVCDKIVPGLTMAALSFGHLPSVFIPSGPMASGLPNKEKVRIRQLYAEGKVDRMALLES

EAASYHAPGTCTFYGTANTNQMVVEFMGMQLPGSSFVHPDAPLREALTAAAARQVTRMTGNGNEWMPLGK

MFDEKVVVNGIVALLATGGSTNHTMHLVAMARAAGIIINWDDFSDLSDVVPLLARLYPNGPADINHFQAA

GGVPVLVRELLKGGLLHEDVHTVAGFGLSRYTLEPWLNNGELDWREGATAPLDDQVIATFEKPFSRHGGT

KVLSGNLGRAVMKTSAVPVENQVIEAPAVVFESQHDVLPAFEAGLLDKDCVVVVRHQGPKANGMPELHKL

MPPLGVLLDRRFKIALVTDGRLSGASGKVPSAIHVTPEAYDGGLLAKVRDGDLIRVNGQTGELTLLVDEA

ELAARQPHIPDLSASRVGTGREMFGALREKLSGAEQGATCITF

>lcl|NZ\_FO834906.1\_prot\_WP\_046043575.1\_3541 [gene=zwf] [locus\_tag=BN49\_RS19345] [protein=glucose-6-phosphate dehydrogenase] [protein\_id=WP\_046043575.1] [location=complement(3609490..3610965)] [gbkey=CDS]

MAVTQTAQACDLVIFGAKGDLARRKLLPSLYQLEKAGQIHADTRIIGVGRADWDKAAYTKVVREALETFM

KEKIDEGLWDTLCGRLEFCNLDVNDTSGFTRLGEMLDQKNRVTINYFAMPPSTFGAICKGLGEAKLNAKP

ARVVMEKPLGTSLETSREINDQVGEFFEECQVYRIDHYLGKETVLNLLALRFANSLFVNNWDCRTIDHVE

ITVAEEVGIEGRWGYFDQAGQMRDMIQNHLLQILCMIAMSPPSDLSADSIRDEKVKVLKSLRRIDRSNVR

EKTVRGQYTAGFAQGKKVPGYLEEEGANKTSNTETFVAIRVDIDNWRWAGVPFYLRTGKRLPTKCSEVVV

YFKTPELNLFKETWQELPQNKLTIRLQPDEGVDIQVLNKVPGLDHKHNLQITKLDLSYSETFNQTHLADA

YERLLLETMRGIQALFVRRDEVEEAWKWVDSITEAWAADRDAPKPYQAGTWGPVASVAMITRDGRSWNEF

E

>lcl|NZ\_FO834906.1\_prot\_WP\_004145554.1\_3542 [locus\_tag=BN49\_RS19350] [protein=hypothetical protein] [protein\_id=WP\_004145554.1] [location=complement(3610976..3611125)] [gbkey=CDS]

MPKSSPNVFTLCGFTAANEGEGFREIRKHSTVQCKKITNIAWQKHQTIN

>lcl|NZ\_FO834906.1\_prot\_WP\_004145555.1\_3543 [locus\_tag=BN49\_RS19355] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_004145555.1] [location=3611285..3612190] [gbkey=CDS]

MKSFPLMSALLLMNMLEKIQSRLEHLSKSERKVAEVILATPEQAIHSSIAALALEAGVSEPTVNRFCRSL

ETRGFPDFKLHLAQSLAHGTLYVNRNVDEDDSVESYTGKIFESAMASLDQVHHSLDMSAVNRAVDLLTQA

KKIAFFGLGSSAAVAHDAMNKFFRFNVPVIYSDDIVLQRMSCMNCDDDDVVVIISHTGRTKSLVELAQLA

RENDAMVIALTSAGTPLAREATLAITLDVPEDTDIYMPMVSRLAQLTVIDVLATGFTLRRGAKFRDNLKR

VKEALKESRFDKEPFVPSDNQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002911440.1\_3544 [gene=pyk] [locus\_tag=BN49\_RS19360] [protein=pyruvate kinase] [protein\_id=WP\_002911440.1] [location=3612316..3613758] [gbkey=CDS]

MSRRLRRTKIVTTLGPATDRDNNLEKVIAAGANVVRMNFSHGTPEDHQLRADKVREIAAKLGRHVAILGD

LQGPKIRVSTFKEGKIFLNVGDKFLLDANLGKGEGDKEKVGIDYKGLPADVVPGDILLLDDGRVQLKVLE

VQGMKVFTEVTVGGPLSNNKGINKLGGGLSAEALTDKDKADIVTAAKIGVDYLAVSFPRCGEDLNYARRL

ARDAGCDAKIVAKVERAEAVCDQDAMDDVILASDVVMVARGDLGVEIGDPELVGIQKALIRRARQLNRSV

ITATQMMESMITNPMPTRAEVMDVANAVLDGTDAVMLSAETAAGQYPSETVAAMARVCLGAEKIPSLNVS

KHRLDVQFDNVEEAIAMSAMYAANHLKGITAIITMTESGRTALMTSRISSGLPIFALSRHERTLNLTALY

RGVTPVFFDSQNDGVAAAHDAVNLLRDKGYLVSGDLVVVTQGDVMSTIGSTNTTRILTVE

>lcl|NZ\_FO834906.1\_prot\_WP\_004175421.1\_3545 [gene=lpxM] [locus\_tag=BN49\_RS19365] [protein=lauroyl-Kdo(2)-lipid IV(A) myristoyltransferase] [protein\_id=WP\_004175421.1] [location=complement(3613799..3614773)] [gbkey=CDS]

METKKNNIEFIPKFEKSFLLPRYWGAWLGVFAFAGIALTPPSFRDPLLGKLGRLVGRLAKSSRRRAQINL

LYCFPEKSEYEREAIIDAMYASAPQAMVMMAELGLRDPQKILARVDWQGKAIIDEMQRNNEKVIFLVPHA

WGVDIPAMLMASGGQKMAAMFHNQGNPVFDYVWNTVRRRFGGRMHARNDGIKPFIQSVRQGYWGYYLPDQ

DHGAEHSEFVDFFATYKATLPAIGRLMKVCRARVVPLFPVYDGKTHRLTVLVRPPMDDLLDADDTTIARR

MNEEVEVFVKPHTEQYTWILKLLKTRKPGEIEPYKRKELFPKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002911444.1\_3546 [gene=mepM] [locus\_tag=BN49\_RS19370] [protein=murein DD-endopeptidase MepM] [protein\_id=WP\_002911444.1] [location=complement(3614891..3616210)] [gbkey=CDS]

MQQIARAVTQAFNNLPRPHRVMLGSLSVLTLAVAVWRPYIYHPESAPIVRTIELEKSEIRSLLPEASEPI

DQAPQEEEAIPQDELDEKADSDAGGHEYVVSTGDTLSSILNQYGIDMGDIAQLSSADKELRNLKIGQQLS

WTLTADGDLQSLTWEMSRRETRTYTRVDNGFKMSSELQKGDWVNSVLKGTVGASFVSSARDAGLTSTEIN

AVIKAMQWQMDFRKLKKGDEFSVLMSREMLDGKREQSQLLGVRLRSDGKDYYAIRAEDGKFYDRNGTGLA

KGFMRFPTARQFRVSSNFNPRRLNPVTGRVAPHRGVDFAMPQGTPVLAVGDGEVVVAKRSGAAGYYVAIR

HGRTYTTRYMHLRKLLVKPGQKVKRGDRIALSGNTGRSTGPHLHYEVWINQQAVNPLTAKLPRTEGLSGS

DRTDYLAQVKEVVPQLRFD

>lcl|NZ\_FO834906.1\_prot\_WP\_004180437.1\_3547 [gene=znuA] [locus\_tag=BN49\_RS19375] [protein=zinc ABC transporter substrate-binding protein ZnuA] [protein\_id=WP\_004180437.1] [location=complement(3616226..3617170)] [gbkey=CDS]

MLHKNTLLCAGLGAVFLFAQVPLASAAVVTSMKPLGFIAAAIADGVTETQVLLPDGASEHDYSLRPSDVK

RLQNADLVVWIGPEMEAFMDKSTQSIAANKKVTIAELDGVKPLLITGADDDDDHHGHDHGAAEKGDGDHH

HGIYNMHLWLSPEIARLSAVAIHDKLLELMPQSRAKLDSNLQQFETALAATDKQVSNELAPLKGKGYFVF

HDAYGYFEKHYGLTSLGHFTVNPEIQPGAQRLHEIRTQLVEQKATCVFAEPQFRPAVIEAVARGTSVRMG

TLDPLGTGITLGKTSYPQFLTQLANQYSSCLKGD

>lcl|NZ\_FO834906.1\_prot\_WP\_002911449.1\_3548 [gene=znuC] [locus\_tag=BN49\_RS19380] [protein=zinc ABC transporter ATP-binding protein ZnuC] [protein\_id=WP\_002911449.1] [location=3617249..3618001] [gbkey=CDS]

MTNLVTLENVSVAFGQRRVLSDISLALTPGKILTLLGPNGAGKSTLVRVVLGLVAPTEGVIKRDARLRIG

YVPQKLHLDATLPLTVSRFLRLRPGTRKDDILPALKRVQAGHLIDAPMQKLSGGETQRVLLARALLNRPQ

LLVLDEPTQGVDVNGQVALYDLINQLRHELDCAVLMVSHDLHLVMAKTDEVLCLNQHICCSGAPEVVSMH

PEFISMFGPRGAEQLGIYRHHHNHRHDLQGRIVLRRGNSR

>lcl|NZ\_FO834906.1\_prot\_WP\_004175419.1\_3549 [gene=znuB] [locus\_tag=BN49\_RS19385] [protein=zinc ABC transporter permease subunit ZnuB] [protein\_id=WP\_004175419.1] [location=3618001..3618786] [gbkey=CDS]

MIELLLPGWLAGMMLACAAGPLGSFVVWRRMSYFGDTLAHASLLGVAFGLLLNVNPFYAVIVVTLLLAGG

LVWLEKRPHLAIDTLLGIMAHSALSLGLVVVSLMSNVRVDLMAYLFGDLLAVTPQDLIAIATGVVIVIGI

LLWQWRNLLAMTISPDLAFVDGVKLQRVKLLLMLVTALTIGVAMKFVGALIITSLLIIPAATARRFARTP

EQMAAVAVGVGMLAVTGGLTFSAFYDTPAGPSVVLCAAVLFILSMTKKAAS

>lcl|NZ\_FO834906.1\_prot\_WP\_014343250.1\_3550 [gene=ruvB] [locus\_tag=BN49\_RS19390] [protein=Holliday junction branch migration DNA helicase RuvB] [protein\_id=WP\_014343250.1] [location=complement(3618850..3619860)] [gbkey=CDS]

MIEADRLVSADSSGFEEAADRAIRPKLLAEYVGQPQVSSQMEIFIQAAKLRGDALDHLLIFGPPGLGKTT

LANIVANEMGVNLRTTSGPVLEKAGDLAAMLTNLEPHDVLFIDEIHRLSPVVEEVLYPAMEDYQLDIMIG

EGPAARSIKIDLPPFTLIGATTRAGSLTSPLRDRFGIVQRLEFYQIPDLQHIVSRSARHMGLEMSDEGAL

EVARRSRGTPRIANRLLRRVRDFAEVRHDGTISADIAAQALDMLNVDAEGFDYMDRKLLLAVIDKFFGGP

VGLDNLAAAIGEERETIEDVLEPYLIQQGFLQRTPRGRMATVRAWNHFGITPPEMP

>lcl|NZ\_FO834906.1\_prot\_WP\_002911454.1\_3551 [gene=ruvA] [locus\_tag=BN49\_RS19395] [protein=Holliday junction branch migration protein RuvA] [protein\_id=WP\_002911454.1] [location=complement(3619869..3620480)] [gbkey=CDS]

MIGRLRGIILEKQPPLVLLETAGVGYEVHMPMTCFYELPEAGQEAIVFTHFVVREDAQLLYGFNNKQERT

LFKELIKTNGVGPKLALAILSGMSAQQFVNAVEREEVASLVKLPGIGKKTAERLIVEMKDRFKGLHGDLF

TPAADLVLTSPAGPTADDAEQEAVAALVALGYKPQEASRMVSKIARPDANSETLIREALRAAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002911456.1\_3552 [gene=ruvC] [locus\_tag=BN49\_RS19400] [protein=crossover junction endodeoxyribonuclease RuvC] [protein\_id=WP\_002911456.1] [location=complement(3620560..3621081)] [gbkey=CDS]

MAIILGIDPGSRVTGYGVIRQVGRQLSYLGSGCIRTKVDDLPSRLKLIYAGVTEIITQFQPDYFAIEQVF

MAKNADSALKLGQARGVAIVAATNQALPVFEYAARQVKQTVVGIGSAEKSQVQHMVRTLLKLPANPQADA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002911459.1\_3553 [locus\_tag=BN49\_RS19405] [protein=YebC/PmpR family DNA-binding transcriptional regulator] [protein\_id=WP\_002911459.1] [location=complement(3621116..3621856)] [gbkey=CDS]

MAGHSKWANTKHRKAAQDAKRGKIFTKIIRELVTAARLGGGDPASNPRLRAAVDKALSNNMTRDTLNRAI

ARGVGGDEDANMETIIYEGYGPGGTAVMVECLSDNRNRTVAEVRHAFTKTGGNLGTDGSVSYLFSKKGVI

SFEKGDEDTIMEAALEAGAEDVVTYDDGAIDVYTAWEEMGAVRDALEAAGLKADAAEVSMIPSTKADMDA

ETAPKLLRLIDMLEDCDDVQEVYHNGEISDEVAATL

>lcl|NZ\_FO834906.1\_prot\_WP\_002911477.1\_3554 [gene=nudB] [locus\_tag=BN49\_RS19410] [protein=dihydroneopterin triphosphate diphosphatase] [protein\_id=WP\_002911477.1] [location=complement(3621884..3622327)] [gbkey=CDS]

MSFKLPVSVLVVIYAEDTKRVLMLQRRDDPAFWQSVTGSLEAGETALQAAAREVKEEVAIDVACEQLTLI

DCQRTVEFEIFSHLRHRYAPGVERNTEFWFCLALPHEREITFTEHLAYRWVSATEAAALTKSWSNRQAIE

EFVINAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002911479.1\_3555 [gene=aspS] [locus\_tag=BN49\_RS19415] [protein=aspartate--tRNA ligase] [protein\_id=WP\_002911479.1] [location=complement(3622329..3624116)] [gbkey=CDS]

MRTEYCGQLRQSHVGQQVTLCGWVNRRRDLGSLIFIDMRDREGIVQVFFDPDRADALKLASELRNEFCIQ

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RAKITSFVRRFMDDHGFLDIETPMLTKATPEGARDYLVPSRVHKGKFYALPQSPQLFKQLLMMSGFDRYY

QIVKCFRDEDLRADRQPEFTQIDVETSFMTAPQVREIMEAMVRQLWLEVKGVDLGEFPIMTFAEAERRYG

SDKPDLRNPMELVDVADLLKSVEFAVFAGPANDPKGRVAALRVPGGASLTRKLIDEYGNFVKIYGAKGLA

YIKVTERAKGMDGINSPVAKFLTAEIVEAILDRTGAQDGDMIFFGADNKKVVADALGALRLKLGKDLSLT

DESKWAPLWVIDFPMFEDDGEGGLTAMHHPFTSPKDMTADELKAAPEEAVANAYDMVINGYEVGGGSVRI

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>lcl|NZ\_FO834906.1\_prot\_WP\_004145564.1\_3556 [locus\_tag=BN49\_RS19420] [protein=hydrolase] [protein\_id=WP\_004145564.1] [location=3624384..3624950] [gbkey=CDS]

MLELNAKNTALVVIDLQEGILPFAGGPHRADEVVARAARLADKCRQQGSPVIMVRVGWSADFAEALKQPV

DAQAGAHTLPENWWTYPATLGKQESDIEVTKRQWGAFYGTDLELQLRRRGIDTIILCGISTNIGVESTAR

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>lcl|NZ\_FO834906.1\_prot\_WP\_004200337.1\_3557 [locus\_tag=BN49\_RS19425] [protein=DUF72 domain-containing protein] [protein\_id=WP\_004200337.1] [location=3624947..3625765] [gbkey=CDS]

MIYIGLPQWSHPKWVRLGITSLEEYARHFNCVEGNTTLYALPKPEIVARWYEQTHDDFRFCFKFPATISH

QAALRHCDELSSEFFARLAPLASRIGQYWLQLPATFGPRDLPALWHFLDGLPKDFTYGVEVRHPEFFAKG

EAEQQLNRGLHERNVNRVILDSRPVHSAAATSPAMIDAQQKKPKVPVHAVMTARQPMVRFIGGDDMVHNR

ELFRVWLQTLAKWHQSGTPWLFLHTPDIAFAPALVDTLWGDLRAALPAAGNAPSIPQQSSLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002911484.1\_3558 [locus\_tag=BN49\_RS19430] [protein=MAPEG family protein] [protein\_id=WP\_002911484.1] [location=3625818..3626213] [gbkey=CDS]

MVSALYAVLGALLLVKFSFDVVRLRTQYHVGYGDGGFSELQVAIRVHGNAVEYVPIGLILLLFMEMNGAQ

TWMVHVCGILLIVGRLMHSWGFHHRVYYWRRSGMSATWCALLLMVLANLWYMPWELVFSLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002911486.1\_3559 [gene=cmoA] [locus\_tag=BN49\_RS19435] [protein=carboxy-S-adenosyl-L-methionine synthase CmoA] [protein\_id=WP\_002911486.1] [location=3626253..3626996] [gbkey=CDS]

MSHRDTLFSAPIASLGDWTFDERVAEVFPDMIQRSVPGYSNIISMIGMLAERFVQPNTQVYDLGCSLGAA

TLSVRRNISHPGCRIIAIDNSPAMVERCRRHIDAYKAPTPVEVIEGDIRDVTIENASLVILNFTIQFLEP

GDRQAILNKVYQGLNPGGALVLSEKFSFEDAHVGELLFNMHHDFKRANGYSELEISQKRSMLENVMLTDS

VETHKARLRQAGFEHAELWFQCFNFGSLVAVKAGEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151451.1\_3560 [gene=cmoB] [locus\_tag=BN49\_RS19440] [protein=tRNA 5-methoxyuridine(34)/uridine 5-oxyacetic acid(34) synthase CmoB] [protein\_id=WP\_004151451.1] [location=3626993..3627997] [gbkey=CDS]

MIDFSNFYQLIAKSPLSHWLETLPAQVAAWQRDALHGKFREWERAVEFLPELTPWRLDLLHSVTAESETP

LSEGHQRRIENLLKNLMPWRKGPYSLYGINIDTEWRSDWKWERVLPHLSDLTGRTILDVGCGSGYHMWRM

IGAGAHLAVGIDPTQLFLCQFEAVRKLLGNDQRAHLLPLGIEQLPALEAFDTVFSMGVLYHRRSPLDHLW

QLKDQLAPGGELVLETLVVEGDENTVLVPGDRYAQMRNVYFIPSAAALKMWLEKCGFIDVRIVDACVTST

EEQRRTEWMTTESLADFLDPQDQRKTVEGYPAPLRAVIIATKPETQQSLAKKAR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043578.1\_3561 [gene=cutC] [locus\_tag=BN49\_RS19445] [protein=copper homeostasis protein CutC] [protein\_id=WP\_046043578.1] [location=complement(3628078..3628821)] [gbkey=CDS]

MAVLEVCCYSVACAREAERYGADRIELCAAPQEGGLTPSYGVLVSAREAITLPVHPIVRPRGGDFCYTEE

EFAAMLNDIRMVRDLGFPGLVTGVLDADGQVDIPRMKKIMAAAGPLAVTFHRAFDLCADPRQAWKTLGTL

GVKRILTSGQQSSAEKGISLITELIAAGDTPIIMAGAGVRAANLPLFLQAGVKEVHSSAGHWLPSEMRFR

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>lcl|NZ\_FO834906.1\_prot\_WP\_015958659.1\_3562 [locus\_tag=BN49\_RS19450] [protein=VOC family protein] [protein\_id=WP\_015958659.1] [location=complement(3628898..3629467)] [gbkey=CDS]

MANWQQNEQLADITADLSRFSDALQRFTARLGLEIAGLDADHISLRCHQNTTAERWRRGLEQCGTLLSEN

MINGRPICLFKLAEPVCVAHWRFHIVELPWPGEKRYPHEGWEHIEIVLPGDPATLNARALALLADDGLSQ

PGIVVKTSSPKGEHERLPNPTLAVTDGSVTVKFHPWSIEQIVASEQADT

>lcl|NZ\_FO834906.1\_prot\_WP\_004151452.1\_3563 [gene=argS] [locus\_tag=BN49\_RS19455] [protein=arginine--tRNA ligase] [protein\_id=WP\_004151452.1] [location=3629703..3631436] [gbkey=CDS]

MNIQALLSEKVSQALIAAGAPADCEPQVRQSAKVQFGDYQANGVMAVAKKLGMAPRQLAEQVLSHLDLNG

IANKVEIAGPGFINIFLDPAFLADNVNRALQSERLGVTKPQAQTIVVDYSAPNVAKEMHVGHLRSTIIGD

ASVRTLEFLGHKVIRANHVGDWGTQFGMLIAYLEKQQQENAGEMALADLEGFYREAKKHYDEDEAFAERA

RSYVVKLQGGDEYFLQMWRKLVDITMSQNQITYDRLNVTLTRDDVMGESLYNPMLPGIVADLKAKGLAVE

SEGATVVFLDEYKNKEGEPMGVIIQKKDGGYLYTTTDIACAKYRYETLHADRVLYYIDSRQHQHLMQAWT

IVRKAGYVPDSVPLEHHMFGMMLGKDGKPFKTRAGGTVKLADLLDEALERARRLVAEKNPDMSADELENL

AKVVGIGAVKYADLSKNRTTDYVFDWDNMLAFEGNTAPYMQYAYTRVLSVFRKAGIDENAMIDAPVVIAE

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TLKLGLDTLGIETVERM

>lcl|NZ\_FO834906.1\_prot\_WP\_004184668.1\_3564 [locus\_tag=BN49\_RS19460] [protein=glycoside hydrolase family 105 protein] [protein\_id=WP\_004184668.1] [location=complement(3631498..3632637)] [gbkey=CDS]

MKVWPVKHSPLLRQPERFIARSELQALIRNVTQNLVNIKDESGQFLLRLDDGRVIDTKGWAGWEWTHGVG

LYGIYQYYQQTGDIEMRDIIDRWFADRFAEGATTKNVNTMAPFLTLAYRFEETGRMAYLPWLESWAEWAM

HEMPRTEQGGMQHMTLAEENHQQMWDDTLMMTVLPLAKIGKLLNRPQYVEEATYQFLLHVQNLMDRETGL

WFHGWNYEGRHNFARARWARGNSWLTMVIPDFLELVDLPEGNAVRRYLITVLDAQIAALAKCQDDSGLWH

TLLDDPHSYLEASATAGFAYGILKAVRKRYVGQHYAGVAEKAIRGIVQNISPQGELLQTSFGTGMGSDLD

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>lcl|NZ\_FO834906.1\_prot\_WP\_016532462.1\_3565 [locus\_tag=BN49\_RS19465] [protein=MFS transporter] [protein\_id=WP\_016532462.1] [location=complement(3632642..3634225)] [gbkey=CDS]

MKTRKIGLANYLAYGAGDFLGAGTTALTAAWLLYFYTTFCGLTPIEATLIFAAARVLDAVVSPLMGFLTD

NFGTTWLGKRFGRRKFFILLGIPCVFSYSAMWVGEMGFWYYLATYLLFDMVYTMILVPYETLVPEMTDDF

KQKTKFSGARISMAQMSAILASFLPGILLSWLGKDNASSFFYASLVFSVLCAVMLTLVWCFTWERPREAW

SEAALRAEAEKQNLTLAQSLNRLVIELSSTLRIKIFRQHLGMYLGGYIAQDVFNAVFTYYVVFVLMQEAA

VASNLLGTMAIFQFIAVIAMIPLCIRFGPAPSYRMVVVLFGLSSLSYALLYYAGLSDVYSLLLLISAVAG

LGRGGINYVPWNTYTYIADVDEAITGQRREGIFAGIMTLTRKASQAGAVMLVGIIMQLSGFVSGQKIQPE

GVSHTILLILSVGTLVMLACGFLVSLRFKLNLHTHSVLRSETLRMRELGYAQSEQTSAEHRAVVELLAGM

PYDCLWGNNNIGYLNRHKPAAPALIKGGALNSTYTRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002911500.1\_3566 [gene=uspC] [locus\_tag=BN49\_RS19470] [protein=universal stress protein UspC] [protein\_id=WP\_002911500.1] [location=3634579..3635007] [gbkey=CDS]

MPYTHLLVAVAPTPESQVLIKKAVSIARPVNAKVSLITLATDPELYNQFAAPMMENLREVMQEETREFLN

ELARHADYPIERMTIACGELGHHIKDFCRSHRVDLVICGNHNHSLFSRATCSAKSIVGSCGVDVLLVSLE

KG

>lcl|NZ\_FO834906.1\_prot\_WP\_004175414.1\_3567 [gene=otsA] [locus\_tag=BN49\_RS19475] [protein=alpha,alpha-trehalose-phosphate synthase] [protein\_id=WP\_004175414.1] [location=complement(3635031..3636455)] [gbkey=CDS]

MSRLVVVSNRIALPDDKKSSAGGLAVGILGALRAAGGLWFGWSGEIGDDQQPLKQVSRGNISWASFNLNE

RDHDEYYNQFSNAVLWPAFHYRLDLVSFQREAWEGYLRVNAMLADKLLPLIEPDDTLWIHDYHLLPFASE

LRKRGVNNRIGFFLHIPFPTPEIFNALPPHAELLEQLCDYDLLGFQTESDRTAFLDSIAMQTRLSDLGDK

RYQAWGKAFSTEVYPIGIDPDEITRNAKGPLPPKLAQLKNELKNVKNIFSVERLDYSKGLPERFLAYETL

LEKYPQHHGKIRYTQIAPTSRGDVQAYQDIRHQLETAAGRINGQFGQLGWTPLYYLNQHFDRKLLMKVFR

YSDVGLVTPLRDGMNLVAKEYVAAQDPDNPGVLVLSQFAGAAQELTSALIVNPYDRDEVAAALDRALSMP

LAERIARHSAMLDVIRENDIHNWQARFVEDLQHISPRSEESRLRGKIATFPKLA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043581.1\_3568 [gene=otsB] [locus\_tag=BN49\_RS19480] [protein=trehalose-phosphatase] [protein\_id=WP\_046043581.1] [location=complement(3636430..3637218)] [gbkey=CDS]

MDNQISVPPALTGNYAFFFDLDGTLADIQPHPDQVVIPDSTLQALNALAQQQEGAVALISGRSMAELDAL

THPWRLPLAGVHGAERRDINGKTYIVSLPTALRDEIAAELTSALEALQGCELESKEMAFALHYRQAPQQQ

SAVLELAQRIVQRYPLLALQLGKCVVEIKPRGVNKGEAITAFMQEAPFAGREPVFVGDDLTDEAGFSVVN

QLQGMSVKVGSGETQAHWRLADAAAVRTWLQHLAYDAQTERRDDHESFSRSL

>lcl|NZ\_FO834906.1\_prot\_WP\_002911507.1\_3569 [gene=araH] [locus\_tag=BN49\_RS19485] [protein=L-arabinose ABC transporter permease AraH] [protein\_id=WP\_002911507.1] [location=complement(3637380..3638360)] [gbkey=CDS]

MSSVTTSGATRSTFSFARIWDQFGMLVVFAVLFIGCVIFVPNFASFVNMKGLGLAISMSGMVACGMLFCL

ASGDFDLSVASVIACAGVTTAVVINLSESLWLGIAAGLLLGALSGLVNGFVIARLKINALITTLATMQIV

RGLAYIISDGKAVGIEDERFFTLGYANWFGLPAPIWLTVACLVVFGLLLNKTTFGRNTLAIGGNEEAARL

AGVPVVRTKIIIFVLSGLVSAAAGIILASRMTSGQPMTSIGYELIVISACVLGGVSLKGGIGKISYVVAG

ILILGTVENAMNLLNISPFSQYVVRGVILLAAVIFDRYKQKAKRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043583.1\_3570 [gene=araG] [locus\_tag=BN49\_RS19490] [protein=L-arabinose ABC transporter ATP-binding protein AraG] [protein\_id=WP\_046043583.1] [location=complement(3638375..3639889)] [gbkey=CDS]

MQQSTPYLSFRGITMTFPGVKALSDISFDCYPGQIHALMGENGAGKSTLLKILSGNYIPTAGHLQIGGQQ

MAFANTMEALNAGVAIIYQELHLIPEMTVAENIYFGQLPHRGGIVNRSLLNYEARLQLEHLGLDIDPETP

LKYLSIGQWQMVEIAKALARNAKIIAFDEPTSSLSAREIDNLFRVIRELREEGRVIIYVSHRMEEIFALS

DAITVFKDGRYVCTFDDMPSVSHDALVQAMVGRNLGDIYGWKPRPYGEERLRLEEVKAPGVRTPVSLSVR

SGEIVGLFGLVGAGRSELMKGLFGGTQITGGQVYIDGQPVSIRKPAQAIQAGMMLCPEDRKAEGIIPVHS

VRDNINISARRKHIHAGCLINNAWEADNADQHIQSLNIKTPGPEQLIMNLSGGNQQKAILGRWLSEEMKV

ILLDEPTRGIDVGAKHEIYNVIYGLAASGVAVVFASSDLPEVLGVADRIVVMREGQIAGELLHEEANEQQ

ALSLAMPTVSQAVA

>lcl|NZ\_FO834906.1\_prot\_WP\_016528848.1\_3571 [locus\_tag=BN49\_RS19495] [protein=arabinose ABC transporter substrate-binding protein] [protein\_id=WP\_016528848.1] [location=complement(3639952..3640932)] [gbkey=CDS]

MHKFTKALAAIGLAAVMSQSAMAENLKLGFLVKQPEEPWFQTEWKFADKAGKDLGFDVIKIAVPDGEKTL

NAIDSLAASGAKGFVICTPDPKLGSAIVAKARGYDMKVITVDDQFVNAKGKPMESVPLVMMAASEIGARQ

GQELYKEMQKRGWDVKDTAVMAITADELDTARRRTTGSIDALKAAGFPDAQIYRVPTKSNDIPGAFDAGN

SMLVQHPQVKHWLIVGMNDNTVLGGVRATEGQGFKAPEVIGIGINGVDAVNELSKAQPTGFYGSLLPSPD

IHGYKTSEMLYNWVTKGVEPPKFTAVTDVVLITRDNFKEELAKKGL

>lcl|NZ\_FO834906.1\_prot\_3572 [locus\_tag=BN49\_RS31165] [protein=hypothetical protein] [pseudo=true] [partial=3'] [location=3641294..>3641389] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004175413.1\_3573 [locus\_tag=BN49\_RS19500] [protein=non-heme ferritin-like protein] [protein\_id=WP\_004175413.1] [location=3641824..3642333] [gbkey=CDS]

MAVPGMAQKLNTQMNLEFHASNVYLNLSEWCARHRFDGAATFLRTRAQSSITLTMRVFDYLKKAGSWPIV

NPDHACNPECTSLEDLFTQTLSDYQQRSRLLSGLAQEAKAQSDDSTWRFLTLLAEEQQQDGLLLQSVLEE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004148869.1\_3574 [locus\_tag=BN49\_RS19505] [protein=succinate dehydrogenase] [protein\_id=WP\_004148869.1] [location=complement(3642404..3642562)] [gbkey=CDS]

MFYIFETLFLYFFMVRQKVTALTNPPYGVTVMREWDRVKTFLFLKGIIGEKK

>lcl|NZ\_FO834906.1\_prot\_WP\_171819496.1\_3575 [locus\_tag=BN49\_RS19510] [protein=MFS transporter] [protein\_id=WP\_171819496.1] [location=3642628..3644139] [gbkey=CDS]

MLRHQLAYGGGNLLGSGALAISGAWLLYFYTTFCGLTLIEASFIFSVASIIDAISNPLMGYLTDNFGKTR

LGKRFGRRRFFLLIGIPLMMFYPLLWVEGLSFWYYLSTYVVFEIIYTSIMVPYETLATEMTDDFSLRSKL

TGYKAIFGKLANFLAAFIPGQFILLYGKDSATPFFLTGLTYGAILIVAISCLWLCSWERERGEEVETSAK

KGLLSTLLSLAKDIRSTFYLRVFRKHLGMYLCGFGAEWLFASIFTYFVIFVLQHDPAMVAGLNSLNSILQ

LISTALFIGLCVKKGFSKPYILALGIVIFAVLLYTSLWFFHLPSGLATVLMFGITVLFGLGTGGVYYIPW

TVYTFLADVDEIYTGRRREGIYAGAMTFSGKILRSIVVFSMGAILSFYGFQSKAHSQPESAVTAIAVVFC

VGVIALALAAIVFSKQMKLDRKAHLVVLQEVARIKAGGKISDIAPDVRVIVEDLVGHRYEECWGNSKLFK

DAAPAPAQTVVSH

>lcl|NZ\_FO834906.1\_prot\_WP\_002911524.1\_3576 [locus\_tag=BN49\_RS19515] [protein=DUF2766 domain-containing protein] [protein\_id=WP\_002911524.1] [location=complement(3644177..3644428)] [gbkey=CDS]

MSQHLTEHDELVSDVVACQLVIKQILDVIDVIAPVEVREKMTTQLKAIDFASHPASADPVTLRAVQKAIA

LIELKFTPQEETH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530097.1\_3577 [locus\_tag=BN49\_RS19520] [protein=MFS transporter] [protein\_id=WP\_016530097.1] [location=3644579..3646000] [gbkey=CDS]

MNTAISSRDERAFSAPALLVAGAFFMEFLDGTVIATALPDMAGDFGVTAVELNIGISAYLITLAVLIPAS

GWIADRFGARAIFTLALAIFTLASVFCGLSTEVHIFVAMRILQGVGGALMVPVGRLAVLRTTPKHQLIKA

IATLTWPALVAPIIGPPLGGFITRYASWHWIFFINVPLGLAAIILSLRIIPDIRETERRSFDLSGFITTS

VAMVSLVTAMERLGDRQPQIWPTLALAALGFGCLLYSIRHFRRAAAPMVRLDALQVPTFRVTMYGGSLFR

ASISAVPFLLPLLFQVGFGMDPFHSGLLVLAVFVGNLTIKPATTPLIRWLGFRRLLLINGALNVCSLLAC

ALLTPQTPVWAIMLILYLGGVFRSIQFTGVSTLAFADVPAAQMSDANTLFSTASQLAVGLGITLGAIGIR

LGEQVGDWLHLTELPGISFRLSFVFIALICLVGMIDSLHLAKTAGSSVSEKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002911528.1\_3578 [locus\_tag=BN49\_RS19525] [protein=RpiB/LacA/LacB family sugar-phosphate isomerase] [protein\_id=WP\_002911528.1] [location=complement(3646050..3646688)] [gbkey=CDS]

MKIALMMENSQANKNAIILKELNAVADEKGFPVYNVGMSDENDHHLTYIHLGIMASILLNSKAVDFVVTG

CGTGQGALMSLNIHPGVVCGYCIDPADAFLFAQINNGNALSLPFAKGFGWGAELNVRFIFEKAFTGRNGE

GYPPERKEPQVRNAGILNQVKAAVVKENYLDTLRAIDPQLVKTAVSGPRFQQCFFENCQDKAIEDFVRQI

VA

>lcl|NZ\_FO834906.1\_prot\_WP\_020801895.1\_3579 [locus\_tag=BN49\_RS19530] [protein=hypothetical protein] [protein\_id=WP\_020801895.1] [location=3646860..3647039] [gbkey=CDS]

MLAHPLRPPLPPAGDKVLTAQAIMNNKLKAFSFIIKLPMRVIPISILNKTFLNLLFANN

>lcl|NZ\_FO834906.1\_prot\_WP\_021313407.1\_3580 [gene=ftnA] [locus\_tag=BN49\_RS19535] [protein=non-heme ferritin] [protein\_id=WP\_021313407.1] [location=3647097..3647594] [gbkey=CDS]

MLKTDMIDKLNEQMNLELYSSLLYQQMSAWCSYHSFEGAAAFLRRHAQEEMTHMQRLFDYLTDTGSLPRI

NAIASPFAEYASLDELFRQTYEHEQLITQKINELAHAAMTGQDYPTFNFLQWYVAEQHEEEKLFKSVIDK

LTLAGKSGEGLYFIDKELATLDAQN

>lcl|NZ\_FO834906.1\_prot\_WP\_004175410.1\_3581 [locus\_tag=BN49\_RS19540] [protein=YecH family protein] [protein\_id=WP\_004175410.1] [location=complement(3647630..3647869)] [gbkey=CDS]

MSSIHGHEVLQMMLASGESWTVASLEAAIRRRFGEEARFHTCSAENLSAAQLVAFLEKKGKFIAREEGFT

TAENKICRH

>lcl|NZ\_FO834906.1\_prot\_WP\_040188717.1\_3582 [gene=tyrP] [locus\_tag=BN49\_RS19545] [protein=tyrosine transporter TyrP] [protein\_id=WP\_040188717.1] [location=3648061..3649272] [gbkey=CDS]

MKNRTLGSILIVAGTTIGAGMLAMPLAAAGVGFTVTLGLLFTLWALMCYTALLLLEVYQHVPADMGLGSL

AACYLGRYGQWVTGFCMLFLLYALTAAYISGAGELLASSLNQWLDWQLPPAAGVLIFTLLGGAVVCIGTA

LVDLFNRFLFSAKIVFLVIMLALLMPHIHQVNLLTLPVEQGLALSAIPVIFTSFGFHGSVPSIVSYLGGD

IRKLRRVFIIGSFIPLVAYIFWQLATLGSIDAPAFTAMLANNAGLNGLLEAIREVVASPHVELAVHLFAD

LALATSFLGVSLGLFDYLADMFQRKNSVGGRLQSGIITFLPPLAFALFYPRGFVMALGYAGVALAVLALI

MPALLVMKSRREHPQATWRVAGGAPTLWLVLLCGIGIVAIQFSIAAGLLPAVG

>lcl|NZ\_FO834906.1\_prot\_WP\_004141106.1\_3583 [locus\_tag=BN49\_RS19550] [protein=YecA family protein] [protein\_id=WP\_004141106.1] [location=complement(3649297..3649965)] [gbkey=CDS]

MNTGPLNENELEWLDDTLAKYAAEGAILDVSELDGLLTAILSAPTDIEPAQWLLAIWGGADNVPRWANDR

ERDRFVNLTLQHMSDIAERLESYPDQFEPLFGTREAEGQELTIVEEWCFGYLRGVALSDWSTLPAELQPE

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SGKKYKQCCLAK

>lcl|NZ\_FO834906.1\_prot\_WP\_023301076.1\_3584 [locus\_tag=BN49\_RS19555] [protein=dihydrodipicolinate synthase family protein] [protein\_id=WP\_023301076.1] [location=complement(3650064..3650945)] [gbkey=CDS]

MFTGLCAFPLTPLHQQDFDEKAFIRILARLTDAGVDSLGILGSTGSYAYLSREQRRRVVQVAKAHAGSIP

MMVGVGAIATNEVLRLVEDAQEAGADALLLPMMSYQPLSAEEIFAFYEEVCRHVSVPVCLYDNPRTTHVM

LADELQGRIAALPAIASIKIPGLPAPQASERVAALRQHLPSRVTLGVSGDAWATAGLQAGCEAWYSVCGG

LFPRCSLALVRAIRSGDVAQTAALNEQLAPLWRCFDRYGGSLRVIASAAAMLGLCDPDSLPRPLLSLGEE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004141115.1\_3585 [gene=pgsA] [locus\_tag=BN49\_RS19575] [protein=CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase] [protein\_id=WP\_004141115.1] [location=complement(3651613..3652161)] [gbkey=CDS]

MQFNIPTLLTLFRVILIPFFVLAFYLPFSWAPFACALIFFVAAVTDWFDGFLARRWNQSTRFGAFLDPVA

DKVMVAIAMVLVAEHYHTWWVTLPAATMIAREIIISALREWMAELGKRSSVAVSWIGKVKTTAQMTALVW

MLWRPYPWVEWAGIALFLVAAVLTLWSMLQYLNAARGDLLDQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002911538.1\_3586 [gene=uvrC] [locus\_tag=BN49\_RS19580] [protein=excinuclease ABC subunit UvrC] [protein\_id=WP\_002911538.1] [location=complement(3652219..3654051)] [gbkey=CDS]

MSDVFDAKAFLKTVTSQPGVYRMYDAGGTVIYVGKAKDLKKRLSSYFRSNLASRKTEALVALIAQIDVTV

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TLALLQKIFPIRQCENSVYRNRSRPCLQYQIGRCLGPCVAGLVSEEEYAQQVEYVRLFLAGKDDQVLTQL

IARMEKASQNLEFEEAARIRDQIQAVRRVTEKQFVSNTGDDLDVIGVAFDAGMACVHVLFIRQGKVLGSR

SYFPKVPGGTELGEVVETFVGQFYLQGSQMRTLPGEILLDFNLGDKTLLADSLSELAGRRINVQTKPRGD

RARYLKLARTNAATALTTKLSQQSTIHQRLQALASVLELPAVKRMECFDISHTMGEQTVASCVVFDSNGP

LRAEYRRYNITGITPGDDYAAMNQVLRRRYGKAIDDNKIPDVILIDGGKGQLAQAKAVFAELDVPWDKHH

PLLLGVAKGSDRKAGLETLFFEPEGEGFSLPPDSPALHVIQHIRDESHDHAISGHRKKRAKVKSTSSLET

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>lcl|NZ\_FO834906.1\_prot\_WP\_002911539.1\_3587 [gene=uvrY] [locus\_tag=BN49\_RS19585] [protein=UvrY/SirA/GacA family response regulator transcription factor] [protein\_id=WP\_002911539.1] [location=complement(3654048..3654704)] [gbkey=CDS]

MINVLLVDDHELVRAGIRRILEDIKGIKVAGEACCGEDAVKWCRANSADVVLMDMNMPGIGGLEATRKIA

RSVAGTKVIMLTVHTENPLPAKVMQAGAAGYLSKGAAPQEVVNAIRCVASGQRYIASDIAQQMALSQIEP

EKTESPFASLSERELQIMLMITKGQKVNEISEQLNLSPKTVNSYRYRMFSKLNIHGDVELTHLAIRHGLC

NAESLASQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002911541.1\_3588 [locus\_tag=BN49\_RS19590] [protein=DUF2594 family protein] [protein\_id=WP\_002911541.1] [location=3655166..3655390] [gbkey=CDS]

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AYRQ

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MRDNDFFSWRRDMLHQFQSMATGEEVYNLLQRETEALEYDYYTLCVRHPVPFTRPRVTFQSTYPRAWMSH

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LPGGYPEDELELRLRTLTELSLLTLLRLEDEMVMPPEMKFSRRELEILKWTAEGKTSAEVAMILSISENT

VNFHQKNMQRKFNAPNKTQIACYAVATGLI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151455.1\_3590 [gene=yecC] [locus\_tag=BN49\_RS19600] [protein=L-cystine ABC transporter ATP-binding protein YecC] [protein\_id=WP\_004151455.1] [location=complement(3656498..3657250)] [gbkey=CDS]

MSAIEVKSLVKKFHGQTVLHGIDLEVQKGEVVAIIGPSGSGKTTLLRSINLLEQPESGTIRVGDVTIDAG

RSLGPQKGLIRQLRQHVGFVFQNFNLFPHRTVLENIIEGPVIVKGEDKQESMARARELLAKVGLSGKENS

YPRRLSGGQQQRVAIARALAMRPDVILFDEPTSALDPELVGEVLNTIRQLAQEKRTMVIVTHEMSFARDV

ADRAIFMDQGRIVEQGEAKALFASPQQPRTRQFLEKFLMQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002911547.1\_3591 [gene=tcyL] [locus\_tag=BN49\_RS19605] [protein=cystine ABC transporter permease] [protein\_id=WP\_002911547.1] [location=complement(3657247..3657915)] [gbkey=CDS]

MQESIQLVIDSAPFLLKGAVFTLQLSIGGMFFGLVLGFILALMRMSPVWPVKWLARMYISIFRGTPLIAQ

LFMIYYGLPQFGIELDPIPAAMIGLSLNTAAYAAETLRAAIASIDKGQWEAAASIGMTPWQTMRRAILPQ

AARVALPPLSNSFISLVKDTSLAATIQVPELFRQAQLITSRTLEVFTMYLAASLIYWVMATVLSSLQNYF

ENQLNRQERDPK

>lcl|NZ\_FO834906.1\_prot\_WP\_004141132.1\_3592 [gene=dcyD] [locus\_tag=BN49\_RS19610] [protein=D-cysteine desulfhydrase] [protein\_id=WP\_004141132.1] [location=complement(3657931..3658917)] [gbkey=CDS]

MSLQNLTRFPRLELIGAPTPLEYLPRLSDHLGREIFIKRDDTTPLAMGGNKLRKLEFLAADALREGADTL

ITAGAIQSNHVRQTAAVAAKLGLHCVALLENPIGTRAENYLSNGNRLLLDLFNTQVEMCDALTDPAAQLD

ELATRIEAQGYRPYVIPVGGSNALGALGYVESALEISQQCEDAVAISSVVVASGSAGTHAGLAVGLEQLM

PQAELIGVTVSRSVADQLPKVEALQQAVANSLELQAKAEIILWDDYFAPGYGTPNEDGMAAVKLLAQLEG

ILLDPVYTGKAMAGLIDGITQKRFKDEGPILFVHTGGAPALFAYHPHL

>lcl|NZ\_FO834906.1\_prot\_WP\_004141135.1\_3593 [gene=tcyJ] [locus\_tag=BN49\_RS19615] [protein=cystine ABC transporter substrate-binding protein] [protein\_id=WP\_004141135.1] [location=complement(3659013..3659813)] [gbkey=CDS]

MKLALLGRQAMMGAMAVVLMAGVSVKTFAAENLLNQIKERGTLRVGLEGTYPPFSFQGDDGKLTGFEVEF

ANELAKHLGVKADLKPTKWDGMLASLDSKRIDVVINQVTISDERKKKYDFSTPYTVSGVQALVKKGNEGV

IKTAADLKGKKVGVGLGTNYEEWLRQNVQGVDVRTYDDDPTKYQDLRVGRIDAILVDRLAALDLVKKTNN

TLAVTGEAFSRQEAGVALRKGNDDLLKAVDGAIADMQKDGSLKALSEKWFGADVTK

>lcl|NZ\_FO834906.1\_prot\_WP\_004899206.1\_3594 [gene=amyA] [locus\_tag=BN49\_RS19620] [protein=alpha-amylase] [protein\_id=WP\_004899206.1] [location=3660014..3661501] [gbkey=CDS]

MKNPTLLQCFHWYYPTGGELWPEVEALAPSLNEIGINMVWLPPAYKGASGGYSVGYDTYDLFDLGEFDQK

GSVATKYGDKAQLLAAINALKEHNIAVLLDVVVNHKMGADEKEALRVQRVDEQDRTQIDEEIIECEAWTR

YTFPVRAGQYSQFVWDYKCFSGIDHIENPTEDGVFKIVNDYTGEGWNEQVDDELGNFDYLMGANIDFRNH

AVTEEIKYWARWVMEQTGCDGFRLDAVKHIPAWFYKAWIEHVQEVAPQPLFIVAEYWSHEVEKLQQYIDL

VEGKTMLFDAPLQMKFHEASRQGRDYDMSQIFSGTLVEADPFHAVTLVTNHDTQPLQALEAPVEPWFKPL

AYALILLRENGVPSVFYADLFGASYEDTGGDGETYAIEMPVIEQLHELIDARQRFAHGVQTLWFDHPNCI

AFSRSGTDDDPGCVVIMSNGDEGEKTLTLGENYGYKRWRDFLGNREEIVETDGEGCATFTCNGGSVSVWV

LEEVL

>lcl|NZ\_FO834906.1\_prot\_WP\_072310868.1\_3595 [locus\_tag=BN49\_RS19625] [protein=lipoprotein] [protein\_id=WP\_072310868.1] [location=complement(3661543..3661977)] [gbkey=CDS]

MMKKLFFAGMVVALAGCVQVDRYEDVVKAPAPAVLAGFWQTKGPQSAMMSPDAIASLIVTKEGDTFDCRQ

WQRVIAQPGKLMNRDSEIYNVTASLDIYPVEREGNTISYDRMTLSRVERLTPECEKAWAKARATGPVSAP

ASTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180447.1\_3596 [gene=rcsA] [locus\_tag=BN49\_RS19630] [protein=transcriptional regulator RcsA] [protein\_id=WP\_004180447.1] [location=3662350..3662973] [gbkey=CDS]

MSTMIMDLCSYTRLGLTGYLTSRGIKKQEIVEVNNAADLQKHCTSCCPAVVFLNEDCFVHDDESNGIIRQ

IITQNPATLFVIFMSLANIHFDRYLRVRKNLLISSKSITPKDLDVILVNYLKYKNTSVGQLTLPTLSLSK

TESNMLQMWMAGHGTSQISTQMNIKAKTVSSHKGNIKKKIQTHNKQVIYHIVRLTENITSGIQVNMR

>lcl|NZ\_FO834906.1\_prot\_WP\_002911586.1\_3597 [gene=dsrB] [locus\_tag=BN49\_RS19635] [protein=protein DsrB] [protein\_id=WP\_002911586.1] [location=complement(3663006..3663197)] [gbkey=CDS]

MQVNDRVTVKTDGGPRRSGVVLAIESFSEGTMYLVSLEDYPLGIWFFNEIGHPDGIFVEKEVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002911589.1\_3598 [locus\_tag=BN49\_RS19640] [protein=DUF2525 domain-containing protein] [protein\_id=WP\_002911589.1] [location=3663331..3663552] [gbkey=CDS]

MKHQLTGQTGDDLDVNVDALLAAINEISESEVHRTLDDPQRASIDGRGSHTWRELAEAFELDIHDFSASE

ANR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043591.1\_3599 [gene=yedQ] [locus\_tag=BN49\_RS19645] [protein=cellulose biosynthesis regulator diguanylate cyclase DgcQ] [protein\_id=WP\_046043591.1] [location=complement(3663852..3665531)] [gbkey=CDS]

MDKPLRLKLKKCYHLARPAHVVNACFIAVVFFSTLLIWREINVLEEAYVANQRNNLSNVAHEMDGLLQFN

IDRMMFFRHGMQAALEQPLDIDVLRKASQRYLSQRHQQAWRVALPNRRTLPVFGISGSVAGHNPILLVDD

PLAADELMATLELGYLLNLTQHDRDFAERMQYISRSGFFTSTLPLRDESQVITHYSQALGAPWFTRQTQR

NNPGRGVIWQTFPDDDPQLEEQVVTASIPLDFAGYWRGVLAMDFSVSEIKAFLVSAMQGGQEGEYQLYDS

HLNLLASSAPGNVLTLLSPREQELLSRAFVHDNQGGLRLLTRYISWAKLRNFDGVLLRIHTLREGVRGNF

GTITIALTLMWVLFTLMLLLSWLVIRRMVRNMSVLQTSLEWQAWHDALTRLLNRGALFEQAMAVASDCQR

SGRPLAVIQLDLDHFKHINDRYGHQAGDRVLSMVASTLSSAVRQGDLLGRVGGEEFCIVMPNTTLQEAAA

VAERLRQRIQGREVFLHNNVTLRVSASLGVSASEERGEYQFEALQSVADGRLYLAKQNGRNQVCFRSAA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529442.1\_3600 [locus\_tag=BN49\_RS19650] [protein=DUF808 domain-containing protein] [protein\_id=WP\_016529442.1] [location=complement(3665647..3666558)] [gbkey=CDS]

MAGSSLLTLLDDIATLLDDISVMGKVAAKKTAGVLGDDLSLNAQQVTGVRANRELPVVWGVAKGSFVNKV

ILVPLALLISAFIPWAITPLLMLGGAFLCFEGVEKVLHSLEARKHKEDPERRQQRLAALAERDPLAFERD

KVKGAIRTDFILSAEIVAITLGIVAEAPLLNQILILSGIAILVTIGVYGLVGVIVKLDDMGYWLAEKRSA

LAQWLGKGLLAVAPRLMKVLSIVGTLAMFLVGGGIVVHGIAPLHHAIEHWSAGPGGVMASTLPVVANLVL

GFIIGAVVLAGVKAVSSLRGAGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529443.1\_3601 [gene=yedA] [locus\_tag=BN49\_RS19655] [protein=drug/metabolite exporter YedA] [protein\_id=WP\_016529443.1] [location=3666742..3667653] [gbkey=CDS]

MSTRQLLPLIGALFALYIIWGSTYFAIAVGVASWPPLMMAGIRFLAAGVLLLGWLLATGHKLPARRPLLN

AALIGVLLLAVGNGFVTLAEHQHVPSGIAAVMVATVPLFTLCFSRFFGIATRKLEWLGIAIGLAGIVMLN

SGGNLNGNPWGALLILIGSLSWAFGSVYGSRIVLPTGMMAGAIEMLAAGIVLLVASWLSGETLTRVPSWS

GIAALAYLAIFGSLIAINAYMFLIRNVTPAVATSYAYVNPVVAVLLGTGFGGESLSLIEWLALAVIIFAV

VLVTLGKYLFPVRSEATPCKASK

>lcl|NZ\_FO834906.1\_prot\_WP\_046044055.1\_3602 [locus\_tag=BN49\_RS19660] [protein=very short patch repair endonuclease] [protein\_id=WP\_046044055.1] [location=complement(3667628..3668122)] [gbkey=CDS]

MADVHDQATRSKNMRAIATRDTAIEKRIAALLTGAGFTFVAQDRALPGRPDFALPDYRCVIFTHGCFWHH

HDCYLFKVPATRTAFWLDKIAGNVARDARDRQKLAEEGWRVLIIWECALRGRLRLSDAALTERLEEWICG

AGHDAQIDTQGIRELTTTSTPYKE

>lcl|NZ\_FO834906.1\_prot\_WP\_171819482.1\_3603 [locus\_tag=BN49\_RS19665] [protein=DNA (cytosine-5-)-methyltransferase] [protein\_id=WP\_171819482.1] [location=complement(3668088..3669503)] [gbkey=CDS]

MSLAEQAGEDAEALLRQLMTIYDVKTLVAELVSVGEQHWSAAILKRVVALGRVAERLRPQEVAHLATLLP

SPPAHHPHYGFRFIDLFAGIGGIRSGFEAIGGQCVFTSEWNKHAVRTYKANWYCDPQQHRFNEDIRDITL

SQRSDVSDEEAARHIRESIPQHDVLLAGFPCQPFSLAGVSKKNAMGRAHGFACETQGTLFFDVVRIIAAR

QPAIFVLENVKNLKSHDQGRTFRIIMQTLDELGYEVADAGHTGPDDPKVIDGRHFLPQHRERIVLVGFRR

DLQLHAGFTLRDIAAQYPAVRPTFGELLEPTVDAKFILTPVLWKYLYRYARKHQARGNGFGYGLVDPANP

HSVARTLSARYYKDGAEILVDRGWDRPLGEKHFDDPLNQQRRPRRLTPRECARLMGFESPQGARFRIPVS

DTQAYRQFGNSVVVPVFAAVAKLLAPRIAQAVARREADDNDGGCSRSSDAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002911594.1\_3604 [locus\_tag=BN49\_RS19670] [protein=phosphohydrolase] [protein\_id=WP\_002911594.1] [location=complement(3669580..3670287)] [gbkey=CDS]

MDLVDWQQRFERWILTHHAQDDAAHDLSHFRRVWATATQLAAGEEVDRLVLLTACYFHDIVSLPKNHPER

SRSSMMAAEKTLAILQSAFADFPADRYPAVSHAIEAHSFSAAIPPRTLEAKIVQDADRLESLGAIGLARV

FAVAGALNTILFDAEDPFADRRALDDRKYALDHFQCKLLRLPETMQTDKGKAMAQHNARFLVEFMAKLSA

ELQGEPLALDEAVLRRFAPQASTDR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151461.1\_3605 [gene=drpB] [locus\_tag=BN49\_RS19675] [protein=cell division protein DrpB] [protein\_id=WP\_004151461.1] [location=complement(3670330..3670611)] [gbkey=CDS]

MEEQAKRSPGGKLALWALYAFCGYCVWVIVRYWWVVGKIHSVPGASVEGDFGTTAGKWLGALLGMLVLGG

IGSILGAVVWYTRPSRGEQDHQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002911596.1\_3606 [gene=ompC] [locus\_tag=BN49\_RS19680] [protein=porin OmpC] [protein\_id=WP\_002911596.1] [location=3671150..3672295] [gbkey=CDS]

MKRKVLALMVPALLMASAANAAEIYNKNGNKLDLYGKVDGLHYFSDDASEDGDQTYVRFGLKGETQITSE

LTGYGQWEYNIQANTSEKEGANSWTRLGFAGLKFADCGSLDYGRNYGVVYDIESWTDMLPEFGGDTYTQT

DVYMTGRTNGVATYRNSDFFGLVDGLHFALQYQGNNENAGSGEGTNNGGKRKLARENGDGFGISSYYDLD

MGISFGAAYSSSDRTHNQLAAARSSQRYANGDKADAWTVGAKYDANNIYLAAMYAETRNMTFYGNDSFGG

IANKTQNFEVVAQYQFDDFNLPLRPSVAYLQSKGKDLYAYSRYGDKDLVKYVDVGMTYYFNKNMSTYVDY

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>lcl|NZ\_FO834906.1\_prot\_WP\_004227143.1\_3607 [gene=mtfA] [locus\_tag=BN49\_RS19690] [protein=DgsA anti-repressor MtfA] [protein\_id=WP\_004227143.1] [location=3672748..3673548] [gbkey=CDS]

MMFKWPWKADDESGNAEMPWEQALAIPVLAHLSSTEQHKLTQMAARFLQQKRLVALQGLELTPLHQARIA

MLFCLPVLELGIEWLDGFHEVLIYPAPFIVDDEWEDDIGLVHNQRVVQSGQSWQQGPVVLNWLDIQDSFD

ASGFNLVVHEVAHKLDTRNGDRASGVPLIPLREVAGWEHDLHAAMNNIQDEIDLVGESAASIDAYAATDP

AECFAVLSEYFFSAPELFAPRFPALWQRFCHFYRQDPLARRRENGLQDEGDRRIVH

>lcl|NZ\_FO834906.1\_prot\_3608 [locus\_tag=BN49\_RS19700] [protein=LysR family transcriptional regulator] [pseudo=true] [location=3674077..3674829] [gbkey=CDS]

MATDFRSGGNRWVCRCVADMEDAENSLSSAAMTPRGRLRVDVPSPLARLILVPALPAFHARYPDIQIDMG

VSDRVVDLIGDNVDCVLRGGQITDQYLIARHVGDLQIGVYVAPSYVERLGAPAHPRELQNTDHCIVGFLS

SRTSKIDPLVLCSENERIEITGN\*VLAVDDGNAYHEAGLVGLGVIALPNYMAAAHQAVGALIPLFTQWRI

SPMPLYLAFPPNRHVNAKLRVFIDWIVELMLQHVPITNNK

>lcl|NZ\_FO834906.1\_prot\_3609 [locus\_tag=BN49\_RS19705] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=<3674866..3675063] [gbkey=CDS]

MGFSGSDCGQACFDNRDSAELIRLIFWIMAIIKGIFAFMDNGSPKKILSNKIKSIGIFADFIIPS

>lcl|NZ\_FO834906.1\_prot\_WP\_032411441.1\_3610 [gene=ldtA] [locus\_tag=BN49\_RS19710] [protein=L,D-transpeptidase] [protein\_id=WP\_032411441.1] [location=complement(3675213..3676154)] [gbkey=CDS]

MTMRRVKLLCTALMLLASHGALAVSYPLPPEGSRLVGSAFTIAVPDNNTQPLESFAAQYGQGLSNMLEAN

PGVDVYLPHSGSTLTIPQQLILPDTVREGIVINVAEMRLYYYPPLGNSVEVLPIGIGQAGRETPRNWVTA

VERKQEGPTWVPTANTRREYAKEGKTLPAMVPPGPDNPMGLYAIYIGRLYAIHGTNANFGIGLRVSQGCI

RLRNDDIKFLFDNVPVGTRVQLIDQPVKYSVEPDGSHWLEVHEPLSRNRAEFESDRKVPLPMTSALRDFT

QGPGVSPAQVEQTLQRRSGMPVNISATAAQGSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004180456.1\_3611 [gene=cbl] [locus\_tag=BN49\_RS19715] [protein=HTH-type transcriptional regulator Cbl] [protein\_id=WP\_004180456.1] [location=complement(3676233..3677183)] [gbkey=CDS]

MNFQQLKIIREAARQDYNLTEVANMLYTSQSGVSRHIRELEEELGIEIFIRRGKRLLGMTEPGKALLSIA

ERILNEASNVRRLADLFTNDASGVLTIATTHTQARYSLPPVIKAFRELFSDVRVELVQGTPQEIEALLHN

GGADIGIASERLSNDPTLAAFPWFRWHHSLLVPKDHPLTQVSPLTLEAIARWPLITYRQGITGRSRIDEA

FNRKGLMPDIVLSAQDSDVIKTYVELGLGVGLVAEQSGDAREADTFTRLDTRHLFDANTVWLGLKRGQLQ

RNYVWRFIELCNAGLSLDEIKRQAMEPEEAAIDYQI

>lcl|NZ\_FO834906.1\_prot\_WP\_002911729.1\_3612 [gene=nac] [locus\_tag=BN49\_RS19720] [protein=nitrogen assimilation transcriptional regulator NAC] [protein\_id=WP\_002911729.1] [location=complement(3677290..3678207)] [gbkey=CDS]

MNLRRLKYFVKIVDIGSLTQAAEVLHIAQPALSQQVATLEGEMDQQLLIRTKRGVTPTEAGKILYTHART

ILRQCEQAQLAVNNVGQTLRGQVSIGLAPGTAASAITMPLLQTVRNELPEVMVYLQESSGTALNDKLLAG

QLDMAVLYERSPVAGIVSQPLLKEDLYLVGTRDCPGQSVDLTAVAEMNLFLPRDYSAVRARVTEAFTLRR

LSAKIIGEIESITTLTAAIASGMGATVLPESAARSLCGAANGWMARISTPSMSLSLSLNMSARGSLSPQA

QAVKEILLSLVSRPSLENRELQLVS

>lcl|NZ\_FO834906.1\_prot\_3613 [locus\_tag=BN49\_RS19730] [protein=tyrosine-type recombinase/integrase] [pseudo=true] [location=3678775..3680031] [gbkey=CDS]

MSLTDAKIRTLKPSDKPFKVSDSHGLYLLVKPGGSRHWYLKYRINGKESRIALGAYPAVSLSDARQQREG

VRKMLALNINPVQQRAAERGSRTPDKVFKNVALAWHKSNRKWSQNTADRLLASMNNHIFPVIGNLPVSEL

KPRHFIDLLKRIEEKGLLEVASRTRQHLSNIMRHAVHQGLIDTNPAANLGGVTTPPVRRHYPALPLERLP

ELL\*RIEAYHQGRELTRLAVLLMLHVFIRSSELRFARWSEIDFTNRVWTIPATREPIIGVRYSGRGAKMR

MPHIVPLSEQSIAILKQIKDITGNNELIFPGDHNPYKPMCENTVNKALRVMGYDTKKDICGHGFRAMACS

ALMESGLWAKDAVERQMSHQERNTVRMAYIHKAEHLEARKAMMQWWSDYLDICRKAYVSPYMMVQENR

>lcl|NZ\_FO834906.1\_prot\_3614 [locus\_tag=BN49\_RS19735] [protein=PhoX family phosphatase] [pseudo=true] [partial=3'] [location=3680216..>3681886] [gbkey=CDS]

MSSPLKLVFKKEHSDEISNHSVNPVFSEVVSAFMSRRRFLQMGMVAGAAVSFPYLVKPENAFAAKANPSA

LSKAVSLGFTTIPVSTADTVTVPEGYIARPFYRWGDAVGIKGNLPEFKFDASNTTDEQAAQAGMHHDGMA

WFRLPQGKENPAHGLLALNHEYIDNGMLFKDGTANWDLDKARKGQNAMGISVIEVKKDNVGWQVARPSSF

ARRITVNTPMQLSGPARHQALMKTAADPQGEVVLGTMQNCANGKTPWGTYLTCEENWSDIFVKKAPRNVL

EKRYGISDSDESYRWSEVDERFSVDKTPNEPNRFGWVVEIDPYDPTSTPRKHTALGRFKHEGAAVTLAGD

NRVVVYMGDDQKFEYIYKFISENKYDPGDRKANMQLLESGTLYVARFNDDGSGDWLPLIFGENGLDQSKG

FDNQGDLLIKTRLAADTVGATKMDRPEWIAVDTHAKGSVYCTLTNNSDRGKEGKAPVDAANPRANNQFGH

IMHWREERADPASAKFTWNILVLAGRTDSDDPKAKGSMQGAEFGSPDGLSFDHRGVLWIQTDVSSST

>lcl|NZ\_FO834906.1\_prot\_WP\_129015087.1\_3615 [locus\_tag=BN49\_RS29295] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_129015087.1] [location=complement(join(3681897..3682810,3682810..3683125))] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAHLHVFL

RRTDDWEDGRRSRHRDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_3616 [locus\_tag=BN49\_RS30530] [protein=DUF839 domain-containing protein] [pseudo=true] [partial=5'] [location=<3683217..3683525] [gbkey=CDS]

STINKKAYEGMGNNQMIATLPGTNEYRRFLTGPRGCEITGIAFTPDNRTLFINIQHPGEGGDDITDPNNP

RAISN\*PDSRSDGRPRSSTVVITKSNGGIIGT

>lcl|NZ\_FO834906.1\_prot\_WP\_223367906.1\_3617 [locus\_tag=BN49\_RS29300] [protein=ATP-binding cassette domain-containing protein] [protein\_id=WP\_223367906.1] [location=3683803..3684324] [gbkey=CDS]

MHDYSLRFANLALGYEGLPAIQNITGTIQKGSLTAIIGPNGSGKSTLLKGIAGILAPLSGSCTVEPKARI

AYLPQISELDRTFPATVSDLVSLGLWPERGLFHHHRIEDRKRLTDALGSVGLAGFEKRQLSALSGGSFNA

RSSHGSFFNRQTSSCLMSLLMPLTPLLLMTCLC

>lcl|NZ\_FO834906.1\_prot\_WP\_001104308.1\_3618 [locus\_tag=BN49\_RS19750] [protein=zinc ABC transporter permease AztB] [protein\_id=WP\_001104308.1] [location=3684536..3685393] [gbkey=CDS]

MNWLHEWVLAPFVGFGFMRRALYGSFLLCLSACPVGVFLTLRRMSLVGDAMSHAILPGAAFGFLLYGLDI

LPMTIGGLVAGLIVAIFAGAVSRLTVQKEDASMAAFYLISLAVGVLIVSLRGSSVDLMHVLFGTVLALNH

EALLLIFSVALLTLLLVSIFWRALIAECLDPLFLRSVSRLGSPVHFIFLALVVLNLVAGFQALGTLLSVG

VMVLPAVTARFWTRRVATMCIASVLIGMLACISGLLFSFHFSLPSGPSIILSVGIMYLVSAAAMMVKNIH

LKKLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004175378.1\_3619 [locus\_tag=BN49\_RS19755] [protein=zinc ABC transporter substrate-binding protein AztC] [protein\_id=WP\_004175378.1] [location=3685425..3686375] [gbkey=CDS]

MRKPGFISLCILTTSMLFLLFTFPAKAKINVIASFSVIGDMAKNIGRDRIELRTIVGPNGDAHVYEPSPA

DAIAMSKADVILVNGLQLEGFISRLIEASETSAPVIETTKGANILQDPAGGHYHFYDGKAVFHAAPFDPH

AWQSVGNSRIYVKNIAEAFCAQDKSNCDFYQANARAYDAKLADLENKIIKTVATIPQEKRTVVVGHNAFK

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>lcl|NZ\_FO834906.1\_prot\_WP\_032105361.1\_3620 [gene=aztD] [locus\_tag=BN49\_RS19760] [protein=zinc metallochaperone AztD] [protein\_id=WP\_032105361.1] [location=3686414..3687664] [gbkey=CDS]

MKKRLLSTSISTLLLGLSVMPAFADEDVTAWRLFVADHDKPVVNVIDALDGDKLATFNVKGPANLSRSES

GATIFAIQGSAGVVSTIASGIAFHDHGDHADIDIDAPKLLPLELTGKKPGHFVERQGKIAQWFDGEDSAQ

ILGESAVLKGQKNITKVNVVAPHHGVAVPYDNYAVVSIPNPDDASKRPVGARVVDLQGKKVGDDALCPGL

HGSAGSGDTFALSCETGLLLITQKNAAPVIRHLPYAKTLPEGSTSTLIGGKGMQYFIGNYGPDRIILVDP

TESDSFRLIQLPTRRVHFVVDPVRAKFAYVFTEDGKLNQIDVLKGEISQSVRVTDPYSMDGHWNDPRPRI

AVADNKIYVTDPLKSKIIVLDATSFKKTSEISVEGQPFNIVAVGGSGKVHGEHHDHEAHHHDDHAH

>lcl|NZ\_FO834906.1\_prot\_WP\_001419900.1\_3621 [locus\_tag=BN49\_RS29305] [protein=hypothetical protein] [protein\_id=WP\_001419900.1] [location=complement(3687888..3688142)] [gbkey=CDS]

MKISKIVAFSLTMASTPALAFQAKDTTGSDLSGKQLRATEDSIISNFYSQHSRQFQTTTLGTCAAVAVPG

CNCPFCSMLRNQKL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529171.1\_3622 [locus\_tag=BN49\_RS19765] [protein=FAD-binding oxidoreductase] [protein\_id=WP\_016529171.1] [location=complement(3688507..3689691)] [gbkey=CDS]

MSVKKIAVIGAGVLGLSVARSLAQQGAKVTVFERSHVGAGTSSTTFAWINSDGKTPESYHHLNALAIDEH

IRLQQERTTEGHWLKATGTYEWAAGAPEQKRLQDRVSRLLELNYPVQNLSADELKRKVPEIRVGSHAGDI

WYFPGECLLVPSVFMAWLVSELHVHNAELKTQSEVTELTEEKNRAEISLANGERWQGDSIVIAAGRWSAE

LASLLGQQLAMIDPNQPNKIACGFLGYTRPVLTQLQANLITPGLNVRPEGGGRLLLQCPDLDSFANPANP

APVDSYIGEEMHKRLRKLFNNMEMAQLERIAVGQRSRPADGLPGLGYISGKRRIYLMVTHSGMTLGPLIG

RLCAEEILHDKRSSLLSDFSPERLLGKTAKDFPAFTTLHFPAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529170.1\_3623 [locus\_tag=BN49\_RS19770] [protein=hypothetical protein] [protein\_id=WP\_016529170.1] [location=complement(3689733..3690068)] [gbkey=CDS]

MVETSKQDRMPYLLFLCENRILAQNIDGHVIDLGGLTKQNGTIDWLLDGNKEKGENLKTEIEALEDLANK

IDFLFLDGQFTSLPDISAEYKDKLTSAPSMEIVLNELGDKP

>lcl|NZ\_FO834906.1\_prot\_WP\_004175376.1\_3624 [gene=hemB] [locus\_tag=BN49\_RS19775] [protein=porphobilinogen synthase] [protein\_id=WP\_004175376.1] [location=complement(3690221..3691243)] [gbkey=CDS]

MSIIIPGSFPARRLRRSRTHSFSRRLVAENQLTVDDLILPVFIIEGQNLRQEVPSMPGVFRLSVDMLLHD

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TDENGYVLNEPTKEILTRQALTHAEAGADIVAPSDMMDGRIGHIRQAFETNGLLNIQIMAYSAKYASNYY

GPFREATKSAVSLGKRDKKSYQMDPANAMEAMHEIAQDLQEGADMVMVKPGMPYLDIIREARKTFAVPVF

AYQVSGEYTMHMAAFRNGWLDEEKTVLESLMCFKRAGADGILTYFANTVAQLLNQHKREY

>lcl|NZ\_FO834906.1\_prot\_WP\_000803506.1\_3625 [locus\_tag=BN49\_RS19780] [protein=dihydroorotase] [protein\_id=WP\_000803506.1] [location=complement(3691304..3692650)] [gbkey=CDS]

MKPLLLTNALIINEDLRYPADILIDKGRIQKIASLIPSRTEWQVIDVRGKWVIPGMIDDQVHFREPGLTH

KGTIASESAAAVMGGITSFMEMPNVTPPTTTLQALREKFQRASHSSLANYSFYFGATNDNLDELKALTAS

QACGVKVFMGASTGNMLVDDEQILESIFANAPCLVATHCEHTPTIKHNEETWRARLGDAIPAGEHAAIRS

VDACLTSSHQAVSLAKKHRTRLHVLHITTADELALFDAAPTLEALRQKTITAEACVHHLFFNYDDYEMLG

HKLKCNPSVKSSFHQEALWRGVNEGIIDVIATDHAPHLLEEKQNDYFAAPSGLPLVQHALPALLDMSSRG

IFTPEMVVRKTSHAVAERFQLKDRGYIREGYWADLVVIDPFSHQQIIREDVAYKCGWSPFEGRILSGGAV

DMTLVNGHVIWNGRTIQQKYGLPLEFCR

>lcl|NZ\_FO834906.1\_prot\_WP\_000595497.1\_3626 [locus\_tag=BN49\_RS29310] [protein=M14 family metallocarboxypeptidase] [protein\_id=WP\_000595497.1] [location=complement(3692647..3693498)] [gbkey=CDS]

MIKQSRSDIPRRESGRHVWPVKEDDTQSNDIDFYKTAFREQSRRWGLSEIILSNTGDGEISLYQSVNQGA

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AEVEPSIEGKVLLNYETLLKNAASHGVLCCHEDILRHKAYLYTFEHATRLGHFSVALRDELERFFPVMEK

ERVDGCECEDGIIFNHFDSSFESWLFSSCSDVAACTETPGLQPFAKRAEANRYLIGAFISSILERNSIGS

GMS

>lcl|NZ\_FO834906.1\_prot\_WP\_050503319.1\_3627 [gene=thrS] [locus\_tag=BN49\_RS19790] [protein=threonine--tRNA ligase] [protein\_id=WP\_050503319.1] [location=complement(3693491..3695449)] [gbkey=CDS]

MKMSEAPITESEPLTFTLPDGSLKHVRKGATLQNVAESIGSSVAKSAVYAEIDGKCVDLLEKAKNSGKLN

IITVFDEEALGPIRRGCLLLLAASVKQLFPSARMVEGQLTKEGFYYDFAVDKPFTRDDLGMIEQHMTSLI

AENPPIIKEQVTRAQAIDCFEQRGEKFKSTELMEILADKSVTLCHLRQFTDGFNGPLVPDLRFLKNMKLL

NVSGAYWRGEANNVQLQRIYGTAWASKKQLDGWLEKTAEAEKRDHRKLGRELDLFHFQDNAPGAVFWHPR

GWTIFQSLIAYMRSRHEVAGYVEVNTPDVMDRSLWEISGHWDNYRDHMFTTQTEDGRNFALKPMNCPGAV

SLFKYGIKSYRDLPVRLSEFGKVHRYEPSGSLHGLLRVRHFTQDDAHIFCTLQQVEGECKSILQLVLDIY

KQFGFEEVAIKLSTRTEKRMGSDADWDRLENALSASLEAQGLQWSVNPGEGAFYGPKLEFVLRDAIGRDW

QCGTLQVDMNLPERFDIGYIAEDGSTKRPVMLHRALFGSLERFTGILLEHYVGKLPAWLSPVQAVVMTIT

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LLLNEAADAIKICCQPPEVHLD

>lcl|NZ\_FO834906.1\_prot\_WP\_000939730.1\_3628 [locus\_tag=BN49\_RS19795] [protein=metal ABC transporter substrate-binding protein] [protein\_id=WP\_000939730.1] [location=3695702..3696616] [gbkey=CDS]

MLQLKTVKIILLSTFITGLTAIHGAYAAEKFKVITTFTVIADMAQNVAGDAAEVSSITRPGAEIHEYQPT

TGDIKRAQGAQLILSNGFNLELWFQKFYQRLKNVPDVVVTTGITPISITEGPYDGKPNPHAWMSPDNALI

YVDNIRDALVKYDQGNAETYKANADAYKQKIRQTLEPLRKQIETLPAEQRWLVSSEGAFSYLARDLGLKE

LYLWPINADQQGTPQQVRNVIDKVRQNKIPAVFSESTVSNKPARQVARETGAHYGGVLYVDSLSAANGPV

PTYLDLLNVTTRTVVQGLHSGMKE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531963.1\_3629 [locus\_tag=BN49\_RS19800] [protein=manganese/iron ABC transporter ATP-binding protein] [protein\_id=WP\_016531963.1] [location=3696620..3697441] [gbkey=CDS]

MSQAAGITVAGLTVVYRNGHKALQNASFSVPKGSNAALLGVNGSEKSTLFRAMMGFVSPSCGTISLLGMP

PAQALRRNIIAYVPQSEEIDWSFPVLVEDVVMMGRYGHMGMLRRAGKEDRRIVNDALERVDMLPYRHRQI

GELSGGQKKRVFLARSIAQRGKVILLDEPFTGVDVNTEKKIITLLGELKEEGSTLVVSTHNLTSVSEYCD

YTVLVKGTVLASGPVATTFTPENIKKTFSANIESESDILPVQGGSTQPNYQPSAEYEDKGRSS

>lcl|NZ\_FO834906.1\_prot\_WP\_016531964.1\_3630 [gene=sitC] [locus\_tag=BN49\_RS19805] [protein=iron/manganese ABC transporter permease subunit SitC] [protein\_id=WP\_016531964.1] [location=3697438..3698298] [gbkey=CDS]

MSWLLEPFGYQYMLNAMWISAMVGGICAFLSCYLMLKGWSLIGDALSHSIVPGVAGAFMLGLPFSVGAFV

SGGLAAGSMFLLNQRTRLKEDVIIGLIFSSFFALGLFIISLNPVSVNIQSIILENILAVPPEDILQLTVI

GIISVITLLLKWRDLLLTFFDENHARAVGLHPERLNILFFLLLTLSTVAALQTVGAFMVICLVVTPGATA

WLLTDRFPRLVCIAVTIGSVTSFLGAWASYYLDGVTGGIIVVAQTLIFLLVFIFAPVHGLLANRRSVSQS

KGPRKC

>lcl|NZ\_FO834906.1\_prot\_WP\_004141222.1\_3631 [locus\_tag=BN49\_RS19810] [protein=metal ABC transporter permease] [protein\_id=WP\_004141222.1] [location=3698292..3699119] [gbkey=CDS]

MLNMLIEPFRFDFINYALIIALLVSVPCALLSVFLVLKGWALMGDAMSHAVFPGVVLAWIVGLPLGTGAF

VAGLSCALLTGYIKDNSRIKQDTLLGIIFSGMFASGLILYVSVRPDVPLEHILFGDMLGINATDILQTGT

IALFILLISGIKWRDFLLYCFDIQQARVSGLRTGWLYYGLLSMISLTVVATLKSVGIILSVSLLIAPGAI

AVLLTQRFNNALFIAVALSALVSTTGVYLSYFIDSAPAPTVVLLFALVFIVIFIYSSFKYNEKYL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531965.1\_3632 [locus\_tag=BN49\_RS19815] [protein=DUF1460 domain-containing protein] [protein\_id=WP\_016531965.1] [location=3699135..3699944] [gbkey=CDS]

MKKAIIFLLSFYSCVGFAEPQQARSDYSIEESQAKVNKILHTTSLYRNGLSYNERVAEISSRFLGTPYQA

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SPRNAQDVTQDISPYTITVNKQLNQKNKKQEYVKGLGIISRRISYIPDSAIDKEVINKLQTGDYVGIYST

KRGLDVSHVGIIIKDHNNIWFRNASSLAKNRKVVDSPFIRYMATKPGIVVLRDKTDQYP

>lcl|NZ\_FO834906.1\_prot\_WP\_151393778.1\_3633 [locus\_tag=BN49\_RS19820] [protein=isocitrate dehydrogenase] [protein\_id=WP\_151393778.1] [location=complement(3699961..3700827)] [gbkey=CDS]

MKLFINDLTVMDFSFLDAESGLIGDSLIVDIILEGDLNAESMVMDFSHAKKSIKHEIDKLADHVLIVPEQ

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LRPESINGDSYHYSHGLKKHRGNCQRIAHGHRSAIRIFVDGERSHMWEQKWATRWNNAYLLSREDVVTVT

TLSPRAVAYWHKGLTCSSWRSSQGYFEIMLCSEVVDILPCDTTVESLALFIRQSIEHGLPAAKIEVHAFE

GVGKGAIA

>lcl|NZ\_FO834906.1\_prot\_WP\_000944851.1\_3634 [locus\_tag=BN49\_RS19825] [protein=carbonate dehydratase] [protein\_id=WP\_000944851.1] [location=complement(3700957..3701517)] [gbkey=CDS]

MLRKNPSGHTPVVSTKAYIDPTAVICGRVIIHDYVYVGPYAVIRADELNADGDMDPIIIHSHSNIQDGVV

IHSKSGAPVTIGSGTSIAHRAIVHGPCQVDERVFIGFNSVLFNCHIQTGCVIRYNAVVDGVTLPENTYIP

STERVGPDSDLKSYSRVDPASLQFSEEVASTNVKLVEGYQKLRNEF

>lcl|NZ\_FO834906.1\_prot\_WP\_016531967.1\_3635 [gene=folE2] [locus\_tag=BN49\_RS19830] [protein=GTP cyclohydrolase FolE2] [protein\_id=WP\_016531967.1] [location=complement(3701507..3702442)] [gbkey=CDS]

MSIAAKQTLCPGMLPDIQSTKGDGEGESLSWVGMEQIDLPIDIAGRPVSAKVNAGINLLSSPEAEKGIHM

SRLYLLLDELTQGEITPALLQHVLKAFLVSHQGRSDEASIEISGDLLLSRKSLNSNHSGWKAYPLTLSAE

LRQSFTVTLKVGIPYSSTCPASAALSRHVAGLQFSKDFGNRIDRLPAAEIADWLVEKGMPATPHSQRSWA

WASIRLNPEAKSLPVIELIDYAEVALGTAVQTVVKRSDEQAFAVANGQNLMFCEDAARRLNNVFRCAPFC

EAFDIRVEHQESLHPHNAVARIHWKGSKNVT

>lcl|NZ\_FO834906.1\_prot\_WP\_004150576.1\_3636 [gene=dksA] [locus\_tag=BN49\_RS19835] [protein=RNA polymerase-binding protein DksA] [protein\_id=WP\_004150576.1] [location=complement(3702506..3702928)] [gbkey=CDS]

MTKPTRAEREKILAMLPEDYMNPVQQDYFRRLIRHERQEVLDHIDQMKQQLQDNPETGDEGDIAIREEQL

RLLFRQIDRESRLLPKYDAALMRLEKGEYGFCRDTGEPIGLQRLLLRSTAELSIEAKIKEEKVEIQYRKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004150577.1\_3637 [locus\_tag=BN49\_RS19840] [protein=GTP-binding protein] [protein\_id=WP\_004150577.1] [location=complement(3702999..3704198)] [gbkey=CDS]

MKRTPLIILNGFLGAGKTTLLKNLLTQAHKRRMTVSVIVNDMSELDVDGVLIANTEIVDAASNNFVSISA

DSISSRSGIQKLDSALKNLLEKRSADFILLETSGSSHPLPLVRYLREHTQVSLKAFLSLVDTVMLNDDYD

GGKKLIPVFQEHLNKGTRGVESLLAEQIMFCNKLLLTKNDRLPFYVVTEVARAIHPLNPQVAIMAVPWGN

LQLDELLSMPDYDFHRVALLIDELQDAIDAVLPDETDKKYDISWRVIEDDRPFHPQRLWDTCHRFMGAGV

YRSKGFFWLPGRDDLALLWNQAAGSINLEFISYWKAGVLTHTDNSLSKEERAAIRQQLAKMPGRFGDRRC

RLTVIGESGEIDDFALALRQCLLTEEEILWWQQGGIFHDPWPTKVARLA

>lcl|NZ\_FO834906.1\_prot\_WP\_000211298.1\_3638 [locus\_tag=BN49\_RS28110] [protein=transcriptional repressor] [protein\_id=WP\_000211298.1] [location=3704296..3704748] [gbkey=CDS]

MTTPVAKTYDWKQTLRTHGLRATPSTLATLQCLEHASQAMSHDDLTQQLGEQAPDRVTLYRILERLMQVS

IVQRYTDSARTQRFALTQRAAVGLFECDNCHHVIPIEQDPALEAAIELVKSHLTGHGMTEREITLSSHGI

CPDCNRTITK

>lcl|NZ\_FO834906.1\_prot\_WP\_004175365.1\_3639 [gene=cysS] [locus\_tag=BN49\_RS19850] [protein=cysteine--tRNA ligase] [protein\_id=WP\_004175365.1] [location=3704830..3706212] [gbkey=CDS]

MIKLTNTLGMQKELLVPVKESKIGMYVCGVTVYDLCHLGHARTFVAFDMIVRYLRFRGYDVTFVRNITDI

DDKIIQRARDTGEDWRSLTERMVHEMHIDFAKLGILPPNIEPRPTEHIPQIISMIERLLHRQFAYIAENG

DVMFSTASAKGYGKLSGQDITMLRAGTRIEVNEYKRDPLDFVLWKRAKPGEPVWPSPWGEGRPGWHIECS

AMNCHYLGTHFDIHGGGSDLIFPHHENEIAQSTSANDGPYVNYWLHTGMVTVNKEKMSKSLNNFFTLRDI

LNRFDAQSVRFFLLSAHYRKPLNYSEENIHLARASLTRLYTACQFADGSRSEQHDAWRARFCEAMDDDFN

TPQALAILFELTREINRLCGTNDDEAAALATTLKDLGNVLGLLEQSADAFLKNRSDLHPAELQLIEKLIH

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>lcl|NZ\_FO834906.1\_prot\_WP\_004141234.1\_3640 [locus\_tag=BN49\_RS19855] [protein=NAD(P)-binding domain-containing protein] [protein\_id=WP\_004141234.1] [location=3706283..3707413] [gbkey=CDS]

MNQPREVVIVGAGPAGVGMAALLRRSAIQDILVVDSHEVGASFMRWPEETRFITPSFFSNPFGQPDLNSV

TPDSSLALFCGEEHPGGKTYASYLKVVLDEYQIPVMAPARIAKVALLSSGNFILTTEAGEKLETRSLIWA

TGEFQFPDRQIFPGADICCHYGDVTSWKDFRKGEYIVIGGYESAVDAAVNLLENGSSVKMLTRSAPWSTN

HISDPSLSLSPYTRERLNRVMNHRLFEIYEDADVCEVIRMPGPGSSYKVHTTNGRAWATDEVPVLATGFQ

CGGGARQLAAFFEWNDDGYPVLTDEDCSTLFPGLYLVGPHVRHAGNIYCFIYKFRQRFPVVAESITRHLG

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>lcl|NZ\_FO834906.1\_prot\_WP\_032105444.1\_3641 [locus\_tag=BN49\_RS19860] [protein=50S ribosome-binding GTPase] [protein\_id=WP\_032105444.1] [location=3707425..3709074] [gbkey=CDS]

MQSFVLMGLESAGKSTLFNILTESAASDERNFRGSTVVCREGLINDAGICLVDTPGIRFQSDSETTKLAL

DALNQHDGILVVLRATHAQQEWQTLCHLIPPQAKHVVILLTFADKIRKGLLEVTEYLSETSGAPVLAVNA

REAGSNVRQGIVQLLLQDKPAPSAVSLPRQKIPVINLLAEFPQQTIFEHRWCGKVAAIVCLFLLFAVPVW

GAWLLSDFIQPVIDSAVIQPLKNITTSWPDVLKTLFVGNYGLFSLGLYSFVWAFPVVVLIGLSLSLTDDS

GLKERITATLDPWLRKLGLSGQDLIPVLSSFGCNVVAVFQSRSCSRCTRHACISMISFGAACSYQTGATL

SLFNAAHQPWLFIPYLSLLFFTGAIHTRLWNGSLKPGQNQRLTELTWLQWPRWRNVTWMLKNILRQFITQ

AMPLFLIICIVAGMLDYAGITRWLSETTAPLLHLFKLPAELMPGIIFSLLRKDGLMVLNQDGGSLIQSLS

TSQLLLLVWLASTLMACLVTVFTIAREINWRFAAAVAGKQVLSSLVVALVISQLFIHEA

>lcl|NZ\_FO834906.1\_prot\_WP\_000005768.1\_3642 [gene=zigA] [locus\_tag=BN49\_RS19870] [protein=zinc metallochaperone GTPase ZigA] [protein\_id=WP\_000005768.1] [location=complement(3709341..3710564)] [gbkey=CDS]

MSEVSANFHGDKRLPVTVLSGFLGAGKTTLLNHILNNREGRRVAVIVNDMSEVNIDAALVREGGAELSRT

DEKLVEMSNGCICCTLREDLLLEVNRLAKEGRFDQLVIESTGISEPLPVAETFTFAGDDGESLSTVARLD

TMVTVVDAYNFLKDYGSEDSIQSRGESLGEGDERSVVDLLIDQIEFCDVLVLNKVDLISEAQKEKLMAIL

RSLNPRARIVVSQFGQVPLGNILNTGLFDFEQAAQAPGWLKELRGEHTPETEEYGITSFVFRARRPFHPT

RFWQVMENELDGVVRSKGYFWLASRPEFAGSWSQAGGIARQGLGGMWWASVPKGRWPEDAESLKFIMSNW

IDGIGDARQELVFIGMDMNESELRNRLDSALLTDAEMAEGPQKWRHYSDPVEPWFEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530997.1\_3643 [gene=hisI] [locus\_tag=BN49\_RS19875] [protein=phosphoribosyl-AMP cyclohydrolase] [protein\_id=WP\_016530997.1] [location=complement(3710601..3711002)] [gbkey=CDS]

MFLLLEKAHAGAVFKLEDILASIPWDSHGLIAAIAQQYDTGEVLMLAWMNQQALDETLLTGRACYWSRSR

SCLWRKGETSGCVQQVHDIRLDCDGDAVLLLVDQKGGACHTGRRSCFYNAIKGDELTVLNDPG

>lcl|NZ\_FO834906.1\_prot\_WP\_021575198.1\_3644 [locus\_tag=BN49\_RS29315] [protein=transcriptional repressor] [protein\_id=WP\_021575198.1] [location=3711153..3711635] [gbkey=CDS]

MSNSPYSLSTRDTALSSTDCSGRRELIESKKIRITPLRERVYNFVSHAKEKGISAYQILELMKKYNPNAK

PATVYRSLDYLQQAGIIVKIECCSKFIKKNNLSSDVVTIFLICSNCGTIIQHTDHLIHTYIEKKAIDYGC

AVQKKDIEVKVICPDCRGKG

>lcl|NZ\_FO834906.1\_prot\_WP\_000930220.1\_3645 [locus\_tag=BN49\_RS19880] [protein=iron ABC transporter permease] [protein\_id=WP\_000930220.1] [location=complement(3711840..3712859)] [gbkey=CDS]

MLMSYRYHWAMWGAMVVLIGLMLFSITRGTVSLSLMQVLGALKLVDEPVSAMVSRIVTDLRVPRMLLSVL

TGAGLAMVGALLQTTTRNDLADPFLFGLSSGASAGAVLVITRFGDRLGVLTLPVSAFVGGVCSAIAVMLL

FHFKKQRGAEHLILCGLAISFLFGALTSYFIFSGDQRAASSVLFWSLGGLGLATWNNLPFAVFSLVLLFA

FVLLRWRSLDGVLAGEQTALSLGINVSRLRIEIFLCCALATSLMVALTGVIGFVGLMVPHLCRHFAGVKH

LLLLPLCGVWGAILLCGGDIVSRTILAPQELPIGIITAGIGGLFIIMLLARNSSRNTAC

>lcl|NZ\_FO834906.1\_prot\_WP\_000732537.1\_3646 [locus\_tag=BN49\_RS19885] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_000732537.1] [location=complement(3712859..3713815)] [gbkey=CDS]

MKKLFISLLAVLSASVASAADFPVTIESCGTPVTFAGPPKRAVINDLNMSEMAFALHLQDRIVGLTGISG

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FTTAHKNKATMDLLYNDVLTLGKIFGKRNDAQSLVSGWKKRLNELPKPAAGTRPLKVFVYDSGEDKPFTS

GKYAMPTAIIEAAGGKNVMEAVDTSWGTTSWESVAATEPDFIILLDYQTGSGADALRHFLENHPLMKLTP

AVQHHRYLKLQYAELTPGPANVDAVEKLARAMYPSTAK

>lcl|NZ\_FO834906.1\_prot\_3647 [locus\_tag=BN49\_RS29325] [protein=ABC transporter ATP-binding protein] [pseudo=true] [partial=5'] [location=complement(3713837..>3714142)] [gbkey=CDS]

PDLVLLDEPTNHLDPPGREELLSLVKTKGITVVAVLHDLTLTESFADRVLLLAQGQSVICDTPERVLVSE

YLYPIFGLTSFTVPHPHTGKALRIFEVPHCA

>lcl|NZ\_FO834906.1\_prot\_3648 [locus\_tag=BN49\_RS31275] [protein=tyrosine-type recombinase/integrase] [pseudo=true] [location=3714328..3715590] [gbkey=CDS]

MSLTDAKIRTLKPSDKPFKVSDSHGLYLLVKPGGSRHWYLKYRISGKESRIALGAYPAISLSDARQQREG

IRKMLALNINPVQQRAAERGSRTPDKVFKNVALAWHKSNRKWSQNTADRLLASMNNHIFPVIGNLPVSEL

KPRHFIDLLKRIEEKGLLEVASRTRQHLSNIMRHAVHQGLIDTNPAANLGGVTTPPVRRHYPALPLERLP

ELL\*RIEAYHQGRELTRLAVLLMLHVFIRSSELRFARWSEIDFTNRVWTIPATREPIIGVRYSGRGAKMR

MPHIVPLSEQSIAILKQIKDITGNNELIFPGDHNPYKPMCENTVNKALRVMGYDTKKDICGHGFRAMACS

ALMESGLWAKDAVERQMSHQERNTVRMAYIHKAEHLEARKAMMQWWSDYLEACRESYAPPYTIGKNKFIP

>lcl|NZ\_FO834906.1\_prot\_WP\_000703034.1\_3649 [gene=ybtS] [locus\_tag=BN49\_RS19895] [protein=yersiniabactin biosynthesis salicylate synthase Irp9/YbtS] [protein\_id=WP\_000703034.1] [location=complement(3715784..3717088)] [gbkey=CDS]

MKISEFLHLALPEEQWLPTISGVLRQFAEEECYVYERQPCWYLGKGCLARLHINADGTQATFIDDAGEQQ

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SADGGRRLCEWVKEASTTTQNAPLAVDTALNGEAYKQQVARAVAEIRRGEYVKVIVSRAIPLPSRIDMPA

TLLYGRQANTPVRSFMFRQEGREALGFSPELVMSVTGNKVVTEPLAGTRDRMGNPEHNKAKEAELLHDSK

EVLEHILSVKEAIAELEAVCLPGSVVVEDLMSVRQRGSVQHLGSGVSGQLAENKDAWDAFTVLFPSITAS

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TREKLASIAPYLMV

>lcl|NZ\_FO834906.1\_prot\_WP\_001286279.1\_3650 [gene=ybtX] [locus\_tag=BN49\_RS19900] [protein=yersiniabactin-associated zinc MFS transporter YbtX] [protein\_id=WP\_001286279.1] [location=complement(3717116..3718396)] [gbkey=CDS]

MSDVQSNVKPLTLTTGRVIFAIAGVYVTQSLVSALSMQSLPALVRAAGGSLALAGATTLFMLPWALKFIW

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DIASDGFCVDQLTRAGYGWGNSVQVGGSYLGMMCGGGVFLMLSAASGWPVAMLMMAMLIMALSFPLWRIT

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IAGTLAGGLLMKYTSPGRALLTAYGVQGIALLAVVMTFMMAPGHLLLPILQCLVIVQSISLACALVCLYA

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CVWLGIFALMILAGFVSMVAEVMILLLGITAPIFIFCLMYGFLRPMFNNWLQNIFAGILTILFAALSLRI

VVNYLNLVLNKATKVADSSTIVELGAQVCLAGIFAAILVYISAKVAAALAGASATVSMQGLAAVGIGAAA

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HGQGRAFIIATKLRTRQPPYLDIPLVDTSAAGDLGEAGVDGWIDSHFWERFGGALMVGMIPDIGAWASNS

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>lcl|NZ\_FO834906.1\_prot\_WP\_000754360.1\_3678 [locus\_tag=BN49\_RS29360] [protein=hypothetical protein] [protein\_id=WP\_000754360.1] [location=3759309..3759614] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_032104908.1\_3680 [locus\_tag=BN49\_RS20035] [protein=type IV secretion system DNA-binding domain-containing protein] [protein\_id=WP\_032104908.1] [location=3760732..3762471] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_000290498.1\_3682 [gene=clbS] [locus\_tag=BN49\_RS20045] [protein=colibactin self-protection protein ClbS] [protein\_id=WP\_000290498.1] [location=complement(3764513..3765025)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043610.1\_3691 [gene=clbH] [locus\_tag=BN49\_RS20090] [protein=colibactin non-ribosomal peptide synthetase ClbH] [protein\_id=WP\_046043610.1] [location=complement(3787561..3792357)] [gbkey=CDS]

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GEEGELYLAGIGLARGYLNNVALTDRCFTVHPTLRHLGKPERLYKTGDLVWRDGESQQIHYIGRNDFQVK

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>lcl|NZ\_FO834906.1\_prot\_3700 [locus\_tag=BN49\_RS30025] [protein=IS3 family transposase] [pseudo=true] [location=3809709..3810766] [gbkey=CDS]

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LCMMP\*SVAVVFARSMSLMILTVRHCRLKSI\*ICQLSEWSVYSTGSRQTVAIRPCFVWITARNLSPWHWL

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QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

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GTLLCVSDKPLHGEIKLPGQANRFYEGAISEHLQIGIRAIDLLRAEGDHMHSRKLRTFNEPPFR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151469.1\_3711 [locus\_tag=BN49\_RS20200] [protein=EmmdR/YeeO family multidrug/toxin efflux MATE transporter] [protein\_id=WP\_004151469.1] [location=complement(3822323..3823759)] [gbkey=CDS]

MNVTSAVRQAVERTSWFKKRQRYRVLYWREISPLAVPILLENACVLLMGVLSTFLVSWLGKEAMAGVGLA

DSFNMVIMSFFAAIDLGTTVVVAFSLGKRDRRRARAAARQSLAIMTLFSILLAGVIHAFGQEIIDFVAGD

ATAQVKDLALTYLELTALSYPAAAIALIGSGALRGAGTTKIPLLINGGMNILNILISSVLIYGIFSWPGL

GFVGAGLGLTIARYIGAIATIWVLMVGLNPALRLSLKGYFKPFNFAIIWEVMGIGIPASIESVLFNGGKL

LTQMFVAGMGTNVIAGNFIAFSVASLINLPGNALGSASTIITGKRLGKGQIGQAEFQAWHVFWLSTIILT

LIAWGSAPFAGFIASFYTHEEDVKEVVKQLLWLNALFMPIWSLSWTLPCAFKGARDVRYTMWVSMLGMWG

CRVVAGYTLGIVLGMGVIGVWLGMVLDWAVRGVLFYFRMVSGRWLWKYPRVKASSEES

>lcl|NZ\_FO834906.1\_prot\_WP\_004225945.1\_3712 [locus\_tag=BN49\_RS31530] [protein=DUF5951 family protein] [protein\_id=WP\_004225945.1] [location=complement(3823794..3823946)] [gbkey=CDS]

MESYLSGEKTFVKHQFACSGATAASIDNLLSFPTIITENTLQDIHFSIII

>lcl|NZ\_FO834906.1\_prot\_WP\_004899245.1\_3713 [locus\_tag=BN49\_RS20215] [protein=integrase arm-type DNA-binding domain-containing protein] [protein\_id=WP\_004899245.1] [location=3824189..3825457] [gbkey=CDS]

MSLNDSKIRNLKPSAKPFKVSDSNGLYLLIKPGGSRHWYLKYRINGKESRIALGAYPAVSLSDARQQREG

IRKMLALNINPAQQRASERRACTPEKVFKTVALAWHKNNKKWSQNTADRLLASMNNHIFPVIGHLSVTEL

KPHHFIDLLKGIEEKGLLEVASRTRQHLSNIMRHAVHQGFIDTNPAANLDGVTAPPMRHHYPALPLERLP

ELIEHIEAYHQGRELTRLAVLLTLHLFIRSSELRFARWSEIDFINRIWTIPATREAIVGVRYSGRGAKMR

TAHIVPLSQQAIAILKRIKEISGAYELVFPGDHNPYRPMCENAVNKALRLMGFDTKQDICGHGFRAMACS

ALMESGLWSQDAVERQMSHQERNTVRLAYIHKAEHLEARKAMMQWWSDYIDTCRVAYVPPFNTGRDKNNE

AA

>lcl|NZ\_FO834906.1\_prot\_WP\_032105408.1\_3714 [locus\_tag=BN49\_RS20220] [protein=sulfite exporter TauE/SafE family protein] [protein\_id=WP\_032105408.1] [location=complement(3825607..3826329)] [gbkey=CDS]

MIALLLLFFVALGAGVLSGVVGTGSSLIMLPVLVATYGPRIAVPVMAIASLFGNIGRVIVWWHEIRWRPV

FAYSLAGVPAAVLGAHTLLTISPGTVEVFLAAFFLAMIPLRRLIRRSNLHLNLWHMSLAGAIVGFMTGFV

LSTGPLSVPVFTGYGMSGGVFLGSEAASAILLYAGKLATFGISGALAQPVLTHGLAIGIALFVGSMIAKR

LVQKLQTHTFELLIDAVLVAGAVGMILALK

>lcl|NZ\_FO834906.1\_prot\_WP\_004899253.1\_3715 [locus\_tag=BN49\_RS20225] [protein=oxidoreductase] [protein\_id=WP\_004899253.1] [location=complement(3826341..3827237)] [gbkey=CDS]

MNTEINTVVAVLGPGAIGTTVAAALHEVGRTPLLCGRTPRDSLTLQDGNRFITVPGPVQTNPAQITRTVD

LIFLAVKSTQIDAAAEWLRALTGPETVICVLQNGVEQLDRLATYSLPGQIVPAVVWFPAQAQSDGSVRLR

GEARLSVPDAPASRVVAAALQGTWCSVDLAANFSSLAWRKLMQNAVAGLMALTHRRSGMFGRADIARLTL

AYLQECLAVARAEGAELGDEVPQEILDKFRAAPADMSTSILTDREAGRPLEWDIRNGVIARRGRVHSIPT

PISDILVPLLAAASDGPG

>lcl|NZ\_FO834906.1\_prot\_WP\_004899254.1\_3716 [locus\_tag=BN49\_RS20230] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_004899254.1] [location=3827314..3828198] [gbkey=CDS]

MNKENGNRISEGEQRLQQWLGSIHARSGDLAASEAKVVDLLLVDPLFVGTSTAAQVATRAGVSPPTVIRA

ARAIGFTGFTELKIEIARARGTAQFFAPPEVLTADATLASVLETSIRAGVDALTALSGAIEISALDEAVD

LIQSARQVFAFGAGPSATVAADAVFRLRTAGVITVSIQDYLSAMIAARLLGPGDVIIVVSSTGRTSSTLS

IADAASSAGASLIAITNQYDTPLATLANVSLVVGGMPLPAQMAAAGSRLAQLVVIDTLVAALTLRDKEQS

RRAERAGIDLPDMS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529049.1\_3717 [locus\_tag=BN49\_RS20235] [protein=DMT family transporter] [protein\_id=WP\_016529049.1] [location=3828198..3829055] [gbkey=CDS]

MQFSTVAMILTAAVAHAVWNIASKYKREDTLVFVWAYSCASALLWVPFSLILIVERQQELDWRLAVGAVI

SSALHIAYSLILQAGYERAELGVVYPIARGSGPVLTILFATLLMGERISPGALLGAFIVIAGIFVVTGNP

FRSGSRPLQGMLWGAATGTAIAGYTLWDGYSVISLHLDPVRYYASTLLLQSLILTPGAMRRRNRIPTAVR

VDIIPILIIAVCSPLAYILVLTAMQSMPLALVAPLRETSIIVGSLLSYWLFRENHLARRIAGAVVVLTGI

AIISL

>lcl|NZ\_FO834906.1\_prot\_WP\_004899261.1\_3718 [locus\_tag=BN49\_RS20240] [protein=winged helix-turn-helix domain-containing protein] [protein\_id=WP\_004899261.1] [location=3829291..3832065] [gbkey=CDS]

MLKTEDLNTMISIDEIHFADWQIWPQLRILLHRGKPVRISARAFDVLVVLVSARGKAVSKESLLTQVWGN

EIVEENNLQAQISAIRRILGHDRHLLVTEFGCGYRFNINKSPTEPLSKSKIPEPAITPFLASILGRDKAV

QELCALLDQYRLVTITGSGGVGKTRLAWEVVSLTHTHFPDGICVAELAHITEASSLLSVISQALHLPLAA

IHNDADSRQQLARRRCLLLIDNCEHVINELEPVITLLLHLAPHIKLLLTSQVALQVAGEQQYLLPPLQVP

ESEEADTQELLNFSSVRLFIERGQANRHDYHPSASELSLIGELCRHLDGLPLAIELAASRLPVMSVKEIY

SRLEDRFQLLSNTHRSLEPRHQKILTALEWTYQLLNTREQRLFCSLGIYTDMFSVKSVSDLLLIKDKHRW

QVVDDLQRLLALSLIQVSTQVPETRFRLLETMRQFACDKLRQQGEYTVLEARFAGYYKVLVEEAQGDWFM

LPTGQWRERYSHMLNDLRSVLQQTLTEGADPSKGLKILQAMTPFWIEYSLYDECQRHIYPLLYENTSQVV

LTLRQRMNLSAVAGKASTWAKGPTPETHSAWKTALTIAEKLDDKEIRLQAHYGLWLYYLRTGELDKALEH

AQSMCELARSITDEEAMATGLRILGVSLHFLGRHDVGRDYLQQSLDWYEHGELSHSFRFGLDQESAGQAF

LSRLLWLQGEYKAAKQMAWRGVKKAARLQHVCSLCCALAEGACMTAALDRNPRWVIKAANWLIHLAKRHD

LYFWKTYGELFLVWAKQFSHTDVSQTTLFSSLRAMGLDWQYSPLLSEIDTGLSLRATHQDHENWCTPELM

RLSATQLPPQKQRLLLEKALDKARQQQAHGWALRIAYSLATLQAEAGEKWAAKQLIQDALHDVDDSDNAT

DVRSAIALCARIGA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530711.1\_3719 [locus\_tag=BN49\_RS20245] [protein=MFS transporter] [protein\_id=WP\_016530711.1] [location=complement(3832042..3833229)] [gbkey=CDS]

MRSDNHELSSTRILMLGIICCIVVANIYFNQSVLNLIAGSFPNEWGAVSLIPMVTQVGYAVGLFFLIPLG

DYIERQRLILRQAQVLFLAMIGMMLSPTATVLVFFSFLTGMAATVAQQIVPLAASLSRTSARGKTVGTVM

SGVLAGILAGRAIGGLIGQYFGWRGVFLSGAIMTLLAIFFILRILPTQSLSTPKFNYLAVLRSLGLLWKN

EPQVRGATLTQAMLFASFSVLWTVLPFWLAYRYDYGAGITGALAALGLIGILCAPLAGSFSDRQGPFRMV

VFGVILMLLAWTVFWRWNSIVGMVVGILLLDAGEQCVLIANQHTIYSLRPDARNRLNTLFMCVMFIGGAC

GSLTATWLWETTHSWALISSAGGGLVIMGMLIAVKRKYSGPYSGT

>lcl|NZ\_FO834906.1\_prot\_WP\_016530710.1\_3720 [locus\_tag=BN49\_RS20250] [protein=SDR family oxidoreductase] [protein\_id=WP\_016530710.1] [location=3833402..3834208] [gbkey=CDS]

MDLKLTGKVALVTGAHTGIGFSICEELAVNGVHLVMVARREPELILAAKKISEKYGVSVLPIAGDVTDPK

LPSLVVEQAEKVFQRIDLLVNNAGRAHAGTLLTTSEEDWQIMTETKFSAMRRFCKVIIPGMQRRNWGRIV

NISSIGGIYPNPQLTVSHALSAAINNLTRSLALSVAPDGILVNAIGVGAVATDNWAQNMLPNVRNRRPEL

ADRTDEEVMALLGKEKTPVGRFGLPEDIAAIATFLLSGRNQFVTGQTIEASGGADRFM

>lcl|NZ\_FO834906.1\_prot\_3721 [locus\_tag=BN49\_RS29405] [protein=hypothetical protein] [pseudo=true] [location=3834443..3835361] [gbkey=CDS]

MSKKQTLSNTNYSSPDWLTIREAVEVINKKGLEIKKK\*YLQACITWQHSSLYLLSVANYITKNTEIELQS

KAQTM\*YVINKSFMPS\*QKSVY\*RT\*FYC\*HYWQIYHSHRESD\*HSIDWI\*ICSSTKITFPIS\*NTIACN

RSY\*F\*SWHNS\*LTRRTISTIR\*NDMGRKNNTKNYATP\*KHFTICT\*RDILKEDK\*LPGERVFPGSYFTS

GCLVCYSTC\*T\*\*SH\*NHNQ\*QSAPIICNANINTTISFFLAGL\*KQ\*SHPSIN\*\*TVQTTIYFRTMGI\*R

RHYRQAQW\*YVKNCTRTRLPHINVGL

>lcl|NZ\_FO834906.1\_prot\_3722 [locus\_tag=BN49\_RS20260] [protein=IS3 family transposase] [pseudo=true] [location=3835781..3837009] [gbkey=CDS]

MIDVLGPERRRRRTPQEKMAIVQQSFEPGMTVSMVARQHGVAASQLFLWRKQYQDGSLTAVTSGEQVVPA

SELAAAMKQIKELQRMLGKKTMEVELLREAVDIGRQKKWIAHVPLLPEGGE\*ASSVAVCGSHVRSFMR\*P

TARLTGRIADASVSPTIRKH\*TVSMLLSVKFRPTATGGYGRCCADSRKMKASQLLTPNESIGSCVSMRYY

LSTGPHWQYQTGRTRAK\*R\*KKVIDVGVPTGSSSVATMERNCGLPLHWTAAIVKRCTGWRVPEGTTARRY

KM\*CWVRWSVASETGYRRPRLNG\*QIMARPIGLTKHAGSQRWWVWSRKQQQCAARKVTVWPRAS\*KR\*SG

TTSASCQNRMG\*QQRGTLRWRSNTITNGIRTVRWGTVHRVNICGVGPVMG\*VINGVWKY

>lcl|NZ\_FO834906.1\_prot\_3723 [locus\_tag=BN49\_RS20265] [protein=helix-turn-helix domain-containing protein] [pseudo=true] [location=complement(3837227..3837626)] [gbkey=CDS]

MKNRKYFVNDLIIWINKNIEMPLKIDDVAIRSGYSKWHLQRLFFF\*NRAEPGRFYQREKIMSYFRGCYHN

K\*TFDKHRDAIWL\*LSAIINQGISEKV\*CPTAPV\*KKCRKY\*KQVF\*GAG\*LLVS\*G\*FFKSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004899294.1\_3724 [locus\_tag=BN49\_RS20270] [protein=HlyD family secretion protein] [protein\_id=WP\_004899294.1] [location=complement(3837739..3838602)] [gbkey=CDS]

MKSLLSLLGRYLLTLSAVAVATLLAFILWKHYVQTPWTRDGRVRADVVQIAPDVSGPVLNVAVRDNQWVN

RGDVLYSIDPHWLRLAVVSAQADVEAKRHEMLMRQDAARRRSQIKGVISSEDLQQTASAASVAAANYHGA

LAALDLAELNLSHAIVRSPVTGYVTHLRLRPGDYATAGETKVSIIDANSFWVVGYFEETKLQHIRTGNTA

HITLMGFKPVITGHVESIGRGIDDNNDETGGLGLPNVEPTFSWVRLAQRIPVRIHIDRLPEGVELVAGLS

ASISITP

>lcl|NZ\_FO834906.1\_prot\_WP\_004899298.1\_3725 [locus\_tag=BN49\_RS20275] [protein=DUF1656 domain-containing protein] [protein\_id=WP\_004899298.1] [location=complement(3838599..3838814)] [gbkey=CDS]

MINDFNIEGVFVPGLLLISLVALTCTLLLVQLFSLSKGYRRLPFRPMIDFSIFIITFYLLLQGLTELGFL

K

>lcl|NZ\_FO834906.1\_prot\_WP\_016529980.1\_3726 [locus\_tag=BN49\_RS20280] [protein=FUSC family protein] [protein\_id=WP\_016529980.1] [location=complement(3838804..3840843)] [gbkey=CDS]

MKKINASYFHFLHTICHRLRGMASPSLLNDANALLYSAKSFTAAMLAYYIALSIGLERPSWAIITVYIVS

QTSVGASLSRSLYRLVGTVIGAGMTVLIVPTFVNSPVFCSVILAGWITFCLYLSLLERTPRAYGFVLAGY

TASLIGFPAVSDPGAIFDIAITRVQEIMIGIFCATLIHRYVLPARISGQFNSKLSQTLLAARQRIAETLI

GKPDPVSSPLHMALALQFLQGISHHIPYDFAFSVPVRQARKRLHDRLARLVIVNCELRDRLALIAKIPVD

VQILMDDVEVWLACKDEGKFKSEGEALKKRSEKLLQRYVVHELTFVEALHVSFMRYLTEAIVLVQQCYRL

SDAIHHANQMPAHSEMNTVKGYVFHRDPLSAARTALGAFTIILSGCMVWIFSAWPDGGTAVSILGVCCTL

FGSFDTPAPHIVKYIIGSLWGVVISLIYSFVLLPQVSDFIVLVVVLAPVYLLAGSLQARPPTTFMAMGIT

LTLPILCELGAHYSGDFAVAVNTSIALFSATGFAVFSMGFLQTVQADAAIKRLLKLCQRDINRSVKGVLN

TDETLWINLMIDRAALVLPRLPRSGQSSEQALNHLLHTLRIGLCVMRLRRWDAHADKEIKEVLTCLTHPT

DINTLLERIVSLTERSLSVADELSRHHVNQLVDLYCALSTQEMEPADDQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004899307.1\_3727 [locus\_tag=BN49\_RS20285] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004899307.1] [location=3840920..3841726] [gbkey=CDS]

MLPPLANTLFDPDTTSCPAVARHLDFVDYAAEVPVHTHRKGQLIIALYGAVICRAENDIWIVPPDCAVWI

PGGVPHSAKATWNAHLNYLFIEPGAAALPERCCTLAISGLIKELIARLTHEGVGYPPESHLARLTRVTLD

ELATMPQQKLSLPVSSHPKIRAMADALVSQPDDRSTFKTWAKRLALSERSLARLMLRETGLTFGRWRQQL

QLIIALRELASGVSVQNVAANLGYESVNAFITMFKKTMGSTPAHYFAERKTSAHLTDI

>lcl|NZ\_FO834906.1\_prot\_WP\_085955508.1\_3728 [locus\_tag=BN49\_RS28115] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_085955508.1] [location=join(3842066..3842324,3842324..3843186)] [gbkey=CDS]

MKKRFSDEQIISILREAEAGVPARELCRKHAISDATFYTWRKKYGGMEVPEVKRLKSLEEENARLKKLLA

EAMLDKEALQVALGRKLLTTDQKREAVMLMCDATGLSQRRACRLTGLSLSTCRYEAHRPAADAHLSGRIT

ELVLERRRFGYRRIWQLLRREGLHVNHKRVYRLYHLSGLGVKRRRRRKGLATERLPLLRPAAPNLTWSMD

FVMDALSTGRRIKCLTCVDDFTKECLTVTVAFGISGVQVSRILDSIALFRGYPATIRTDQGPEFTCRALD

QWAFEHGVELRLIQPGKPTQNGFIESFNGRFRDECLNEHWFSDIVHARKIINDWRQDYNECRPHSALNYQ

TPSEFAARWRNGKCEGKQTDLTN

>lcl|NZ\_FO834906.1\_prot\_WP\_016532370.1\_3729 [locus\_tag=BN49\_RS20305] [protein=hypothetical protein] [protein\_id=WP\_016532370.1] [location=3843259..3843582] [gbkey=CDS]

MTHAQKGGHSGGLDKPNFRFSLPISQLMAKAIPVRGAKFKKPAFEQAFCFFASLTLTQHRIQPGKHLVDN

DARYAFQTLAFPYRLPTPRVSSVSAPQLSLKKRLPVG

>lcl|NZ\_FO834906.1\_prot\_WP\_004214694.1\_3730 [locus\_tag=BN49\_RS20310] [protein=AarF/UbiB family protein] [protein\_id=WP\_004214694.1] [location=3843652..3844755] [gbkey=CDS]

MNLRQQQQQAFDRSGEPLIVGNVSHCPLPPETLAALGPDSPYVVQVYGSGLTGEVYRLRIAGKEYNLKKR

RAVAGVANLNGQLSFLNEVQRRQALQQLKDDPVTAPRFTHIVPTLYADYRLGILLSPWIDGEPIHQLTPP

LIAQLFTTLEACEEQGLMEWDLCSGNLLVDRQEQLWLFDFGYMYPFDPLREFNSNGLADPLFHFVERFET

RFFFSWLMTRIPDAEQQLAHYRDLKRLAVESYRRKLVWLRARRADPLVLAHFQQLTARWESALADPAALS

RLFAVEAFRSHVLDIEDDLHGQSCTLLTLQRIDWVINQLEQHYRFITDEGGLFYDNEGKSQQALLSSYAQ

KRQQAQQYLLSATAAKD

>lcl|NZ\_FO834906.1\_prot\_WP\_002911798.1\_3731 [locus\_tag=BN49\_RS20315] [protein=sensor domain-containing diguanylate cyclase] [protein\_id=WP\_002911798.1] [location=complement(3844752..3845723)] [gbkey=CDS]

MKLAGLHPDEQRRLQSLRSSGLLNSGKEERFDRLTRLARSLYNLPVASISLVGEDLLHIKSCAGLDVDTV

PRDISFCAHTILQTDPLIVNDMQQDERFHDNPLVIEAPFIRFYAGYPVQLPDGATVGSFCLMDHQPRSFS

AHEMQILSDLAAIVEDEFKVLDAATSDELTGLFNRRGFLTLAEYALLTAQRRHEPVSLAFVDLDRFKHIN

DTWGHEEGDRALIAIADLMKAAFRESDILARQGGDEFIILFANTSRHDAATAMETLSHNVARFNQQAANP

WQLAFSWGCVEYDPASHPSLNALVATADRLMYQAKQKQGRERR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180471.1\_3732 [locus\_tag=BN49\_RS20320] [protein=alpha/beta hydrolase] [protein\_id=WP\_004180471.1] [location=complement(3845930..3846766)] [gbkey=CDS]

MAFVTTQDGVNIYFKDWGPKEAQPIVFHHGWPLSADDWDNQMLFFLAEGFRVIAIDRRGHGRSDQVSEGH

DMDHYAADVSAVVEHLDLHNAVHVGHSTGGGQVARYVARYGQPQGRVAKAVLISAVPPLMVKTEQNPGGT

PIEVFDGFRKALAANRAQFYLDVASGPFYGFNRDGAEISQGTIQNWWRQGMIGSAKAHYEGIKAFSETDQ

TEDLKSITLPVLVMQGDDDQVVPYKNAAILQDKLLPNSQLKIYPGFPHGMHTSHADTINADLLAFIRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532101.1\_3733 [locus\_tag=BN49\_RS20325] [protein=hypothetical protein] [protein\_id=WP\_016532101.1] [location=complement(3846959..3847534)] [gbkey=CDS]

MHVVSRYTAAEAAATIDPRGRAIALSVVIAAGALLLIMPPVIGVTGTLSLLTALIAAFSVGWGFTRGQSW

LYRSPLAATRWAFLLSAAGWLLALVAWYGGQDWPALLPGVACGGAGAAVAWRIAAGRTALPGMRVSGATV

LSVAIAIAATLLTWHTAGGGRHGVCFAFAVLLDWALLGALMVRIRQQESAA

>lcl|NZ\_FO834906.1\_prot\_3734 [locus\_tag=BN49\_RS20330] [protein=LysR family transcriptional regulator] [pseudo=true] [location=3847666..3848580] [gbkey=CDS]

MRPPRLPPLGALRAFHAVARHRSFKQAAEALGVSATAVSHQIKLLESVLECRVCERSAQGVSLTADGEIL

YAATQRAFSALEQAVVQIAHARQPPSLTVTTTSNFLTHWLVPRLADFTARFPAIDLRLHTSVERVDLHLG

TVDAAIRYREKPEPDLYCTLLYEDRFIVVASPTLGLSRPEDLQRVTLFHVANRRVPADSPSWENWRRRYG

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DIIALREWLLSQMASGDGGHPTAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002911862.1\_3735 [locus\_tag=BN49\_RS20335] [protein=DUF1869 domain-containing protein] [protein\_id=WP\_002911862.1] [location=complement(3848586..3848921)] [gbkey=CDS]

MTSENKGYTLALENGRLHQKQEKIFLKPMVLYIPQQAVEAVNDLLSKLPDDREEGEFLLTVTNNNNGVSV

DKTFSSLAALRDPLTAADAVKDLINIVRGYESDEETNVCGW

>lcl|NZ\_FO834906.1\_prot\_WP\_002911866.1\_3736 [locus\_tag=BN49\_RS20340] [protein=DUF1971 domain-containing protein] [protein\_id=WP\_002911866.1] [location=complement(3848928..3849260)] [gbkey=CDS]

MQRIIIPTHYVHTRSTPLWTKETAPASIWRRHLDAGTRQGVYPRLSVMQGAIRYLGYADETSPEPVETLT

IEAGQFGVFPPEKWHCIEALSEDTVFNVDFYVDPKILIEG

>lcl|NZ\_FO834906.1\_prot\_WP\_032433877.1\_3737 [locus\_tag=BN49\_RS31170] [protein=hypothetical protein] [protein\_id=WP\_032433877.1] [location=3849358..3849486] [gbkey=CDS]

MWNFTPTPFYTSQGLALRENKKGDFRILKSPERIKVDTLKIC

>lcl|NZ\_FO834906.1\_prot\_WP\_042942662.1\_3738 [locus\_tag=BN49\_RS20350] [protein=EAL domain-containing protein] [protein\_id=WP\_042942662.1] [location=complement(3849483..3851393)] [gbkey=CDS]

MNRILTAIILSLFVVTGYITYLVHERQSELQKFTRYTDSWSMSQMVSEYMRLESRLAGMAIGAEGADHDE

VRLRLEIMMSQIELLQEGDLGKFINKSEQRKTVVAKLIRNLHLLDKQVDTMMPEQVRQILPVLSELDGPL

TSMAAATLTQDINIVNITHDKIQHLYYIYSVISILLIAMCITLGLLMLRQNNNLRRAHVRMKTLANDLQA

SKEKLQVQNRRLQYDAYHDSLTGMPNRLSFWQRLQEIVNQVRPYKGCAVVMLFDLDSFKDVNDTLGHDAG

DKLLQDLASRLSFFRKTSETLYRLGGDEFAMLSYDLTEEMALERANVIREKISQPYQSYDAQINIDACIG

IVISDGESRTDYLYKCADLALYEAKKEGSGHVQIFRPGMLQRLQENKSFEDDLLQALAHDEFKVYYQPIA

DTVTREIYGYEALVRWFHPVRGAVPPTVFIPVAEKIGLINALGEWVLKTACAEAASWATPLKVSVNVSPI

QLMNTSLTDTIIEVLHQTGLDPRRLDLEITESDVFNENTRSLEILSQLREQGIQISIDDFGTGYSSLSRL

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KPSPLR

>lcl|NZ\_FO834906.1\_prot\_WP\_014907250.1\_3739 [locus\_tag=BN49\_RS20355] [protein=molybdopterin-dependent oxidoreductase] [protein\_id=WP\_014907250.1] [location=complement(3851404..3851865)] [gbkey=CDS]

MLPSAYAEKLPAPTGKPVLTISGKIGNMNVGDKAVFDLAMLEKLGMKTIETTTPWYTGKVRFDGIPLNKL

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SRSAWQVSKMIIE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532099.1\_3740 [gene=shiA] [locus\_tag=BN49\_RS20360] [protein=shikimate transporter] [protein\_id=WP\_016532099.1] [location=3852208..3853527] [gbkey=CDS]

MDSTISVQPGEAPDSLHRARRAAWGSFAGAVVDWYDFLLYGITATLVFNREFFPQIGPAMGTLAAFATFG

VGFLFRPLGGIIFGHFGDRLGRKRMLMMTVWMMGIATACIGLLPSFNQIGWWAPVLLVFLRAVQGFAVGG

EWGGAALLSVENAPQGKKAFYSSGVQVGYGVGLLLSTGLVSLISSLTSDQQFLSWGWRLPFLFSVVLVLI

ALWIRNGMAESQEFEAQQSQGNAPQMKKRLPVVEALLRHPGAFLLIIALRLCELLTMYIVTAFALNYSTQ

NLGLPRELFLNIGLLVGGLSCLTIPCFAWLADRFGRRRIYITGALIGTLSGFPFFMALESQSVFWILFFA

LMLANIAHDMVVCVQQPMFTELFGASYRYSGAGVGYQVASVVGGGFTPFIAAALVTFSGGSWHSVALYLT

AGCLLSALTALMMKKHPVD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043621.1\_3741 [locus\_tag=BN49\_RS20365] [protein=lipoate--protein ligase A] [protein\_id=WP\_046043621.1] [location=3853574..3854314] [gbkey=CDS]

MSQLTLADCWPRRFSPSSLALQFCEDPTQAEQPLFAKASAGEAVAKLWQAPQGLVVPGSYRQFTDLPAVS

AHFAARGWPVWLRRSGGGLVPQGPGIINLSLAWPVQQPLGEAAEPIYHSLCAVLQRTLARFGVASHPRAV

SGSFCDGRYNLACGEDAEARKIVGTAQYWRPLAAGGGHVVLAHAVILIDADLSAAHQAANAFEAQLGSER

VYCADKTVTLAQLLPGERHLLPRFSETLAQELDAAR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043623.1\_3742 [locus\_tag=BN49\_RS20370] [protein=LysR family transcriptional regulator] [protein\_id=WP\_046043623.1] [location=complement(3854274..3855230)] [gbkey=CDS]

MSESRPESYWIHLYWLTVLEEQKSYTRAAEKLGISKSAISQKISELERVTGKTLVHRTTRSVSLSDDGLR

LVAELNEPFGQLRDIFTGACDEGGPLRGTLRLTAPVAFSRQQLVPAIAPFLHQHPQLHLQLEVTDRLVSL

ASEGFDLAIRHCRREALPDTHVAWPLCHTATLTVASADYIRRHGRPETPEDLRHHQCLTYPRGPQRPQWT

FASRQSPDARVTINVQGPFATNNSESLRDAVLAGLGVALLPDFSAREAIGRGLVQELLPAWQPVEVFADR

LYVIRPYTPRVSRAVETFSRYLKATFSEPRPAPAPASR

>lcl|NZ\_FO834906.1\_prot\_WP\_004175282.1\_3743 [locus\_tag=BN49\_RS20375] [protein=tautomerase family protein] [protein\_id=WP\_004175282.1] [location=3855346..3855735] [gbkey=CDS]

MPLLTFDLIEGRTEQEVKTLLDAAHRAVLRAFEVPERDRYQIVHENKAHHMVIEDTGLGLTRTRDLVVVR

VYTSPRSEAQKQRFFAILQEELAEHCGLSGDDLMVSIISNQKGDWSFGRGVAQYLTGDL

>lcl|NZ\_FO834906.1\_prot\_WP\_002911879.1\_3744 [locus\_tag=BN49\_RS20380] [protein=HPP family protein] [protein\_id=WP\_002911879.1] [location=complement(3855757..3856488)] [gbkey=CDS]

MLSVIPAGIFSRLRIFLGRLKPHALPVARRHIVLGSIGAGTGLAVTSMFSHWLLGEVNLWFIAPMGASAV

LLFGVPSSPLAQPWSIVGGNVLSALIGVTVGMLVPDAALACGLAAALAIAGMYFLRCLHPPGGAVALTAI

LGGAGVHSEGYHFVLTPVLLNSLMLALLAIVFNNLVGRRYPHPLAAEEVKSRAVPLGISVTREDIHAALL

EGQFLDIDEDDVQELLENIEQQARQRIATAARR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532095.1\_3745 [locus\_tag=BN49\_RS20385] [protein=adenosylhomocysteinase] [protein\_id=WP\_016532095.1] [location=3856687..3857796] [gbkey=CDS]

MNNKISLAKEVAWASQNMPRTLRQVAALPDLSGVRLACCMHLDMKMIPLVQGILDKGAQVFLTTCNPTTV

QDDVVAWLVERGAEACAWRNMSDADWQQSWEKAIAWQPTHLCEMGADITTLLHQRGEFGNIVAGLEATGS

GINRLGDIQPGYPIFNWDDLPVKEGLHNRHMVGLTAWHTFFQTTHLTLHEKKVLVIGYGLVGQGVAAAAK

AFGGQVMVAEIDPARRLQAAYDGWHVVDLQEAIASADVVATATGGKNVVNRQALDRAKAGVFILNVGHVA

EEIDGDYLRQYPQEEVMPYINAYRMADKTVYLLANGSMLNLTAGFGDSLNAFDVTLAVMASGIRHIVTEG

MRAPAKVYLLPQAVWQQAL

>lcl|NZ\_FO834906.1\_prot\_WP\_032418694.1\_3746 [gene=cobT] [locus\_tag=BN49\_RS20390] [protein=nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase] [protein\_id=WP\_032418694.1] [location=complement(3857839..3858906)] [gbkey=CDS]

METLSALLAAIPQPDVAGMARAQQHIDGLLKPPGSLGRLEALAVQLAGLPGLQGQLALAEKAIVVMCADH

GVWHEGVTPSPQGVTAIHAGNMVRGNTGVCVLAAQAGARVQVVDVGIDADPLPGLINLKVARGSGNIART

AAMSRQQAETVLLASMQLTRQLAADGVKAFGVGELGMANTTPAAATISVLTGSDPDAVVGCGANLPLAQR

GHKVTVVRQAIAHNQPNPADGLDVLAKVGGYDLVGMTGVILGAASCGLPVVLDGFLSYASALAACRMAPS

AHPYLIPSHLSAEKGAQIALDALGLRPYLDMDMRLGEGSGAALAMHLLDAASVMYNQMGTLAQSNIVLPD

SAPSS

>lcl|NZ\_FO834906.1\_prot\_WP\_004144121.1\_3747 [gene=cobS] [locus\_tag=BN49\_RS20395] [protein=adenosylcobinamide-GDP ribazoletransferase] [protein\_id=WP\_004144121.1] [location=complement(3858934..3859674)] [gbkey=CDS]

MIKSFFAALSFISRLPVPARLSQGLEIEQYQRSIVTFPLVGLLLGAIAGAVALLLQPWCGVPLAALFGVL

ALALLTGGFHLDGLADTCDGIFSARTRDRMLEIMRDSRLGTHGGLALIFVLVAKVLVVGELLLRDIHPIA

ALAAACAVGRGMAVLLMYRHRYAREKGLGNLFIGKISLQQTLVTMAMAIALATALMGLQGLRAALITLVL

IWGLGWALKRTLGGQTGDTLGAAIELGELLFLLALL

>lcl|NZ\_FO834906.1\_prot\_WP\_002911883.1\_3748 [locus\_tag=BN49\_RS20400] [protein=DUF496 family protein] [protein\_id=WP\_002911883.1] [location=complement(3859989..3860312)] [gbkey=CDS]

METTKPSFQDVLEFVRLYRRKNKLQREIQDVEKKIRDNQKRVLLLDNLSDYIKPGMSVEAIQGIIASMKS

DYEDRVDDYIIKNAELSKERRDISKKLKVMGEAKVEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002911885.1\_3749 [locus\_tag=BN49\_RS20405] [protein=FUSC family protein] [protein\_id=WP\_002911885.1] [location=complement(3860480..3861538)] [gbkey=CDS]

MRADKSLKPFEIRLYRHYRVVHGVRIALAFVLTFLLVRLLNVPEGTWPLITLVVVMGPISFWGNVVPRAF

QRIGGTILGSALGLVALKLELISLPLMVLWCAAAMFLCGWLALGKKPYQALLIGITLSVVVGAPPGDMHT

ALWRSGDVIFGSLLAMLFTGIWPQRAFIHWRIQMASYVTNFNRLYQAGFSPNLVDRPRLEKHLQQALNDV

VKMRGLITPASKETHIQKAIFEAIQTVSRNLVCMLELQINAWWATRPGHFVMLNAHTLRETQQMTQQTLL

SIAHALYEGNPQPVRANNEKLTEIVLELRQLLKEQGDDGLAETPVHGYVWLSIELARQLELLSHLICRAL

RK

>lcl|NZ\_FO834906.1\_prot\_WP\_004144123.1\_3750 [gene=sbmC] [locus\_tag=BN49\_RS20410] [protein=DNA gyrase inhibitor SbmC] [protein\_id=WP\_004144123.1] [location=complement(3861637..3862110)] [gbkey=CDS]

MNYSITTLGKKTIAGFHLVGPWDHTVKQGFEQLMMWVENHQVPAREWVAVYYDNPEEVPAEKLRCATAVA

VDEDYVIPANSEGVILAAIAGGDYACARARVVDYDFATPWMQFFDSLQQSTAYRIAPQPCFEVYLNDGNH

DGYWDIDMYVPVERVAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004153104.1\_3751 [gene=dacD] [locus\_tag=BN49\_RS20415] [protein=serine-type D-Ala-D-Ala carboxypeptidase DacD] [protein\_id=WP\_004153104.1] [location=complement(3862287..3863450)] [gbkey=CDS]

MKGRLFIAVSLLASSVSCAFAVDLPATVAPPSIQAGSWVLMDYTTGQVLTAGNEHQQRNPASLTKLMTGY

VVDRAIDSHRITFDDIVTVGKDAWAKGNPVFDGSSLMFLKPGDRVSVRDLSRGLIVDSGNDACVALADYV

AGGQPQFVALMNQYVEKLHLRDTHFETVHGLDAPGQHSSAYDLAVLSRAIIHGEPDVYHMYSQKSLTWNG

ITQQNRNGLLWDKTMNVDGLKTGHTSGAGFNLIASAVDGQRRLIAVVMGADSPKGREQQAAKLLHWGQQN

FDTVQVLQKGQKVGTERIWYGDKEQIKLGTDQDFWLALPKAEVSRIKAKYVLDKKDLEAPIAANQRVGEI

SLYDGDKVVGHYPLVTLESINKGGVFSRMSDYLHHEL

>lcl|NZ\_FO834906.1\_prot\_WP\_016531201.1\_3752 [gene=sbcB] [locus\_tag=BN49\_RS20420] [protein=exodeoxyribonuclease I] [protein\_id=WP\_016531201.1] [location=3863631..3865055] [gbkey=CDS]

MQDSVNQPGFLFHDYETFGTSPSLDRPAQFAAIRTDAELNVLGEPEVFYCKPADDYLPQPQAVMITGITP

QEALAKGDNEATFARRIHDLFTVPQTCIVGYNNVRFDDEVTRNIFYRNFYDPYAWSWQHDNSRWDLLDVM

RACYALRPEGIAWPENDEGLPSFRLEHLTVANGIEHQNAHDAMADVYATIAMAKLVKTRQPRLFDYLYSH

RNKRKLATLIDVPQMKPLVHVSGMFGAARGNTSLVAPLAWHPENRNAVIMVDLAGDMAPLLELDADALRE

RLYTPRAELGDLLAAPIKLVHLNKCPVLAQANTLRPQDADRLGISIQRCLENAQLLRANPQVREKVVAVY

AEAEPFVPSENVDAQLYNGFFSDADRAAMKIVLETEPRNLPALDITFADKRIERLLFNYRARNFPGTLDE

HEQQRWLEHRRQVFTPEFLQAYADELQMLYQQYADDKEKLAQLKALWQYAQDIV

>lcl|NZ\_FO834906.1\_prot\_WP\_020804128.1\_3753 [gene=fusA] [locus\_tag=BN49\_RS20425] [protein=elongation factor G] [protein\_id=WP\_020804128.1] [location=complement(3865279..3867381)] [gbkey=CDS]

MPRPIPLERYRNIGISAHIDAGKTTTTERILFYTGMSHKLGEVHDGAATTDWMAQEQERGITITSAAVSC

FWPGMDRSFEPHRINIIDTPGHVDFTIEVERSMRVLDGAVMVYDSVGGVQPQSETVWRQANKYHVPRLAF

VNKMDRPGADFFRVVQMMIDRLKANPVPIVIPIGAEEHFTGVVDLVKMRAILWDDATQGMTFSYGPVPDE

LLATAQQWREKMVSAAAEASDELMDKYLETGELDEAEIVAGLRQRTVKGEIQAVLCGSAFKNKGVQRMLD

AVVELMPSPLDIPAIQGVDEQGQPAERHPSDDEPLSALAFKLMTDPYVGQLTFIRVYSGTLKKGDAVWNP

VKGKKERIGRIVLMQANDRHEVDELHAGDIAACVGLKDVTTGDTLCDPDAVITLERMEFPEPVISLAIEP

KTKADQEKMGIALQRLAAEDPSFRLHTDEESGQTIISGMGELHLEIIVDRMKREFGVEANIGRPQVTYRE

TLRKKVTDVEGKFVRQSGGKGQYGHVVLTLEPLEPGSGFVFEDATKGGVVPREYIPSVEKGLREAMGTGV

LAGYPVVDVKATLTFGSYHDVDSSEMAFRMAAIFGFREGARKADPVILEPVMHVEVETPEEYAGNIMGDL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002912109.1\_3754 [locus\_tag=BN49\_RS20430] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_002912109.1] [location=3867621..3867932] [gbkey=CDS]

MIANHPEREQIRLENVLSALGNPLRLEIIRTLADGSELSCNALRQEEVAKSTMTHHWRVLRDSGVIWQRP

QGRENMISLRREDLDARFPGLLDTLLKVMVQAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004148994.1\_3755 [gene=plaP] [locus\_tag=BN49\_RS20435] [protein=putrescine/proton symporter PlaP] [protein\_id=WP\_004148994.1] [location=complement(3868115..3869473)] [gbkey=CDS]

MSHNATPNTSRVELRKTLTLVPVVMMGLAYMQPMTLFDTFGIVSGMTDGHVPTAYAFALIAILFTALSYG

KLVRRYPSAGSAYTYAQKSISPTVGFMVGWSSLLDYLFAPMINILLAKIYFEALVPSIPSWVFVIALVAF

MTAFNLRSIKSVANFNTVIVVLQVVLIAVILGMVIYGVFEGEGAGTLASSRPFWSGDAHVIPMITGATIL

CFSFTGFDGISNLSEETKDAERVIPRAIFLTALIGGLIFIFATYFLQLYFPDISRFKDPDASQPEIMLYV

AGKAFQVGALIFSTITVLASGMAAHAGVARLMYVMGRDGVFPKSFFGYVHPTWRTPAMNIILVGAIALLA

INFDLVMATALINFGALVAFTFVNLSVISQFWIREKRNKTLKDHFQYLFLPMCGALTVGALWVNLEESSM

ILGLIWAGIGLVYLACVTKSFRNPVPQYEDVA

>lcl|NZ\_FO834906.1\_prot\_WP\_096335043.1\_3756 [gene=yoeI] [locus\_tag=BN49\_RS30550] [protein=membrane protein YoeI] [protein\_id=WP\_096335043.1] [location=complement(3869463..3869525)] [gbkey=CDS]

MGQFFAYALAFTVKGDNYVA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043630.1\_3757 [locus\_tag=BN49\_RS20440] [protein=LysR family transcriptional regulator] [protein\_id=WP\_046043630.1] [location=complement(3869763..3870653)] [gbkey=CDS]

MKPLLDVLVILDALEKEGSFAAASAKLFKTPSALSYTIHRLESDLNIQLLDRRGHRARFTPSGQMLLEKG

REVLHIARELENRAVKLQQGWENSLRLAVDSTFPVALLSPPIAAFYQQQPLTRLHFTLNPSLLDWRPLTD

GQADLLLGALGEPPPLSGYDYLPLGELELLLVVAPQHPLARHRAPLSWRTLRRYRAVATGEGGALLSDQE

TLTVCDAAGQLALLRLGLGWGCLPRYQVQGLLDSGELVCMTVRGLSPPQRVWIAWNDATCGLAGKWWRET

LLANSAIFTIYHTETV

>lcl|NZ\_FO834906.1\_prot\_WP\_004152513.1\_3758 [locus\_tag=BN49\_RS20445] [protein=SDR family oxidoreductase] [protein\_id=WP\_004152513.1] [location=complement(3870692..3871516)] [gbkey=CDS]

MKKVAIVGLGWLGMPLALSLTARGWQVTGSKTTQDGVEAARMCGIDSYPLRLEPQLVCDTEDLDALMNVD

ALVITLPARRTGAGEGFYLQAVQEIVDTALAYHIPRIVFTSSTSVYGNVNGTVKENSPRLPQTASGQVLK

ELEDWLHNLPGTSVDILRLAGLVGPSRHPGRFFAGKSAPDGQHVVNLVHLQDVVAAIELLLQAPKGGHIY

NLCAPRHPARGLFYPQMARELGLPPPVFSDSPDGGQGKIVDGNRICNELGFEYQYPDPLVMPME

>lcl|NZ\_FO834906.1\_prot\_WP\_004899375.1\_3759 [gene=hisL] [locus\_tag=BN49\_RS30555] [protein=his operon leader peptide] [protein\_id=WP\_004899375.1] [location=3871693..3871743] [gbkey=CDS]

MNRVQFKHHHHHHHPD

>lcl|NZ\_FO834906.1\_prot\_WP\_002912152.1\_3760 [gene=hisG] [locus\_tag=BN49\_RS20450] [protein=ATP phosphoribosyltransferase] [protein\_id=WP\_002912152.1] [location=3871889..3872788] [gbkey=CDS]

MLDNTRLRIAIQKSGRLSEDSRELLSRCGIKVNLHTQRLIALAENMPIDILRVRDDDIPGLVMDGVVDLG

IIGENVLEEELLSRRAQGEDPRYFTLRRLDFGGCRLSLATPVDEAWNGPAALDGKRIATSYPHLLKRYLD

QKGISFKSCLLNGSVEVAPRAGLADAICDLVSTGATLEANGLREVEVIYRSKACLIQRDGEMADAKQQLI

DRLLTRIQGVIQARESKYIMMHAPTERLEEVVALLPGAERPTILPLAGDKQRVAMHMVSSETLFWETMEK

LKALGASSILVLPIEKMME

>lcl|NZ\_FO834906.1\_prot\_WP\_046043632.1\_3761 [gene=hisD] [locus\_tag=BN49\_RS20455] [protein=histidinol dehydrogenase] [protein\_id=WP\_046043632.1] [location=3872828..3874132] [gbkey=CDS]

MSFNTIIDWNGCSADQQQQLLTRPAISASDSISKTVTEILNNVKANGDAALREYSAKFDKTTVAALQVSE

AEIAAAGERLSDELKQAMAVAVNNIETFHNAQQLQAVDVETLPGVRCQQVTRPIASVGLYIPGGSAPLFS

TVLMLATPARIAGCQQVVLCSPPPIADEILYAAQLCGVKTIFNVGGAQAIAALALGTESVPKVDKIFGPG

NAYVTEAKRQVSQRLDGAAIDMPAGPSEVLVIADSGANPDFVASDLLSQAEHGPDSQVILLTPDADMGSR

VAEAVERQLAALPRAETARVALSASRIIVARDLAQCVAISNLYGPEHLIIQTRQARELVDSITSAGSVFL

GDWSPESTGDYASGTNHVLPTYGYTATCSSLGLADFQKRMTVQELSRDGFAALASTIEILAAAERLDAHK

NAVTLRVAALKEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004149000.1\_3762 [gene=hisC] [locus\_tag=BN49\_RS20460] [protein=histidinol-phosphate transaminase] [protein\_id=WP\_004149000.1] [location=3874129..3875190] [gbkey=CDS]

MSIEDLARANVRALTPYQSARRLGGKGDVWLNANEFPTAVAFQLTEQTLNRYPEPQPKAVIESYARYAEV

KPEQVLVSRGADEGIELLIRAFCEPGEDAVLYCPPTYGMYSVSAETIGVECRTVPTLADWQLDLPGIEAR

LDGVKVVFVCSPNNPTGQIIDPQSMRDLLEMTRGKAIVVADEAYIEFCPQATLAGWLSDYPHLVVLRTLS

KAFALAGLRCGFTLANAEVINVLLKVIAPYPLSTPVADIAAQALSPEGIAAMRQRVAQILDERRYLVEQL

RGIACVEQVFDSETNYVLARITASSAVFKSLWDQGIILRDQNKQPSLSGCLRITIGTRAESQRVIDALTA

ENV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529437.1\_3763 [gene=hisB] [locus\_tag=BN49\_RS20465] [protein=bifunctional histidinol-phosphatase/imidazoleglycerol-phosphate dehydratase HisB] [protein\_id=WP\_016529437.1] [location=3875187..3876254] [gbkey=CDS]

MTQKYLFIDRDGTLISEPPEDFQVDRFDKLAFEPQVIPALLKLQQEGYKLVMITNQDGLGTDSLPQEAFD

GPHNLMMQVFASQGVNFEEVLICPHFPGDNCACRKPKTQLVLPWLEEGVLDKSHSYVIGDRATDLELADN

MGITGLRYDRETLDWPTICEQLTRRDRYAHVERITKETQVDVKVWLDREGGSKIHTGVGFFDHMLDQIAT

HGGFRMEVNVGGDLYIDDHHTVEDTGLALGEALKLALGDKRGINRFGFVLPMDECLARCALDISGRPHLE

YKADFTYQRVGDLSTEMVEHFFRSLSYTMAVTLHLKTKGKNDHHRVESLFKAFGRTLRQAIRVQGDALPS

SKGVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002912227.1\_3764 [gene=hisH] [locus\_tag=BN49\_RS20470] [protein=imidazole glycerol phosphate synthase subunit HisH] [protein\_id=WP\_002912227.1] [location=3876254..3876844] [gbkey=CDS]

MNVVILDTGCANLNSVKSAIGRHGYEPVVSRDPEVVLRADKLFLPGVGTAQAAMDQLRDRELIDLIKACT

QPVLGICLGMQLLGKRSEENNGVDLLGIIEEEVPKMTDHGLPLPHMGWNRVYAKAGDRLFRGIEEGAYFY

FVHSYAMPVNPYTIAQCNYGEAFTAAVQKDNFFGVQFHPERSGSAGAQLLKNFLEM

>lcl|NZ\_FO834906.1\_prot\_WP\_016529436.1\_3765 [gene=hisA] [locus\_tag=BN49\_RS20475] [protein=1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino]imidazole-4-carboxamide isomerase] [protein\_id=WP\_016529436.1] [location=3876844..3877581] [gbkey=CDS]

MIIPALDLIDGTVVRLHQGDYGQQRDYGSDPLPRLQAYAAQGAEVLHLVDLTGAKDPAKRQIPLLKSLVA

GVDVPVQVGGGVRTEADVAALLEAGVARVVVGSTAVKSPEEVKGWFKRFGPERLVLALDVRIDADGNKQV

AVSGWQENSGVTLEELVKSYLPVGLQHVLCTDISRDGTLAGSNVSLYEEVCARYPQVAFQSSGGIGDLND

IAALRGTGVRGVIVGRALLEGKFNVTEAIQCWQNG

>lcl|NZ\_FO834906.1\_prot\_WP\_004180497.1\_3766 [gene=hisF] [locus\_tag=BN49\_RS20480] [protein=imidazole glycerol phosphate synthase subunit HisF] [protein\_id=WP\_004180497.1] [location=3877563..3878339] [gbkey=CDS]

MLAKRIIPCLDVRDGQVVKGVQFRNHEIIGDIVPLAKRYADEGADELVFYDITASSDGRVVDKSWVSRVA

EVIDIPFCVAGGIKSLEDAAQILSFGADKISINSPALADPTLITRLADRFGVQCIVVGIDTWFDAETGKY

HVNQYTGDESRTRVTQWETLDWVEEVQKRGAGEIVLNMMNQDGVRNGYDLQQLAKVRAVCHVPLIASGGA

GTMEHFLEAFRDADVDGALAASVFHKQIINIGELKAYLAAQGVEIRVC

>lcl|NZ\_FO834906.1\_prot\_WP\_016529435.1\_3767 [gene=hisIE] [locus\_tag=BN49\_RS20485] [protein=bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP diphosphatase HisIE] [protein\_id=WP\_016529435.1] [location=3878333..3878932] [gbkey=CDS]

MLTEQLDWEKTDGMMPAIVQHAVSGEVLMHGYMNKEALEKTEATGKVTFYSRTKQRLWTKGETSGNVLNV

VSITPDCDNDTLLVLVNPIGPTCHKGTTSCFGETGHQWLFLYQLEQLLAERKHADPESSYTAKLYASGTK

RIAQKVGEEGVETALAATVNDRFELKNEASDLIYHLLVLLQDQGLDLGEVIDNLRARHR

>lcl|NZ\_FO834906.1\_prot\_WP\_032448054.1\_3768 [locus\_tag=BN49\_RS20490] [protein=GtrA family protein] [protein\_id=WP\_032448054.1] [location=3879155..3879502] [gbkey=CDS]

MKYGLVGIVNTLITAVVIFLLMHLGLGIYLSNAMGYVVGIVFSFIANTIFTFTQPISIHRLIKFLCVCFI

CYVANIIVIKIFFVFMPEKIYSAQILGMFTYTITGFILNKFWAMK

>lcl|NZ\_FO834906.1\_prot\_3769 [locus\_tag=BN49\_RS20495] [protein=glycosyltransferase family 2 protein] [pseudo=true] [location=3879499..3880479] [gbkey=CDS]

MTTSTDIKSTPSLAIVVPCYNEQEAFPFCLEKLSNVLNLLIARNKINNNSYLLFVDDGSRDNTWAQIKDA

STAYHYVRGIKLSRNKGHQIALMAGLRSVDTDVSISIDADLQDDVNCIEKMIDAYSQGYDIVYGVRGNRD

SDTFFKRTTANAFYAIMSHLGVNQTPNHADYRLLSNRALEALKQYKEQNIYLRGLVPLVGYPSFEVQYSR

EERIAGE\*KYPIKKMLALALEGITSLSVTPLRIIAMTGFITCIISTIAAIYALIQKTTGTTVEGWTSVMI

AIFFLGGVQMLSLGIIGEYVGKIYIETKNRPKYFIDESVGNNSNGK

>lcl|NZ\_FO834906.1\_prot\_WP\_004899393.1\_3770 [locus\_tag=BN49\_RS20500] [protein=hypothetical protein] [protein\_id=WP\_004899393.1] [location=3880481..3881941] [gbkey=CDS]

MQNLINPLAEGNKKNVYIFYFFLLMLTFSPVIFFSYAFSDDWSTLFDATTRNGSSFQWDVQSGRPVYAVF

RYYGKMLINDISSFSYLRLFNILSLVVLSCFIYNFIDSRKIFDNPVFKIIFPLLICLLPAFQVYASWATC

FPFTISVLLAGISYNKCFPHSKQRSSLPEKLASIVVLWVAFAIYQPTAITFLFFFMLDSCIKKESSLTVK

KVGTCFIILVIGVAGSFIMSKVLPVWLYGESLSRAELTADIGGKMKWFINESLINAVNNYNIQPVKIYSW

FSSLAILIGLYTIFVGKSGRWKTFTVIAIGIGSYAPNLATKENWAAFRSLVALELIISTLFLIGINSLVS

RISKQAFVWPLIALTIMIIAQYNIINGFIIPQRSEIQALAAEITNKIPKNYTGKLMFDLTDPAYNAFTKT

QRYDEFGNISLAAPWALKGMAEEIRIMKGFNFKLSNNVIISETNRCIDDCMVIKTSDAMRRSTINY

>lcl|NZ\_FO834906.1\_prot\_WP\_046043635.1\_3771 [locus\_tag=BN49\_RS20505] [protein=glycosyltransferase] [protein\_id=WP\_046043635.1] [location=complement(3882011..3883219)] [gbkey=CDS]

MAHEKSDIIVSVVIPVYNAEEYIADTLKNIVSQSLYEIEIIIINDHSSDNTLDILKEIASSDERIRIIDN

AVNIGAGISRNIGLSEAKGEYIIFLDDDDYVDTNMLKHMSDCAELSGADIVVCRSRSFNLQSLQYAPMPD

SIRKDLLPEKAVFSPGDIERDFFRAFIWWPWDKLFRREFIIQHSLSYQDLRTSNDLFFVCASMLSAEKVT

ILDEILIAHTINRKTSLSSTRSVSYHCALDALVALRDFLFKNGMMQKRQRDFYNYIVVFLEWHLNTLSGE

AFNKLFQDVKLFISSFDINNEDFYDEFILSAYRRIADMSAEEYLFSLKDRVLNELEDAQRNILTLQNEVE

EIKQQLQQKDEMIASMNRENLAIKADNKILENYNEELKTVQTKFLKLLSSKD

>lcl|NZ\_FO834906.1\_prot\_WP\_171819483.1\_3772 [locus\_tag=BN49\_RS20510] [protein=glycosyltransferase family 4 protein] [protein\_id=WP\_171819483.1] [location=complement(3883315..3884457)] [gbkey=CDS]

MGIAMRKLCYFINSDWYFDLHWIDRAIASRDAGYEIHIISHFIDDNIINKFKTFGFICHNVTLDAQSFNA

LVFFRTYHDVQKIIKNIKPDLLHCITIKPCLIGGVLAKKFNLPVIVSFVGLGRVFSSDSMPLKLLRQFTI

AAYKYIASNKRCIFMFEHDRDRKKLAKLVGLEEQQTIVIDGAGINPEIYKYSLEQNHDVPVVLFASRMLW

SKGLGDLIEAKKILRSKNIHFTLNVAGILVENDKDAISLQLIENWHQQGLINWLGRSNNVCDLIEQSNIV

ALPSVYSEGVPRILLEASSVGRACIAYDVGGCDSLIIDNDNGIIVKSNSPEELADKLAFLLSNPKARVEM

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>lcl|NZ\_FO834906.1\_prot\_WP\_004899405.1\_3773 [locus\_tag=BN49\_RS20515] [protein=glycosyltransferase] [protein\_id=WP\_004899405.1] [location=complement(3884458..3885351)] [gbkey=CDS]

MKYTALIVTFNRLGKLKKTVEETLKLEFTNIVIVNNGSTDGTQAWLSSIVDTRVIVLTLTENTGGAGGFK

TGSQYICAQLASDWVFFYDDDAYPYPDTLKSFSQLDKRGCRVFSGLVKDPQGKPCPMNMPFSRVPTSLGD

TVRYLRYPAEFIPAANRSMFVQTVSFVGMVIHRDLLATSLDYIREQLFIYFDDLYFGYQLSLAGEQIMYS

PELLFYHDVSIQGKLIAPEWKVYYLCRNLILSKKIFQKNGVYSNSAIAIRILKYILILPWQRQKYSYMKF

ILRGISHGIKGISGKYH

>lcl|NZ\_FO834906.1\_prot\_WP\_004890861.1\_3774 [gene=rfbD] [locus\_tag=BN49\_RS20520] [protein=UDP-galactopyranose mutase] [protein\_id=WP\_004890861.1] [location=complement(3885348..3886502)] [gbkey=CDS]

MKRKKILIVGAGFSGAVIGRQLAEKGHQVHIIDQRDHIGGNSYDARDSETNVMVHVYGPHIFHTDNETVW

NYVNKHAEMMPYVNRVKATVNGQVFSLPINLHTINQFFSKTCSPDEARALIAEKGDSTIADPQTFEEQAL

RFIGKELYEAFFKGYTIKQWGMQPSELPASILKRLPVRFNYDDNYFNHKFQGMPKCGYTQMIKSILNHEN

IKVDLQREFIVDERTHYDHVFYSGPLDAFYGYQYGRLGYRTLDFKKFIYQGDYQGCAVMNYCSVDVPYTR

ITEHKYFSPWEQHDGSVCYKEYSRACEENDIPYYPIRQMGEMALLEKYLSLAENETNITFVGRLGTYRYL

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043637.1\_3775 [locus\_tag=BN49\_RS20525] [protein=DUF4422 domain-containing protein] [protein\_id=WP\_046043637.1] [location=complement(3886518..3888413)] [gbkey=CDS]

MNNSVKIYTSHHKPSAFLNAAIIKPLHVGKANSCNEIGCPGDDTGDNISFKNPFYCELTAHYWVWKNEEL

ADYVGFMHYRRHLNFSEKQTFSEDTWGVVNHPYIDEEYEKIFGLNEETIQRCVEGIDILLPKKWSVTAAG

SKNNYDHYERGEYLHIRDYQAAIAIVEKLYPEYSAAIKTFNDASDGYYTNMFVMRKDIFVDYSEWLFSIL

DNLEDAISMNNYNAQEKRVIGHIAERLFNIYIIKLQQDGELKVKELQRTFVSNETFNGALNPVFDSAVPV

VISFDDNYAVSGGALINSIVRHADKNKNYDIVVLENKVSYLNKTRLVNLTSAHPNISLRFFDVNAFTEIN

GVHTRAHFSASTYARLFIPQLFRRYDKVVFIDSDTVVKADLGELLDVPLGNNLVAAVKDIVMEGFVKFSA

MSASDDGVMPAGEYLQKTLNMNNPDEYFQAGIIVFNVKQMVEENTFAELMRVLKAKKYWFLDQDIMNKVF

YSRVTFLPLEWNVYHGNGNTDDFFPNLKFATYMKFLAARKKPKMIHYAGENKPWNTEKVDFYDDFIENIA

NTPWEMEIYKRQMSLAASIGLTHSEPQQQILFQTKIKNVLMPYVNKYAPIGTPRRNMMTKYYYKVRRAIL

G

>lcl|NZ\_FO834906.1\_prot\_WP\_004175264.1\_3776 [gene=rfbB] [locus\_tag=BN49\_RS20530] [protein=O-antigen export ABC transporter ATP-binding protein RfbB] [protein\_id=WP\_004175264.1] [location=complement(3888429..3889169)] [gbkey=CDS]

MHPVINFSHVTKEYPLYHHIGSGIKDLIFHPKRAFQLLKGRKYLAIEDVSFTVGKGEAVALIGRNGAGKS

TSLGLVAGVIKPTKGTVTTEGRVASMLELGGGFHPELTGRENIYLNATLLGLRRKEVQQRMERIIEFSEL

GEFIDEPIRVYSSGMLAKLGFSVISQVEPDILIIDEVLAVGDIAFQAKCIQTIRDFKKRGVTILFVSHNM

SDVEKICDRVIWIENHRLREVGSAERIIELYKQAMA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912373.1\_3777 [gene=rfbA] [locus\_tag=BN49\_RS20535] [protein=O-antigen export ABC transporter permease RfbA] [protein\_id=WP\_002912373.1] [location=complement(3889169..3889936)] [gbkey=CDS]

MKYNLGYLFDLLVVITNKDLKVRYKSSMLGYLWSVANPLLFAMIYYFIFKLVMRVQIPNYTVFLITGLFP

WQWFASSATNSLFSFIANAQIIKKTVFPRSVIPLSNVMMEGLHFLCTIPVIVVFLFVYGMTPSLSWVWGI

PLIAIGQVIFTFGVSIIFSTLNLFFRDLERFVSLGIMLMFYCTPILYASDMIPEKFSWIITYNPLASMIL

SWRDLFMNGTLNYEYISILYFTGIILTVVGLSIFNKLKYRFAEIL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529644.1\_3778 [locus\_tag=BN49\_RS20540] [protein=NAD-dependent epimerase] [protein\_id=WP\_016529644.1] [location=3890982..3891986] [gbkey=CDS]

MKFLITGAAGFIGFHIAQRLLNEGHDVVGIDNMNDYYDVSLKQARLDRLASPAFHFQQLDLADREGMAKL

FATEQFDRVIHLAAQAGVRYSLENPYAYADANLMGYLNILEGCRHTKVKHLVYASSSSVYGLNRKMPFST

EDSVDHPVSLYAATKKANELMAHTYSHLYGIPTTGLRFFTVYGPWGRPDMALFKFTKAMLEGKSIDVYNY

GKMKRDFTYIDDIVEAVVRVQDVIPQANANWTVESGSPATSSAPYRVYNIGNSSPVELMDYITALEEALG

MEAQKNMMPIQLGDVLDTSADPQPLYDLVGFKPQTSVKEGVKNFVEWYKDYYQI

>lcl|NZ\_FO834906.1\_prot\_WP\_004144151.1\_3779 [locus\_tag=BN49\_RS30740] [protein=small membrane protein] [protein\_id=WP\_004144151.1] [location=3892386..3892508] [gbkey=CDS]

MENLFFLVVAAILLAVSVYFLISYLKDRKKTKLTFNKRKW

>lcl|NZ\_FO834906.1\_prot\_WP\_009484573.1\_3780 [gene=ugd] [locus\_tag=BN49\_RS20555] [protein=UDP-glucose 6-dehydrogenase] [protein\_id=WP\_009484573.1] [location=complement(3892931..3894097)] [gbkey=CDS]

MKITISGTGYVGLSNGILIAQNHEVVALDIVQAKVDMLNQKISPIVDKEIQEYLAEKPLNFRATTDKHDA

YRNADYVIIATPTDYDPKTNYFNTSTVEAVIRDVTEINPNAVMIIKSTIPVGFTRDIKERLGIDNVIFSP

EFLREGRALYDNLHPSRIVIGERSARAERFADLLKEGAIKQDIPTLFTDSTEAEAIKLFANTYLALRVAY

FNELDSYAESQGLNSKQIIEGVCLDPRIGNHYNNPSFGYGGYCLPKDTKQLLANYESVPNNIIAAIVDAN

RTRKDFIADSILARKPKVVGVYRLIMKSGSDNFRASSIQGIMKRIKAKGIPVIIYEPVMQEDEFFNSRVV

RDLNAFKQEADVIISNRMAEELADVADKVYTRDLFGND

>lcl|NZ\_FO834906.1\_prot\_WP\_004899416.1\_3781 [gene=rfbK1] [locus\_tag=BN49\_RS20560] [protein=O9 family phosphomannomutase RfbK1] [protein\_id=WP\_004899416.1] [location=complement(3894261..3895631)] [gbkey=CDS]

MTQLTCFKAYDIRGELGEELNEDIAYRIGRAYGEFLKPGKIVVGGDVRLTSESLKLALARGLMDAGTDVL

DIGLSGTEEIYFATFHLGVDGGIEVTASHNPMNYNGMKLVRENAKPISGDTGLRDIQRLAEENQFPPVDP

ARRGTLRQISVLKEYVDHLMGYVDLANFTRPLKLVVNSGNGAAGHVIDEVEKRFAAAGAPVTFIKVHHQP

DGHFPNGIPNPLLPECRQDTADAVRAHQADMGIAFDGDFDRCFLFDDEASFIEGYYIVGLLAEAFLQKQP

GAKIIHDPRLTWNTVDIVTRSGGQPVMSKTGHAFIKERMRQEDAIYGGEMSAHHYFRDFAYCDSGMIPWL

LVAELLCLKNSSLKSLVADRQAAFPASGEINRKLGNAAEAIARIRAQYEPAAAHIDTTDGISIEYPEWRF

NLRTSNTEPVVRLNVESRADTALMNAKTEEILALLK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529407.1\_3782 [locus\_tag=BN49\_RS20565] [protein=mannose-1-phosphate guanylyltransferase/mannose-6-phosphate isomerase] [protein\_id=WP\_016529407.1] [location=complement(3895654..3897069)] [gbkey=CDS]

MLLPVIMAGGTGSRLWPMSRELYPKQFLRLYGQNSMLQETITRLSGLEIHEPMVICNEEHRFLVAEQLRQ

LNKLSNNIILEPVGRNTAPAIALASLQATRHGDDPLMLVLAADHIINNQPVFHDAIRVAEQYADEGHLVT

FGIVPNAPETGYGYIQRGVALTDSAHTPYQVARFVEKPDRERAEAYLASGEYYWNSGMFMFRAKKYLSEL

AKFRPDILEACQVAVNAADNGSDFISIPHDIFCECPDESVDYAVMEKTADAVVVGLDADWSDVGSWSALW

EVSPKDGQGNVLSGDAWVHNSENCYINSDEKLVAAIGVENLVIVSTKDAVLVMNRERSQDVKKAVEFLKQ

NQRSEYKRHREIYRPWGRCDVVVQTPRFNVNRITVKPGGAFSMQMHHHRAEHWVILAGTGQVTVNGKQFL

LTENQSTFIPIGAEHSLENPGRIPLEVLEIQSGSYLGEDDIIRIKDQYGRC

>lcl|NZ\_FO834906.1\_prot\_WP\_004899420.1\_3783 [gene=gndA] [locus\_tag=BN49\_RS20570] [protein=NADP-dependent phosphogluconate dehydrogenase] [protein\_id=WP\_004899420.1] [location=complement(3897312..3898718)] [gbkey=CDS]

MSKQQIGVVGMAVMGRNLALNIESRGYTVSVFNRSREKTEEVIAENPGKKLVPYYTVQEFVESLETPRRI

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MPGGQKEAYELVAPILKHIAAVAEDGEPCVTYIGADGAGHYVKMVHNGIEYGDMQLIAEAYALLKGGLAL

SNEELAQTFTEWNEGELSSYLIDITKDIFTKKDEEGKYLVDVILDEAANKGTGKWTSQSSLDLGEPLSLI

TESVFARYISSLKDQRVAASKVLSGPQAQPAGDKAEFIEKVRRALYLGKIVSYAQGFSQLRAASDEYNWD

LNYGEIAKIFRAGCIIRAQFLQKITDAYAQNAGIANLLLAPYFKQIADDYQQALRDVVAYAVQNGIPVPT

FSAAIAYYDSYRSAVLPANLIQAQRDYFGAHTYKRTDKEGVFHTEWLE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529410.1\_3784 [gene=wcaJ] [locus\_tag=BN49\_RS20575] [protein=undecaprenyl-phosphate glucose phosphotransferase] [protein\_id=WP\_016529410.1] [location=complement(3898882..3900279)] [gbkey=CDS]

MTISQHRFRSNANASIISMLQRFSDILIIFLGIYFSCFINDYFFNLHYVLMALVALVVFQMIGGITDFYR

SWRGVEFSVELILILKNWSLSFLLTLGFVTLFSDFDLTFRTFIFWYLAVCAGFVVTRSLIRALAGFFRRI

GYNKRRVAFAGSLPAGISLLETFRKQPWLGFEVKGIYEDSFSGTYDLELYVGKISDLINEARKGTIDRIY

IAMHMRDEVAIKNMVSQLTDTTCSVLYIPDVFTFNILQSRTEEINGVPVVPLFDSPLNGINMVFKRLEDI

IVSSLILILISPILLVIATAVKTTSKGPVIFRQVRYGMDGKPIKVWKFRSMTVMENDDKVIQATKNDIRV

TKVGKFLRSTSLDELPQFFNVLFGQMSVVGPRPHAVSHNEQYRSLIQGYMLRHKVKPGITGLAQINGWRG

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>lcl|NZ\_FO834906.1\_prot\_WP\_227504834.1\_3785 [locus\_tag=BN49\_RS29420] [protein=acyltransferase] [protein\_id=WP\_227504834.1] [location=complement(3900357..3900884)] [gbkey=CDS]

MKIKNIKNIKFHKNSNLIVGLSNVSHVNNNSICYINNRGEMHVSGNVFIAKSVRVDIADSSKIILNDCYI

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VVASHSVVNGVFLEKNCLIAGVPARVIKRNISWQH

>lcl|NZ\_FO834906.1\_prot\_WP\_071829961.1\_3786 [locus\_tag=BN49\_RS29425] [protein=hypothetical protein] [protein\_id=WP\_071829961.1] [location=complement(3901048..3902787)] [gbkey=CDS]

MKLLMSKRYFLKKLIPSLTLFPVLTSYASSNKDVIESPQSKRYTIESIKQYISLFIGECVFISGQEATQD

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CLPLKFIPGHIYQVKKTYEIDVSKTSWFSSDLSTLKWFNDFNADFAIRLFSSQKDYSKRFQNVKVAIKSI

AIIGAGIKNLLDSCAIKIGGDERNSSLFTIDSVSIQGWRTTLAFDNNSWRIKFCDCHFLWGNIIAPPGNK

NSGECMVFDNCMFADNRSYTELHYGDWFFSKCSFDNHEVKLFGDANVFINQSHMENPGRKTTDFTIVSIN

SINSFASVIDSFIFISPTPKIINTPLFYVISDNENGLYVRNLRFQATENYNPSKGTENALVLVGGDGKSY

LENVRVSLNNKSYLALNKNDSSVLMNSRFKDGLRYWDFNDGVSLQARISSNDSETIVFSKNGASLSQSVL

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SFGQSVDVKLSTILMDIIS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043642.1\_3787 [locus\_tag=BN49\_RS20585] [protein=MOP flippase family protein] [protein\_id=WP\_046043642.1] [location=complement(3902818..3904275)] [gbkey=CDS]

MSLKLKTIKSTKWSALSSLTIIVLGFLQMVILSRILEPFEFGVLSIMIVVFLFTDMLADCGLSNAIIQKK

NITLDELSALYWVNIFLGVFLFVVTIILSYEISSWMRLDRLSFLIQLTALVFIIMPHGQQYRALMQKELE

FDILSKIESFSYLTGFCLTVIIGIITKNASCAVFGYLLTVSMRTVILSFVGRKYYHPTWKRSKLREIKKQ

LLFSFYLTLDSILNYINSSITTPIVARVLGAIYVGGYNLSFNVAVNPPSKISPIITRVLFPALSKIQDDK

ERLRINFFKLLHVISYINFPALLGLCIIAKDFVYLVFGEKWLFIVPTLQLLCIAGAMRMVANPIGSLLMA

KAKMELSVRFNFVKIIIFIPVLYFSTIWNGMVGAAIGFLICQAINALLSYFFLLKPVLGNCIVDYINSFF

IPFVHTLPMILLLLVCDNYIDKISLTFFILKIVIGGGVYILTIIISPNKLLAEMKGLFRQLLLKR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043644.1\_3788 [locus\_tag=BN49\_RS20590] [protein=O-antigen ligase family protein] [protein\_id=WP\_046043644.1] [location=complement(3904293..3905537)] [gbkey=CDS]

MHNIIRLLFRNPFFFLFCLFIPFDNTSLQSIGGIMTASPSALILLPGLFVSILSKGLKVNKNILLCFFGV

LLISFLYYFYWVFYFPELDPIFILDRGSRYFLLYVFYFLALYYSLRQNIKDIRAGAALIIIVDIFSVLLN

YLDPAIINNKSIIQYNDFISPERLRGFSLEASVFGYQIVCSILLLAVLLNWSTFFLVTVTIVIAILTTSK

GAALSFLICICFYFSLKGKLMFRVLLSLCSIVISYIIFKYYFLDALASDIDTYSSVATRGTMFIVGLKIF

LFNPLGVGFFGYLPSIYDFTSGVIDFIKSHFPFLNFDEVYTYTIPGEYKTVGTKSLILDLLIIYGVFFLI

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>lcl|NZ\_FO834906.1\_prot\_WP\_004180514.1\_3789 [locus\_tag=BN49\_RS20595] [protein=glycosyltransferase] [protein\_id=WP\_004180514.1] [location=complement(3905539..3906705)] [gbkey=CDS]

MAKIIVVSTDCPYPANHGGRLDILMRLELLSSTGHDVDLIVTYKEEIDEASKQYLERICKNVYYAQRLGM

IRSAFNDMLKFLPLQVKSRSRLREIKLNKKYDYVLCESEYVYSILKNSTLDAKNKLLRVHNDEVVYYKAL

FNDEKSIFKKIYYFYEMLAFKYNKKDINSSFDKLLFISKDECDKESKGIWLPSHIPVMHPFKYDKFDLHN

CNVLFVGNLFMPNNLQGLIWYLNKVHPMVIKENPDIKLTIAGNAKNGISEELKKAISIYDGNAINLITSP

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>lcl|NZ\_FO834906.1\_prot\_WP\_042941590.1\_3790 [locus\_tag=BN49\_RS20600] [protein=glycosyltransferase family 4 protein] [protein\_id=WP\_042941590.1] [location=complement(3906711..3907832)] [gbkey=CDS]

MNIILVNTLYYPYKIGGAEVSVQILAESLIEKGHSVTVVSIHEHNERKDTEHNGVKIIYLPYSNIYWGLS

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IHPNCKLYKNGSEMSVKSIAVSLWSLSKKILGKNVDVYVGISNYIKDKHIEAGFFKSTEKYTIYNSVKSN

VILDLTAANDKRLGFIGRLTYEKGFDQFCKLAQLNKTKKFIAAGEFDKNSASLKQLALDSNVELLGYCPV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004180517.1\_3791 [locus\_tag=BN49\_RS20605] [protein=glycosyltransferase] [protein\_id=WP\_004180517.1] [location=complement(3907862..3908938)] [gbkey=CDS]

MNVIHIAETVKGGVATVINNLTENNEIDSHVICPESQSKEIYCAQKTLFSRTGRNISSLSSLFLVIIKTL

KYNKFDVIHLHSSFAGFIVRALFAFKLINKKKYKVIYTPHCFSFIMDTKKWKKKAYIYIERILAKQTDCI

IANSYYEYKCAVDAGISKNKIKVVYNAVSLDGQEKLERIKKCNENEVQKEKINILFVGRFDKQKGYDYLL

NVIKVADVSKYTFNIIGDSVHDVFEKIEKENVVYYGWVDNKELPAYFCENDVLLMPSRWESFGLVAVEAQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043646.1\_3792 [locus\_tag=BN49\_RS20610] [protein=polysaccharide biosynthesis tyrosine autokinase] [protein\_id=WP\_046043646.1] [location=complement(3908998..3911166)] [gbkey=CDS]

MTSISKKKQPETVDDLDFGRMVGELIDHRKIIIALTSFATLIALLYAFFATPIYKADALIQVEQKQANAI

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VSSSIGDEENPPEFTLKVKDSNRYVIEFGGEEINGKVGELIEKDGITLKIDEINAKPGAEFTIKYVSKLK

AIADLQENLSVADQGKDTGILILSYLGDDPLKIKNIVDSISENYLAQNISRQAAQDEKSLEFLNKQLPMV

RSDLDSAEDKLNDFRKRNDSVDLSLEAKSVLDQIVNVDNQLNELTFRESEISQLYTKEHPTYKALMEKRK

TLQDERGKLNKRVATMPETQQEILRLSRDVESGRAVYMQLLNRQQELNIAKSSAIGNVRIIDSAVTQHKP

VKPKKIIVVLAGLFIGLVISVSLVLVRILLRKGIETPEQLEELGINVYASIPVSESNPKNVIAKRLNKRD

DSRPKVLLATENPADLAIEAMRGLRTSLHFAMLEARNNLLMISGASPNAGKTFVSSNLSSVISQTGKKVI

FIDADLRKGYTHKLFNIKNTNGLSDYLSGRVALDKIINNLQTEGFDYISRGSVPPNPAELLMHNRLAELL

EWANKSYDIVILDTPPILAVADAAIIGNYVGTTLLVARFEENTPKEIDISVKRFQNSGVNIKGCILNGVV

KKASNKYGYGYNYYDYSYSDKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004213675.1\_3793 [locus\_tag=BN49\_RS29430] [protein=protein-tyrosine-phosphatase] [protein\_id=WP\_004213675.1] [location=complement(3911185..3911619)] [gbkey=CDS]

MFSTILIVCTGNICRSPIGERYLQQLLPSKNISSAGTQALVDHEADQSAVEVARKNGISLAGHLGRQFTS

KLSKEYELILVMEKNHIEQISNIAPEARGKTMLFGHWLEQRDIPDPYRKSEEAFASVFKLIEQSALLWAE

KLKA

>lcl|NZ\_FO834906.1\_prot\_WP\_004180522.1\_3794 [locus\_tag=BN49\_RS20615] [protein=polysaccharide export protein] [protein\_id=WP\_004180522.1] [location=complement(3911621..3912757)] [gbkey=CDS]

MKKKIVRFSALALAIGFLSGCTIVPGQGLNSLRKNVVELPDSDYDLDKLVNVYPMTPGLIDQLRPETILA

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LSQVRQDIASRLTTYIESPQVDVSVAAFRSQKAYVTGEVAKSGQQPITNIPLTVMDAINAAGGLAPDADW

RNVVLTHNGKDTKVSLYALMQKGDLTQNHLLYPGDILFVPRNDDLKVFVMGEVGKQSTLKMDRSGMTIAE

ALGNAEGMSQAFSDATGVFVIRQLKGDKQGKIANIYQLNAQDASAMVLGTEFQLQPYDIVYVTTAPLVRW

NRVISQLVPTITGVHDMTETAKFIKDWP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529750.1\_3795 [locus\_tag=BN49\_RS20620] [protein=capsule assembly Wzi family protein] [protein\_id=WP\_016529750.1] [location=complement(3912903..3914336)] [gbkey=CDS]

MIKIARIAMTLGLLTSLGAKAYAAGLVVNDNDLRNDLAWLSDRGVIHLSLSTWPLSQEEIARALKKAKPS

YSSEQVVLARINQRLSALKADFRFTGYTSTDQPGTPQGFGQTQPADNSLGLAFNNSGEWWDVHLQGNVEG

GERISNGSRFNANGAYGAVKFWNQWLSFGQVPQWWGPGYEGSLIRGDAMRPMTGFLMQRAEQAAPETWWL

RWVGPWQYQISASQMNQYTAVPHAKIIGGRFTFTPFQSLELGASRIMQWGGEGRPQSFSSFWDGFTGHDN

TGTDNEPGNQLAGFDFKFKLEPTLGWPVSFYGQMVGEDESGYLPSANMFLGGIEGHHGWGKDAVNWYVEA

HDTRTNMSRTNYSYTHHIYKDGYYQQGYPLGDAMGGDGQLFAGKVELITENNQRWSTRLAYAKVNPKDQS

INKAFPHSDTLKGVQLGWSGDVYQSVRLNTSLWYTNANNSDSDDVGASAGIEIPFSL

>lcl|NZ\_FO834906.1\_prot\_3796 [locus\_tag=BN49\_RS31535] [protein=hypothetical protein] [pseudo=true] [partial=5'] [location=<3914677..3914751] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529749.1\_3797 [locus\_tag=BN49\_RS20625] [protein=phosphatase PAP2 family protein] [protein\_id=WP\_016529749.1] [location=complement(3915298..3915927)] [gbkey=CDS]

MNWQLISFFGDSTVLLPSAAALFIVLMLRKTSRLLAWQWSLLFGITGAIVCASKLAFMGWGLGIRELDYT

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LFLVLQKRTPDPESVNISWDGVACLVMVPLILLHSGSKAPTQSLLGQIATAVGPLDKPFTRTDLHKQAW

>lcl|NZ\_FO834906.1\_prot\_3798 [gene=galF] [locus\_tag=BN49\_RS20630] [protein=GalU regulator GalF] [pseudo=true] [location=complement(3916243..3917216)] [gbkey=CDS]

MNMTNLKAVIPVAGLGMHMLPATKAIPKEMLPIVDKPMIQYIVDEIVAAGIKEIVLVTHSSKNAVENHFD

TSYELEALLEQRVKRQLLAEVQAICPPGVTIMNVRQAQPLGLGHSILCARPVVGDNPFVVVLPDIILDGG

TADPLRYNLAAMIARFNETGRSQVLAKRMPGDLSEYSVIQTKEPMVAEGQVARIVEFIEKPDEPQTLDSD

LMAVGRYVLSADIWAELERTEPGAWGRIQLTDAIAELAKKQSVDAMLMTGESYDCGKKMGYMQAFVTYGM

RNLKEGTKFRESIKKMLA\*QLA\*R\*AAGQSLSARRS\*RYAEIIH

>lcl|NZ\_FO834906.1\_prot\_WP\_002912435.1\_3799 [locus\_tag=BN49\_RS20635] [protein=TerC family protein] [protein\_id=WP\_002912435.1] [location=3917975..3919558] [gbkey=CDS]

MEWIADPSIWAGLVTLVVIELVLGIDNLVFIAILAEKLPPAQRDRARITGLMLAMVMRLLLLASISWLVT

LTKPLIVFHDFSFSARDLIMLFGGLFLLFKATVELNERLEGKDSDNPTQRKGAKFWAVVAQIVVLDAIFS

LDSVITAVGMVDHLAVMMAAVVIAISLMLMASKALTRFVNSHPTIVILCLSFLLMIGFSLIAEGFSFIIP

KGYLYAAIGFSVMIEALNQLAQFNRRRFLSANMTLRQRTTEAVMNLLSGQKEKAELDADTASLVADQDQH

PLFNPQERLMIERVLNLNQRSVSSIMTSRHDIERINLSAPEEEIRSLVEKNQHTRLVVTGGKDNEDLLGV

VHVIDLLQQSLRQEPLDLQALVRQPLVFPEGLPLLSALEQFRQARTHFAFVVDEFGSVEGIVTLSDVMET

IAGNLPNEVEEIDARHDIQHHQDGSWTVNGHMPLEDLVQYVPLPLDDKREYHTVAGLLMEYLQHVPQVGE

TIEIDGYTLRTLQVDSHRVQKVQIVPPAKQDELDYEV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043649.1\_3800 [gene=asmA] [locus\_tag=BN49\_RS20640] [protein=outer membrane assembly protein AsmA] [protein\_id=WP\_046043649.1] [location=complement(3919895..3921742)] [gbkey=CDS]

MRRILTTLMILLAVIVAGLTSLVLLVNPNDFRAYMVHEVAERSGYQLDLDGPLRWHVWPQLSILSGRMTL

TARGAEEPVIRADNMRLDVALLPLLSHQLQVKQVMLKGAVIQLTPKTEAVRDSSAPVVPHDNTLPLAPED

RGWSYDVRQLQVADSVLFFQHQNGEQVTVRDIRLQMEQDENHRATVDFSGRVNRDQRDLALNFSATVQGG

DYPHSLKADFTQLSWQLRGAELPPDGINGQGSLQASWQEDDKTLRFDNLNLMANRSTVTGSGSVVLGDRP

DWSLDLHATTLDLDSLLAQRSPATDSSASQQGQSQTRPLRPVIADSDEREDYQSLRGFNGRMALSADQLQ

WRGLNFTQVQSEISNQQGLLTVSKMQGNLDGGQLSLPGTLDARGDTPLATFQPALQNVEIGSLIKAFNYS

LNLTGKLSLSGEFSGTRIDADDFRRHWQGQAQLQMADTRTEGLNFQQLVQQAVERSTNVRAQENYDNATR

LDSVSSRLTLDNGLVTLNRLQGQSDVMAMTGEGQLDLQKENCDMRFNVRVLGGWKGEGKLIDRLKQTAIP

LRIYGEWQSLSYSLQVDQILRKQLQDEAKQRLNDWVERNKGSKDGNDAKKLLDKL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151145.1\_3801 [gene=dcd] [locus\_tag=BN49\_RS20645] [protein=dCTP deaminase] [protein\_id=WP\_004151145.1] [location=complement(3921773..3922354)] [gbkey=CDS]

MRLCDRDIEAWLDEGRLAINPRPPVERINGATVDVRLGNKFRTFRGHTAPFIDLSGPKAEVSAALDRVMS

EEIVLPEGEAFFLHPGELALAVTYESVTLPADLVGWLDGRSSLARLGLMVHVTAHRIDPGWSGCIVLEFY

NSGKLPLALRPGMPIGALSFEPLSGPAARPYNRREDAKYRDQQGAVASRIDKD

>lcl|NZ\_FO834906.1\_prot\_WP\_002912442.1\_3802 [gene=udk] [locus\_tag=BN49\_RS20650] [protein=uridine kinase] [protein\_id=WP\_002912442.1] [location=complement(3922445..3923086)] [gbkey=CDS]

MTDMSHQCVIVGIAGASASGKSLIASTLYRELREQVGDEHIGVIPEDSYYKDQSHLSMEERVKTNYDHPS

SMDHSLLFQHLQMLKSGQPIELPVYSYVEHTRTPNTIHVEPKKVIILEGILLLTDARLRNELNFSIFVDT

PLDICLMRRIKRDVNERGRSMDSVMAQYQKTVRPMFLQFIEPSKQYADIIVPRGGKNRIAIDILKAKISQ

FFE

>lcl|NZ\_FO834906.1\_prot\_WP\_023301766.1\_3803 [gene=alkA] [locus\_tag=BN49\_RS20655] [protein=DNA-3-methyladenine glycosylase 2] [protein\_id=WP\_023301766.1] [location=complement(3923201..3924049)] [gbkey=CDS]

MVLLPWTPPYDWAWMVGFLQARAVAGVERFDEGGYSRSFGVEGHRGLIHLAPDEEAQGLRVTLSPGLQPV

AEICYARIGQLFDLACDPRQVAGALGPLAEARPGLRLPGALDAFEQAVRAVLGQLVSVAMAARLTAKVAA

GWGEPLAEAPGYVLFPTPEALSRADPQALKALGMPLRRAEALIHLARAALSGELPLKAPADIDAGLRQLQ

SMPGIGRWTANYFALRGWQAKDIFLPDDYLIKQRFPGMTPAAIARYARRWQPMRSYALLHIWYTDDWIPA

AE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531337.1\_3804 [gene=yegD] [locus\_tag=BN49\_RS20660] [protein=molecular chaperone] [protein\_id=WP\_016531337.1] [location=3924187..3925539] [gbkey=CDS]

MFIGFDYGTANCSVAVMRENTPQLLTLENGSALLPSMLCAPTREAVSEWLYRHHDVPTHSDENQALLRRA

IAANRDEDIEVLRNSVQFGLASLHQYVEDPEEVYFVKSPKSFLGASGLKPQQVALFEDLVCAMMLHIKLQ

AESQLPEQIDQAVIGRPINFQGLGGDDANAQAQGILERAALRAGFRDVVFQFEPVAAGLDFEATLNEEKR

VLVVDIGGGTTDCSLLLMGPQWRERADRQQSLLGHSGCRIGGNDLDIALAFKCLMPLLGMGGETEKGTAL

PILPWWNAVAINDVPAQSDFYSTANGRLLNDLLRSARDADKVALLLKVWRQRLSYRLVRSAEESKIALSS

AASVETALPFIQDELATAIAQQGLEAALDQPLTRIMEQVQLALDSSQTTPDVIYLTGGSARSPLIKKALT

AQLPGIPLAGGDDFGSVTAGLARWAQVVFR

>lcl|NZ\_FO834906.1\_prot\_WP\_032429747.1\_3805 [locus\_tag=BN49\_RS20665] [protein=sensor histidine kinase] [protein\_id=WP\_032429747.1] [location=3925829..3927685] [gbkey=CDS]

MLLVAPQAQAATRQVGIDIPVQWYADASGQMTIDRFAALPIYQLATTRQIPSFGYSRKTWWLRSELPGTW

FAGEPRWLQLGPSFVDHLTIYYRPLGSDAPWAQRTFGDRDGARESDLHCRESVLILPPPPTAAGYEVVFR

LQSTSTLILLASLSSPQEFVQRATADTAFWSFYFGLAAVASGVALWLALALRRRLLWGICLFSLNYPLVA

ALHGFPEWFFGHAALPFQDFMISSLSLFSYATALWLHSEIFDLKKNMPRLHQLLIAAVVLNLVLQVSIPL

GFYGFAMQIEGVVFIIITPVLLFTSWWLWRKKAIDRTTLLLGLLPPFYVVAAVLVQLSIHGIIPFHMAIF

SLWQYALIVHIITVLIIAILRVRAENRQLEQKQRLARELQIEREASFHQRQFMGMVAHEFRTPLAVIQAA

LENLRLSAASTSQEARFDRIGRAATRLVQLTDNCLADARLASHDLHVERQQTALLTVINMAASVVAISHD

HYLNIRQHGAVESPQLQADAGLLCIAIANLLDNAVKYSPPGEIAIDIHSDAGQTELRIRDHGPGLPAGQA

ELIFERYRRGEHTSPVPGGTGLGLYVARQIVQAHDGKLWLAEHGPDGCTFILTLPTVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004899452.1\_3806 [locus\_tag=BN49\_RS20670] [protein=response regulator transcription factor] [protein\_id=WP\_004899452.1] [location=3927700..3928401] [gbkey=CDS]

MALRLAIIEDNADLLDELLAWLGYRGFEVWGTRSAEAFWRQLHSHPVDIVLVDIGLPGEDGFSVLNYLHE

LGHYGLVVVSARGQQQDKLQALSLGADAYLIKPVNFAHLAETLTALGARLRQDRPAAPPAEAIGTPPAVS

PGSWRLQEDKLISPDARTLELTQQEYRLVQLLMRNRNEVCSKLDLHACLFSHESEPDLHRIDVVVSRLRH

KARQQGIHLPVRAIFGKGLAFIS

>lcl|NZ\_FO834906.1\_prot\_WP\_032411492.1\_3807 [locus\_tag=BN49\_RS30745] [protein=small membrane protein] [protein\_id=WP\_032411492.1] [location=3928639..3928779] [gbkey=CDS]

MAMQTWLVLLLCIFFFSISVYSFISYLKDRRRLKLTFNDKRSMRRK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531112.1\_3808 [locus\_tag=BN49\_RS20680] [protein=positive transcription regulator] [protein\_id=WP\_016531112.1] [location=3928895..3929506] [gbkey=CDS]

MRNINVTINTRNAFVRESLVAMVNDLTRGDLRARFSWHNTDLSAEDIIICEVIPGEIYLCNTLIKNRKRG

SSLIILHSYDQLPEDEFMINCLKGVIFVSLKTASIPQLLTIIKSELQHCMAPTATDAAGRELSCASCPHR

VLSRSQTAVVHGILEGLDMSKIAALQRVSPRTAAYHKNKLMEKYSLNNNHEFFQFMNLLRERW

>lcl|NZ\_FO834906.1\_prot\_WP\_004149053.1\_3809 [locus\_tag=BN49\_RS20685] [protein=dicarboxylate/amino acid:cation symporter] [protein\_id=WP\_004149053.1] [location=complement(3929780..3931054)] [gbkey=CDS]

MANANKLTLFIVIFMLMGILSGAAIHAYATPTTVSAWADNITLLTDLFLRLIKMVIAPLVFSTLTVGIMR

LGETATIGRVGGKAMVWFITSSVLSILVGLVIVTFQHPGAGLNLAVPKEAVDTGLAVSGMSLKGFLSHTI

PTSITEAMANNEILQIVVFSMFFGIAGASLGEKFNAPLVAALNVVSHIMLKVTGYVMYVAPLAIFAAISS

VIASQGLGILLNYASFIGGYYLAVLLTSAVLIAVGYMVLKKEVFRLLNMLKDPVLVAFTTSSSEAAYPKT

LERLVKFGCSRNIVSFVLPIGYSFNLVGSMVYCSFAAMFIAQAYNVPLSFSEITVMMLTLMLASKGIAGV

PRSALVVLAATIPSFNIPVAGILLLMGIDHFLDMGRSAINVLGNGIATAMLSKNEGLLTDEEAQPDWEVE

KAEA

>lcl|NZ\_FO834906.1\_prot\_WP\_032439405.1\_3810 [locus\_tag=BN49\_RS20690] [protein=MdtA/MuxA family multidrug efflux RND transporter periplasmic adaptor subunit] [protein\_id=WP\_032439405.1] [location=3931355..3932593] [gbkey=CDS]

MKGSNIRRWGAALAVVIIAGAAYWFWHDRGTGGSGTPAAGQGPQGPGGARHGRFGAALAPVQAATATEEA

VPRYLTGLGTVTAANTVTVRSRVDGQLLSLHFQEGQQVKAGDLLAQIDPSQFKVALAQAQGQLAKDQATL

ANARRDLARYQQLVKTNLVSRQELDTQQSLVVESAGTVKADEAAVASAQLQLDWTRITAPIDGRVGLKQV

DIGNQISSGDTTGIVVLTQTHPIDVVFTLPESSIATVVQAQKAGKALSVEAWDRTNKQKISVGELLSLDN

QIDATTGTIKLKARFSNLDDALFPNQFVNARLLVDTQQNAVVIPAAALQMGNEGHFVWVLNDENKVSKHS

VTPGIQDSQKVVISAGLSAGDRVVTDGIDRLTEGAKVEVVTASSGEQAQPAPRQSGKHGARS

>lcl|NZ\_FO834906.1\_prot\_WP\_016531116.1\_3811 [locus\_tag=BN49\_RS20695] [protein=MdtB/MuxB family multidrug efflux RND transporter permease subunit] [protein\_id=WP\_016531116.1] [location=3932593..3935715] [gbkey=CDS]

MQVLPPGRTGGPSRLFIMRPVATTLLMVAILLAGIIGYRFLPVSALPEVDYPTIQVVTLYPGASPDVVTS

AITAPLERQFGQMSGLKQMSSQSSGGASVVTLQFQLTLPLDVAEQEVQAAINAATNLLPSDLPNPPIYSK

VNPADPPIMTLAVTSSAIPMTQVEDMVETRVAQKISQVSGVGLVTLAGGQRPAVRVKLNAQAIAALGLTS

ETVRTAITSANVNSAKGSLDGPARAVTLSANDQMQSAEDYRRLIIAYQNGAPIRLGDVASVEQGAENSWL

GAWANQQRAIVMNVQRQPGANIIDTADSIRQMLPQLTESLPKSVKVQVLSDRTTNIRASVRDTQFELMLA

IALVVMIIYLFLRNVPATIIPGVAVPLSLVGTFAVMVFLDFSINNLTLMALTIATGFVVDDAIVVIENIS

RYIEKGEKPLAAALKGAGEIGFTIISLTFSLIAVLIPLLFMGDIVGRLFREFAVTLAVAILISAVVSLTL

TPMMCARMLSHESLRKQNRFSQASERFFERVIAVYGRWLSRVLNHPWLTLGVALSTLALSIILWVFIPKG

FFPIQDNGIIQGTLQAPQSVSFASMAERQRQVASIILKDPAVESLTSFVGVDGTNPALNSARLQINLKPL

DERDDRVQTVISRLQQAVDGVPGVALYLQPTQDLTIDTTVSRTQYQFTLQANSLEALSTWVPPLLSRLQA

QPQLADVSSDWQDKGLAAYIKVDRDSASRLGISMADVDNALYNAFGQRLISTIYTQANQYRVVLEQDTEA

TPGLAALENIRLTSSDGGIVPLTAIATVEQRFTPLSVNHLDQFPVTTISFNVPDNYSLGEAVEAILAAEQ

SLDFPTDIRTQFQGSSLAFQSALGSTVWLVVAAVVAMYIVLGVLYESFIHPITILSTLPTAGVGALLALW

LAGSELDVIAIIGIILLIGIVKKNAIMMIDFALAAEREQGMPPREAIYQACLLRFRPILMTTLAALLGAL

PLMLSTGVGAELRRPLGIGMVGGLMLSQVLTLFTTPVIYLLFDRLSLHLKRRFPRQEEEA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043653.1\_3812 [gene=mdtC] [locus\_tag=BN49\_RS20700] [protein=multidrug efflux RND transporter permease subunit MdtC] [protein\_id=WP\_046043653.1] [location=3935716..3938793] [gbkey=CDS]

MKFFALFIYRPVATILISLAITLCGILGFRLLPVAPLPQVDFPVIMVSASLPGASPETMASSVATPLERS

LGRIAGVNEMTSSSSLGSTRIILEFNFDRDINGAARDVQAAINAAQSLLPSGMPSRPTYRKANPSDAPIM

ILTLTSDTYSQGELYDFASTQLAQTIAQIDGVGDVDVGGSSLPAVRVDLNPQALFNQGVSLDAVRTAISD

ANVRKPQGALEDSAHRWQVQTNDELKTAADYQPLIVHYQNGAAVRLGDVATVSDSVQDVRNAGMTNAKPA

ILLMIRKLPEANIIQTVDSIRARLPELQQTIPAAIDLQIAQDRSPTIRASLEEVEQTLVISVALVILVVF

LFLRSGRATLIPAVAVPVSLIGTFAAMYLCGFSLNNLSLMALTIATGFVVDDAIVVLENISRHLEAGMKP

LQAALQGSREVGFTVLSMSLSLVAVFLPLLLMGGLPGRLLREFAVTLSVAIGISLAVSLTLTPMMCGWLL

KSGKPHQPTRNRGFGRLLVAVQGGYGKSLKWVLKHSRLTGLVVLGTIALSVWLYISIPKTFFPEQDTGVL

MGGIQADQSISFQAMRGKLQDFMKIIREDPAVDNVTGFTGGSRVNSGMMFITLKPRDQRHETAQQVIDRL

RKKLANEPGANLFLMAVQDIRVGGRQSNASYQYTLLSDDLSALREWEPKIRKALAALPELADVNSDQQDN

GAEMDLVYDRDTMSRLGISVQDANNLLNNAFGQRQISTIYQPLNQYKVVMEVDPAYTQDVSALDKMFVIN

SDGKPIPLAYFAKWQPANAPLSVNHQGLSAASTISFNLPTGRSLSEASEAIDRAMTQLGVPSSVRGSFAG

TAQVFQKTMNAQVILILAAIATVYIVLGVLYESYVHPLTILSTLPSAGVGALLALEIFDAPFSLIALIGI

MLLIGIVKKNAIMMVDFALEAQRNGNLTPEEAIFQACLLRFRPIMMTTLAALFGALPLVLSGGDGSELRQ

PLGITIVGGLVMSQLLTLYTTPVVYLFFDRLRLRFSRHSSQPVSE

>lcl|NZ\_FO834906.1\_prot\_WP\_004149057.1\_3813 [locus\_tag=BN49\_RS20705] [protein=MFS transporter] [protein\_id=WP\_004149057.1] [location=3938795..3940210] [gbkey=CDS]

MTDLPASVRWQLWIVAFGFFMQSLDTTIVNTALPSMAKSLGESPLHMHMIIVSYVLTVAVMLPASGWLAD

RVGVRNIFFTAIVLFTAGSLFCAQASTLDQLVMARVLQGVGGAMMVPVGRLTVMKIVPRDQYMAAMTFVT

LPGQVGPLLGPALGGVLVEYASWHWIFLINIPVGIVGAIATLCLMPNYTMQTRRFDLSGFLLLAAGMATL

TLALDGQKGLGISPAWLAGLVAVGLCALLLYLWHARGNARALFSLNLFRNRTFSLGLGGSFAGRIGSGML

PFMTPVFLQIGLGFSPFHAGLMMIPMVLGSMGMKRIVVQVVNRFGYRRVLVASTLGLAAVSLLFMFSALA

GWYYVLPLVLFLQGMINASRFSSMNTLTLKDLPDDLASSGNSLLSMVMQLSMSIGVTIAGLLLGLYGQQH

MSLDAASTHQVFLYTYLSMAAIIALPALIFSRVPDDVGSNTVLRRRNRSGS

>lcl|NZ\_FO834906.1\_prot\_WP\_004149058.1\_3814 [gene=baeS] [locus\_tag=BN49\_RS20710] [protein=two-component system sensor histidine kinase BaeS] [protein\_id=WP\_004149058.1] [location=3940207..3941685] [gbkey=CDS]

MKFWRPGITGKLFLAIFATCIVLLISMHWAVRISFERGFIDYIKRGNEQRLTMLSDALSEQYAQHGSWAF

LRNNDRFIFQLLRTFERDNDDRSPPGHAMKPDAAPDGPPPDGPPDGPRPRPEMPPHGWRTMFWVVDQSGR

VLVGPRERVPEDGTQRSIVVNGAEVGKVIASPVERLTRNTDINFDRQQKRTSWLIVALATLLAALATFPL

ARGLLAPVKRLVEGTHKLAAGDFSTRVTVTGGDELGRLAQDFNQLASTLERNQQMRRDLMADISHELRTP

LAVLRGELEAIQDGVRRFTPESIPSLQAEVATLTKLVDDLHQLSMSDEGALAYQKTSLDIITLLEVAAGA

FRERFASRQLSIQVSLPEQAMIFGDRDRLMQLFNNLLENSLRYTDSGGSLHITARRSGRMLVIDFADSAP

GVSDEQLARLCERFYRAEGSRNRASGGSGLGLAICLNIVAAHGGTLRADHSPFGGVSIKVELPLEHDLPR

DV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529103.1\_3815 [gene=baeR] [locus\_tag=BN49\_RS20715] [protein=two-component system response regulator BaeR] [protein\_id=WP\_016529103.1] [location=3941682..3942404] [gbkey=CDS]

MTELPVDKNTPRILIVEDEPKLGQLLIDYLQAAGYAPALINHGDKVLPYVRQTPPHLILLDLMLPGTDGL

TLCREIRRFSDVPVVMVTAKIEEIDRLLGLEIGADDYICKPYSPREVVARVKTILRRCKPQRDLQTLDAQ

SPLIVDEGRFQASWRDKLLDLTPAEFRLLKTLSQEPGKVFSREQLLNHLYDDYRVVTDRTIDSHIKNLRR

KLEALDAEQSFIRAVYGVGYRWEADACRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529104.1\_3816 [gene=yegQ] [locus\_tag=BN49\_RS20720] [protein=tRNA 5-hydroxyuridine modification protein YegQ] [protein\_id=WP\_016529104.1] [location=3942723..3944084] [gbkey=CDS]

MFKPELLSPAGTLKNMRYAFAYGADAVYAGQPRYSLRVRNNEFNHENLQLGINEAHALGKKFYVVVNIAP

HNAKLKTFIRDLKPVVEMGPDALIMSDPGLIMLVREHFPEMPIHLSVQANAVNWATVKFWQLMGLTRVIL

SRELSLDEIEEIRRQVPEMEIEIFVHGALCMAYSGRCLLSGYINKRDPNQGTCTNACRWEYNVAEGKEDD

VGNIVHKYEPIPVQTVEPTLGIGAPTDKVFMIEEAKRPGEYMTAFEDEHGTYIMNSKDLRAIAHVERLTQ

MGVHSLKIEGRTKSFYYCARTAQVYRKAIDDAAAGKPFDTSLLETLEGLAHRGYTEGFLRRHTHDDYQNY

EYGYSLSERQQFVGEFTGERNGPLAAVAVKNKFSVGDSLELMTPQGNVNFTLEHMENGKGEAMPVAPGDG

YTVWLPVPDDLPLQYALLMRNFTGQTTRNPHGN

>lcl|NZ\_FO834906.1\_prot\_WP\_004151134.1\_3817 [gene=yegS] [locus\_tag=BN49\_RS20725] [protein=lipid kinase YegS] [protein\_id=WP\_004151134.1] [location=3944327..3945223] [gbkey=CDS]

MMSTFPASLLILNGKGANEPQLREAVNLLRDEGIDIHVRVTWEKGDAARFIDEALQLNVETVIAGGGDGT

INEVATALVERGGKMALGILPLGTANDFATSVGIPQDLASALKLAIVGRDVPIDIARVNDKTGFINMATG

GFGTRITTETPEKLKAALGGVSYLIHGLMRMDTLKPDRCEIRGENFHWQGDALVIGIGNGRQAGGGQQLC

PEALINDGLLHLRIFTGEELIPALFSTLANPENSPNIVDGVSSWFEITAPHEMTFNLDGEPLSGKTFRME

LLPAALRCRLPPDCPLLR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180550.1\_3818 [locus\_tag=BN49\_RS20730] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_004180550.1] [location=complement(3945465..3946238)] [gbkey=CDS]

MIEVQHLNLAFGEGEKRNQVLYDVSFHVKPGEIYGLVGESGSGKTTVLKCLAGLFTHWQGELTIDAQPLG

HEISRERCRQVQMVFQDPYGSLHPRHTIGDILEEPLQIHRINDRDRRINVLLDKVGLNRAFRERYPHQLS

GGQRQRVAIARALILEPQVLLLDEPTSALDVSVQAEILNLLAELQREAKLTYLMVTHDLGVIAHLCQKVA

VMQYGKILETLTVDALVSGQAQTAYTQMLVNASRQYTREMAREVAEY

>lcl|NZ\_FO834906.1\_prot\_WP\_042940510.1\_3819 [locus\_tag=BN49\_RS20735] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_042940510.1] [location=complement(3946249..3947112)] [gbkey=CDS]

MTSSIPVVNNAPLLDVRDLCVDFVNGSAVTHAVRGVSFQLGHEKLAIVGESGSGKSTVGRALLQLHPKKA

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LEMLEVVRIRQPERVYQLYPHEISGGQGQRIMIAMMLITDPELIIADEPTSALDVSVRLQVLGLLDDLVQ

SRGLGLIFISHDINLVRSFCDRVLVMYAGRVVESIAAKDLDHARHPYTQGLINSLPDMQHRRPILPVLQR

QASWFTD

>lcl|NZ\_FO834906.1\_prot\_WP\_004200464.1\_3820 [locus\_tag=BN49\_RS20740] [protein=ABC transporter permease] [protein\_id=WP\_004200464.1] [location=complement(3947084..3947989)] [gbkey=CDS]

MTVSLDSPLSGGAGEGRQRLQRAAARAVGFIGKMARNPLTAIGGGIIFMLLVVAIFAPLIAPYNPLVQDL

NSALVAPNAQHWFGTDEFGRDIFSRLVYGSRITLYIVLLVSVTVGPLGLLLGVSAGYFGGKVDMVLMRVT

DIFISFPSLVLALAFVAALGPGLEHVVIAITLTAWPPIARLARAETLSLRQADFISAVRLQGASSARVLW

RHIVPLCLPSVIIRITMNMAGIILTAAGLGFLGLGAQPPEPEWGAMISSGRTYMMECWWVVTIPGLAILI

NSLAFNFLGDGLRDILDPRSE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151133.1\_3821 [locus\_tag=BN49\_RS20745] [protein=ABC transporter permease] [protein\_id=WP\_004151133.1] [location=complement(3947986..3949023)] [gbkey=CDS]

MSTAILAPGSRGRRLSKRLLQVVITLFGLLLLTFTIGRVMPIDPVLAIVGPDADQSTYQQVYQQLGFDKS

LTTQFGIYFVNLLHGDLGNALLTGKPVVDDIIRVFPATMELATMAIIVGAGLGIPLGVLAAARRNSVSDY

VVRIISLAGYSTPIFWVGMMGLLVFYAWLGWVGGAGRVDLGLDGVVPRRTGLITVDALLAGNGQVFWNAI

NHLILPASLLGFHSLAYISRMTRSFMLAQLSQEFIITARVKGLTERQVIWNHAFRNILVQLLTVVALAYG

ALLEGAVLIETVFSWPGFGSYLTGSLLLGDMNAVMGCVLLVGVIFVMLNLLSDMLYQFFDPRTKS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529107.1\_3822 [locus\_tag=BN49\_RS20750] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016529107.1] [location=complement(3949020..3950642)] [gbkey=CDS]

MKKTSLLGACILALAMSMGSGEAVAKTPPDQLIIGMNMNNLLTLDPAAMTGNEVVGIVVNLYDSLVELDP

EQLTTVRPALAKSWDISPDGKTLTFHLRDDVKFHSGNPLTAADVVWSMRRILHLNLAQASVWKSYGFSKK

NIDSQVSAPDRFTVQIVLPKDNDPQLVIYSLAALGNLGVLDSKTVQSHQQDNDWGNRWLTTHEAGSGPFI

LETWQAKDVLRMKRNPDYWRGEAKMSRVVLRHFQESQTLRLMIEKGDLDIANNMAVSDINALRSDPQLTV

DAVQRGTMYYVAMSMKEAHFANPKVREAVRYLIDYQGINKALMPGYGVLHQRPIKAGMPSTLPDPGYRLD

VARAKKLLAEAGYPNGFDTTLRVLSDQPFLNIAIAVQSTLMQAGINAKIITGTGNQIYGAMRERKFDLLV

GRGGSGMEPHPHSSLRALVYNPDNSDKARLTNFQGWRTGFYDPQLNMMIDQALLERDPQKQVADYQAIQT

RYDQLVPALIPLSQMVDSVVVRNEVREYQPHPSATTFLRDVYKVREGEKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002912648.1\_3823 [locus\_tag=BN49\_RS20755] [protein=mandelate racemase family protein] [protein\_id=WP\_002912648.1] [location=complement(3950762..3951916)] [gbkey=CDS]

MKIESVNVTVFQYPTRRVSDSAGHSHPGVESMAKMAMLTITADDGAQGFSFAPPEVVRPFVVNTFFRKVL

VGQDPFNRERIWQDLNHWQRGSAHQLTERALSFVEQALWDLIGRSLKMPVYKLLGGYRDTVPAYGSTMCG

DDLPGGLSTPEEYAAFAEKLVARGYKAIKLHTWMPPISFAPNPKMDIKACAAVREAVGPDIDLMIDGYHW

YSRAEALWIGKELEKLNFAWFEEPMEEDSMSSYAWLAENLSIPIVGPESFGGKHHMRAEWVKAGACDILR

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DPMDDQGFVHLSQRPGLGEDINFAYIEANTVSHD

>lcl|NZ\_FO834906.1\_prot\_WP\_016529108.1\_3824 [locus\_tag=BN49\_RS20760] [protein=HAD-IA family hydrolase] [protein\_id=WP\_016529108.1] [location=complement(3952214..3952876)] [gbkey=CDS]

MSMQAVIFDMDGVIIDSEALWRQAQIDALAQWGATASVAECETLTKGKRLDDIAGTWCRYFQLDLAPQRL

EDAILQRITRLIAAKGEPMRGGQEALRYFREAGYKIALATSSSRQVIAAVLNKLSLWHFFDAISSADDEP

RGKPHPAVYLTTLRKLNLNASQCLVIEDSFTGFCAAQSAGIATIVIAEDSQHARFQAAAGRYQTLPELLE

ALSAEPAAAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529109.1\_3825 [gene=dalT] [locus\_tag=BN49\_RS20765] [protein=D-arabinitol transporter] [protein\_id=WP\_016529109.1] [location=complement(3952925..3954202)] [gbkey=CDS]

MSINNKQWLGLPLNLLWGYIAIAVFMTGDGFELAFLSHYIKALGFSPAEASFAFTLYGLAAALSAWISGV

VAEIITPLKTMMIGFVLWCVFHVLFLVFGLGHANYALILLFYGIRGFAYPLFLYSFIVAIVHNVKSDNAS

SAIGWFWAVYSIGIGVFGSYIPSFTIPHIGEMGTLWLALAFCLTGGVIALVSLRHIQTPQHMQNLTTREK

FSELGRAATLLYTNRNILLSSMVRIINTLSLFGFAVIMPMMFVDELGFSTSEWLQVWAVFFFTTIFSNVL

WGILGEKLGWMKVVRWFGCIGMALSSLAFYYIPQHFGHSFAMALIPAIALGIFVAAFVPLAAVFPALEPK

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QVEYS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043658.1\_3826 [gene=xylB] [locus\_tag=BN49\_RS20770] [protein=xylulokinase] [protein\_id=WP\_046043658.1] [location=complement(3954273..3955736)] [gbkey=CDS]

MYLGIDLGTSEVKALVIDENHEVIASHSAPLSIQRPHPHWSEQAPELWWEATEYLMATLREKCAQHWPAI

KAIGLSGQMHGAVLLDAEGKAIRPAILWNDTRCAAECAELEAMAPELHQVAGNLAMPGFTAPKLLWVRRH

EPQHFQRTATVLLPKDYLRYRMTGKKVSDMSDAAGTLWLDVAKRDWSDALLDKCGLSRSQMPKLVEGCEV

SATLDPQVAARWGLNASVMVAGGGGDNAVSAIGVGAVSPGDAFISLGTSGVLFVVTDAYRPAPQSAVHAF

CHVLPNLWHQMSVMLSAASCLQWFCRLTGTTEVALLAEIAELSEEDKANAPFFLPYLSGERTPHNDPDAR

GIFWGMTHASLRAQLGYAVLEGVSFGINDGLQALKESGTPIAQCSLVGGGARSPFWAQLLADILAMPVVT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530934.1\_3827 [locus\_tag=BN49\_RS20775] [protein=mannitol dehydrogenase family protein] [protein\_id=WP\_016530934.1] [location=complement(3955746..3957113)] [gbkey=CDS]

MNNQFTWLHIGLGSFHRAHQAWYLHRLIASGDNRWRIAAGNIRNDAEQVVQALAAQGGRYVLETVSPEGE

REYEEITSIQKLLPWQTGLQPLINEGANPQTKVIAFTVTEGGYYLNTRHQLETSNPDLQADLQGECKTIY

GTLARILEKRMADNAGPLTLLNCDNVRHNGERFHDGMVEFLQLTGKQAVIDWMAANTTCPNTMVDRITPR

PAADLPARIKAQTGIDDKAPVMGETFIQWVVENNFRDTRPNLEAVGVEMVESVIPYEEAKIRILNASHSC

IAWAGTLIGQQYIHESTLTDVIYAIADRYVTEDVIPCLGNNGIDLPTYRDVVLKRFTNPYIQDTNQRVAA

DGFSKIPAMIAPTLQECYQRGVRPEATAMLPALFFVFMEQWHKGTLPYQYQDGILDAQAVHEMFEAQDPV

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>lcl|NZ\_FO834906.1\_prot\_WP\_004144198.1\_3828 [locus\_tag=BN49\_RS20780] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_004144198.1] [location=3957320..3958261] [gbkey=CDS]

MSKEDDIRLDQKVRAAWMYYIAGQNQSEIASQLGTSRPVVQRLIAAAKEEGIVSINLHHPVANCLDYAQL

LQEKYRLIECNVVPAFSEESTLDSVSFGCYQLMARYLQDDKEKIIGLGSGLTLKKALQRIDFDSLNTRCV

ALISAMNADGQCNYYDDVPLLLTRKIKAKYYQWPAPRYAQSADEYEMWCTNRLFRSVSGVAREADVIFVG

IGPLGTQSPIFKDGFINQAQMDELTARGGIGEILGRFIDAQGDVVDSEINRMITSYDIRQSHCPRIAAAC

GEHKRPAILAALKGGWINGLVTDEHTARWLLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530935.1\_3829 [locus\_tag=BN49\_RS20785] [protein=LacI family DNA-binding transcriptional regulator] [protein\_id=WP\_016530935.1] [location=complement(3958284..3959285)] [gbkey=CDS]

MKKITIYDLAELSGVSASAVSAILNGNWKKRRISAKLAEKVTRIAEEQGYAINRQASMLRSKKSHVIGMI

IPKYDNRYFGSIAERFEEMARERGLLPIITCTRRRPELEIEAVKAMLSWQVDWVVATGATNPDKISALCQ

QAGVPTVNLDLPGSLSPSVISDNYGGAKALTHKILANSARRRGELAPLTFIGGRSSDHNTSERLRGFHDA

HRELGLSVPQANILAPGYSKGHVEACLQERFSSEKTLLQGIFVNSTISLEGVVRWLSQVGLTGSEQPPMG

CFDWDPFVYLLGHDIDMVQQDVPAMLDSVFSIIDAGEASQQRIEIPPRLMSSS

>lcl|NZ\_FO834906.1\_prot\_WP\_004180592.1\_3830 [locus\_tag=BN49\_RS20790] [protein=SDR family oxidoreductase] [protein\_id=WP\_004180592.1] [location=3959540..3960289] [gbkey=CDS]

MNHSVSSMNTSLSGKVAAITGAASGIGLECARTLLGAGAKVVLIDREGEKLNKLVAELGENAFALQVDLM

QADQVDNLLQGILQLTGRLDIFHANAGAYIGGPVAEGDPDVWDRVLHLNINAAFRCVRSVLPHLIAQKSG

DIIFTSSIAGVVPVIWEPVYTASKFAVQAFVHTTRRQVAQYGVRVGAVLPGPVVTALLDDWPKAKMDEAL

ANGSLMQPIEVAESVLFMVTRSKNVTVRDIVILPNSVDL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043660.1\_3831 [locus\_tag=BN49\_RS20795] [protein=FGGY-family carbohydrate kinase] [protein\_id=WP\_046043660.1] [location=3960316..3961923] [gbkey=CDS]

MQNDTQNIIGVDVGSGSVRAGVFNLRGELLAHATREITLFRSAGNKVEQSSREIWQAVCYCIKTAVASAG

VSPSSIAGIGFDATCSLVVIGDNDAPLAVGPSDDADRNIIVWMDHRATGQAEKINATGHPVLRYVGGKIS

PEMQTPKILWLKENRPHIYQQARHFFDLADYLTWRSTGDEARSVCTVTCKWTYLAHEQRWDAGYFRQIGL

AELADEDFVRIGQRIVDPGTPCGDGLCATAAEEMGLPIGTPVAVGMIDAHAGGIGTVGVLNGAVNNMAYV

FGTSSCTMTTTQEAVFVPGVWGPYYSAMVPGYWLSEGGQSAAGAAIDQLLSFHPAAAEAREQAKAAGVPL

PVWLADRVLTQVASPSEAVTLAAGLHVVPEFLGNRAPLADPHAKALIAGLGMERDLDNLTALYVAGLCGI

GYGLRQIIDAQRAYGIESENIVISGGAGQHPLVRQLLADACGVSIVSTASREPVLLGSAILGAVAGRVAA

SLPEAIKQFTQVDATYHSETAFSPLHQRRYAAYKALQQAGRLIRE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530940.1\_3832 [locus\_tag=BN49\_RS20800] [protein=RbtT/DalT/CsbX family MFS transporter] [protein\_id=WP\_016530940.1] [location=3962005..3963288] [gbkey=CDS]

MSVNNKQWYGLPLNLIWGYVAIAVFMTGDGFELAFLSHYIKALGFTPAQASFAFTLYGLAAALSAWVSGV

VAEIITPRKAMLIGFVLWCVFHVLFLVFGLGRANYALILLFYGIRGLAYPLFLYSFIVAIIHNVRSDSSS

SALGWFWAVYSVGIGVFGSYIPSFTIPHIGEMGTLWLALLFCATGGIIALVSMRHTETPRHMQNLTTREK

FAELGRAATLLYTNSSILFSSIVRIINTLSLFGFAVIMPMMFVDELGFTTSEWLQVWAAFFFTTIFSNVF

WGIVAEKMGWMKVIRWFGCIGMALSSLAFYYLPQHFGHNFAMALVPAIALGIFVAAFVPMAAVFPALEPN

HKGAAISVYNLSAGLSNFLAPAIAVVLLPYFSTIGVVIAYTALYILAFFLCPLIRVEQPGFTSDQHAKPF

TANAAES

>lcl|NZ\_FO834906.1\_prot\_WP\_002912704.1\_3833 [gene=fbaB] [locus\_tag=BN49\_RS20805] [protein=class I fructose-bisphosphate aldolase] [protein\_id=WP\_002912704.1] [location=complement(3963347..3964399)] [gbkey=CDS]

MTDITQLLGKDAESLLQHRCITIPSDQLYLPGADYVDRVMVDNNRPPAVLRNMQTLYNTGRLGGTGYLSI

LPVDQGVEHSAGASFAANPLYFDPKNIVELAIEAGCNCVASTYGVLASVSRRYAHRIPFLVKLNHNETLS

YPTEYDQTLYASVEQAFNMGAVAVGATIYFGSEQSRRQIEEISAAFERAHELGLVTVLWAYLRNSAFKKD

GVDYHVSADLTGQANHLAATIGADIVKQKMAENNGGYKAVNFGYTDDRVYSKLTSDNPIDLVRYQLANCY

MGRAGLINSGGAAGGETDLADAVRTAVINKRAGGMGLILGRKAFKKSMADGVKLINAVQDVYLDGKVTIA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912707.1\_3834 [gene=thiD] [locus\_tag=BN49\_RS20810] [protein=bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase] [protein\_id=WP\_002912707.1] [location=complement(3964547..3965347)] [gbkey=CDS]

MKRINALTIAGTDPSGGAGIQADLKTFSALGAYGCSAITALVAQNTRGVQSVYRIEPDFVAAQLDSVFSD

VRIDTTKIGMLAETDIVEAVAERLARYRVANVVLDTVMLAKSGDPLLSASAVETLRQRLLPQVSLITPNL

PEAAALLDAPHARNEREMLEQGRALLALGCGAVLMKGGHLDDAESPDWLFTREGEQRFTAPRVQTKNTHG

TGCTLSAALAALRPRHADWAATVIEAKAWLSAALAQADSLEVGHGIGPVHHFHAWW

>lcl|NZ\_FO834906.1\_prot\_WP\_012541053.1\_3835 [gene=thiM] [locus\_tag=BN49\_RS20815] [protein=hydroxyethylthiazole kinase] [protein\_id=WP\_012541053.1] [location=complement(3965344..3966117)] [gbkey=CDS]

MPELLNPAPVAHLRHLLRAHSPLVHCMTNDVVQTFTANVLLAVGASPAMVIDPREAAQFAAIADALLINV

GTLTEDRAVAMRAAVEHARQAGKPWTLDPVAVGALTVRTAFCHELLALQPAAIRGNASEILALAGMSAGG

RGVDTTDTAAAALPAAQALARRLATVVAVTGEVDYVTDGERVLSVAGGNPLMTRVVGTGCALSAVVAASA

ALPGDRLENVAAACGLMKQAGEIAARQGGPGSFIPAFLDALYQEVQG

>lcl|NZ\_FO834906.1\_prot\_WP\_004189084.1\_3836 [locus\_tag=BN49\_RS20825] [protein=universal stress protein] [protein\_id=WP\_004189084.1] [location=3966435..3966857] [gbkey=CDS]

MAVYHHALVLINSSQDGVPLLQHAARMAEENGMRITIAHISTDYRALNYVSDSLRDDRVSQEVIQAKALL

NELACTVSLPVDTLSLVTTRRFEDVETCVRQRQIDLIIAGHHNRLLGVLSSHSLEYINHLTVDVLIKHLP

>lcl|NZ\_FO834906.1\_prot\_WP\_019705226.1\_3837 [locus\_tag=BN49\_RS20830] [protein=LysR family transcriptional regulator] [protein\_id=WP\_019705226.1] [location=complement(3966854..3967768)] [gbkey=CDS]

MMNEPWQRLPALSLKQLQYFVTLAQLRHFTDTASRLAISQPALSSALRQIETVLGGKLVNRTAATVTLTE

LGAAILPHAQRILSVAQAAFSDMQQIVEAGGDGTVRIGLVPSVSSLLFPLLPQTLAEAFPRLRIEFHDQT

NDALIQALQRGEIDFGIGAIDSSLPAELLVYPLREDPFVAVLHRDDPLAAQAHLPWKQLVGRDIAVFSKG

NIQRLVAALVESHRLTLTTRYQVDYIETLYGLVRSRLAVAILPALYTTHLQDQALRVAHLQQPALARTVA

LMRGPQALPPLIEDCFSLLQAALR

>lcl|NZ\_FO834906.1\_prot\_WP\_032415250.1\_3838 [locus\_tag=BN49\_RS20835] [protein=amidohydrolase family protein] [protein\_id=WP\_032415250.1] [location=3967889..3969700] [gbkey=CDS]

MSSNAQVRRRAVQAARGESPFDLLLIDAQIIDMATGEIRPADVGIVGEMIASVHPRGSREDAHEVRSLAG

GYLSPGLMDTHVHLESSHLPPERYAEIVLTQGTTAVFWDPHELANVLGVAGVRYAVDASRHLPLQVMVAA

PSSVPSTPGLEMSGADFAGAEMETMLGWPEVRGVAEVMDMHGVLHGSERMQEIVQAGLNSGKLIEGHARG

LSGADLQAYLAAGVTSDHELTSADDALEKLRAGLTIEIRGSHPYLLPDIVAALKTLPHLSSQITVCTDDV

PPDMLLEKGGIIALLNLLIEHGLPAVDALRFATLNAAIRLQRHDLGLIAAGRRADLVVFDSLEKLVAREV

YIGGKLLARAGNLLTPIAPAAGVTPPRDTLQIAPLRADDFILRVQGIRHGIARLRHIRGARFTQWGEVEV

QVRDGIVQLPAGFSLIWVKHRHGRHQATPQIALLEGWGELRGAIATSYSHDSHNLVVLGRDANDMALAAN

QLIASGGGMALAQQGEILAHVAMPIAGMLSDLPAAELARQFRELRDLSSQVADWEPPYRVFKAIEGTCLA

CNAGPHLTDLGLTDGGSRQIVDPLIACREIPEPTDHNNNPQGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912743.1\_3839 [locus\_tag=BN49\_RS20840] [protein=NCS2 family permease] [protein\_id=WP\_002912743.1] [location=3969703..3971046] [gbkey=CDS]

MADNTLHSSARANWLERRFALRSRGGTLRTECLAGITGFLAAAYLLVVIPGLLAIGGMDKGAATTGTILV

FVVGSLLMAFYANLPFIVGPGIGGSVLVGVTLAGSEGIGWQTGLGIACWSGILFFLLTRFGLREVVTRSV

PQSIKLGLTASIGLFVAVLGFRNAGLVLANAKTNALMLGDFLAPGALVALCGLFLAIALQARKVPGAILW

AILCATLVGIPFGVTKLPTHFIDAPHSLAPVLGQVDLLGALNIAFLPFLFVFFASEFFSTMGTTLAVGGE

AGLLDEEGNMPQINRPFMVDSIAAALGPWVGIPAATALIESSAAAEAGGKTGLTALSAAVMFLLMLLFTP

VALMIPKEATAPALILIGLNMFSGLRKVDLANFTDGLPVLMMVMITLIANSFGTGIAGGLLFYIVIKAIA

GKWREIPIGLWVLAVPLVYYFATLVRH

>lcl|NZ\_FO834906.1\_prot\_WP\_004149074.1\_3840 [locus\_tag=BN49\_RS20845] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004149074.1] [location=complement(3971036..3971935)] [gbkey=CDS]

MFRLEDLTLFVRAAALGSFSDAAREAGQQPAQVSAAIKRLETILNIRLFARSTRSLRLTPEGETWLPYAT

QMLDTLEAGLQKIQTPDDEVRGMLQIAVPSDLGRNLLLTLFRDFRQRHPALRLRLLFSDQLTDVFKDPVD

VAFRYGNNDDASFISLPVAPENRRVLVASPEWIARHGEPQTLEELSQHNALIYILRGRPFDRWSLSLDGV

VQQQKVSGTVMSDDAEVIRRLAIAGEGIAYKSMLDVSDDLRAGRLRRLLPRYQGDVVPLNLICPHRKQLS

AAVRLLYEEVKSHCEGLNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912749.1\_3841 [locus\_tag=BN49\_RS20850] [protein=RcnB family protein] [protein\_id=WP\_002912749.1] [location=3972119..3972436] [gbkey=CDS]

MRKTKMMLLGVLLATAGASWTATAAGIDQYALKEFTADFTQFHIGDTVPAMYLTPEYNIKQWQQRNLPAP

DAGSHWTYMGGNYVLITDTEGKILKVYDGEIFYHR

>lcl|NZ\_FO834906.1\_prot\_WP\_021440469.1\_3842 [locus\_tag=BN49\_RS20855] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_021440469.1] [location=3972408..3972872] [gbkey=CDS]

MMARSSIIVDPRNLHVRPGEPADSPALRQIFLRARSLSWTWLPAAAWRLEDFDAATADEQLWVAECDGQP

VGFAAVWTADNFLHHLFVDPDWQGKHIGSALLAQVERTFTASGTLKCLMENKNALRFYQRHGWTIEAQGA

SPEGRYWLMRSPRP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529233.1\_3843 [gene=apbC] [locus\_tag=BN49\_RS20860] [protein=iron-sulfur cluster carrier protein ApbC] [protein\_id=WP\_016529233.1] [location=complement(3972869..3973978)] [gbkey=CDS]

MNSQSQAKSPERLRAMVAGTLANFQHPTLKHNLTALKALHHVAWLDDTVHIELQMPFVWSSAFEALKEQC

SAELLRITGAKAIDWKLTHSIATLKRVKNQPGVNGVKNIIAISSGKGGVGKSSTAVNLALALAAEGAKVG

ILDADIYGPSIPTMLGAEDSRPTSPDGTHMAPIMKYGLATNSIGYLVTNDNAMVWRGPMASKALMQMLQE

TLWPDLDYLVLDMPPGTGDIQLTLAQNIPVTGAVVVTTPQDIALIDAKKGIVMFEKVEVPVLGIVENMSM

HICSNCGHHEPIFGTGGAQKLAEKYHTQLLGQLPLHITLREDLDNGTPTVVARPDSEFTDIYRQLAGRVA

AQMYWQGEVIPGEIAFRAI

>lcl|NZ\_FO834906.1\_prot\_WP\_002912753.1\_3844 [gene=metG] [locus\_tag=BN49\_RS20865] [protein=methionine--tRNA ligase] [protein\_id=WP\_002912753.1] [location=3974132..3976165] [gbkey=CDS]

MTQVAKKILVTCALPYANGSIHLGHMLEHIQADVWVRYQRMRGHEVNFICADDAHGTPIMLKAQQLGITP

EQMIGEMSQEHQTDFAGFDISYDNYHSTHSDENRELSELIYTRLKENGFIKNRTISQLYDPEKGMFLPDR

FVKGTCPKCKSPDQYGDNCEVCGATYSPTELIDPKSVVSGATPVMRDSEHFFFDLPSFSEMLQAWTRSGA

LQEQVANKMQEWFESGLQQWDISRDAPYFGFEIPNAPGKYFYVWLDAPIGYMGSFKNLCDKRGDTTSFDE

YWKKDSTAELYHFIGKDIVYFHSLFWPAMLEGSNFRKPTNLFVHGYVTVNGAKMSKSRGTFIKASTWLNH

FDADSLRYYYTAKLSSRIDDIDLNLEDFVQRVNADIVNKVVNLASRNAGFISKRFDGVLAAELADPALYK

TFTDAAESIGEAWDSREFGKAIREIMALADVANRYVDEQAPWVVAKQEGRDADLQAICTMGLNMFRVLMT

WLKPVLPQLAARAEAFLNSELSWDAIQQPLLAHKVNPFKALYNRIEMKQVEALVEASKEEVKATAAPVTG

PLADDPIQETITFDDFAKVDLRVALIENAEFVEGSDKLLRLTLDLGGEKRNVFSGIRSAYPDPQPLIGRL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002912756.1\_3845 [locus\_tag=BN49\_RS20870] [protein=DUF1456 family protein] [protein\_id=WP\_002912756.1] [location=complement(3976279..3976749)] [gbkey=CDS]

MLSNDILRSLRYTLKVNNNDMVRILALSAMESTAASFDTWTTKEDEEGFVRCPDIILSGFLNGLIYDKRG

KDDSAPELALERRVNNNTVLKKLRIAFSLKTDDIQAIMSEQKYRVSVPEITAMMRSPDHKNYRECGDQFL

RNFLRGLTQRVHNPKA

>lcl|NZ\_FO834906.1\_prot\_WP\_004144215.1\_3846 [gene=btsR] [locus\_tag=BN49\_RS20875] [protein=two-component system response regulator BtsR] [protein\_id=WP\_004144215.1] [location=complement(3976797..3977516)] [gbkey=CDS]

MLRVLIVDDEPLARENLRILLETQRDIEIVGECGNAVEAIGAVHKLRPDVLFLDIQMPRISGLEMVGMLD

PEHRPYIVFLTAFDEYAVKAFEEHAFDYLLKPIEAARLEKTLARLRQERNLQDVSLLDDAQQTLKYIPCT

GHSRIWLLQMEDVAFVSSRMSGIYVTDREGKEGFTELTLRTLESRTPLLRCHRQYLVNMAHLKEIRLEEN

GQAELLMRAGQTVPVSRRYLKSLKEAIGL

>lcl|NZ\_FO834906.1\_prot\_WP\_002912760.1\_3847 [locus\_tag=BN49\_RS20880] [protein=sensor histidine kinase] [protein\_id=WP\_002912760.1] [location=complement(3977510..3979198)] [gbkey=CDS]

MYEFDLVLLLLQQMCVFLVIAWLMSKTRLFIPLMQVTVRLPHKLLCYVTFSIFCIMGTYFGLHIEDSIAN

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LTAGAITFVAELVQMMIILLIARPFQDALHLVQSIAAPMMVTNTVGAALFMRILLDKRAMFEKYTSAFSA

TALKVAASTEGILRQGFNEENSMKVAQVLIQELDIGAVAITDRDKLLAFTGIGDDHHLPGKPISSSYTQR

AIETGEVVYADGNEVPYRCSIHPHCKLGSTLVIPLRGENQRVIGTIKLYEAKNRLFSSINRTLGEGIAQL

LSAQILAGQYERQKALLTQSEIKLLHAQVNPHFLFNALNTLKAVIRRDSDQAGQLVQYLSTFFRKNLKRP

TEIVTLADEIEHVNAYLQIEKARFQANLQIQMAVPEGLAHHQLPAFTLQPIVENAIKHGTSQHLGVGEIT

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AC

>lcl|NZ\_FO834906.1\_prot\_WP\_002912762.1\_3848 [locus\_tag=BN49\_RS20885] [protein=protein YohO] [protein\_id=WP\_002912762.1] [location=3979428..3979541] [gbkey=CDS]

MKPAKIAVVTLFLLMAIGGISGVMLAGYSFIVRGGVG

>lcl|NZ\_FO834906.1\_prot\_WP\_004151128.1\_3849 [locus\_tag=BN49\_RS20890] [protein=ABC transporter permease] [protein\_id=WP\_004151128.1] [location=complement(3979516..3980253)] [gbkey=CDS]

MKALREPLWWLIALFIGLLAGLPYSAPLFSRLFPELPRPVYQQESFWALTLDHGWLVVASSLAATAIGLG

AGVAVTRPAGSAFRPLVETIAAIGQTFPPVAVLAMAVPVLGFGWLPALIALALYGILPVLQGTLAGLGSI

PPGVSGVAEGMGMTGWQRLYKVELPLAAPVILAGIRTSVIVNIGTATIASTVGASTLGTPIIIGLSGFNT

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>lcl|NZ\_FO834906.1\_prot\_WP\_020956604.1\_3850 [locus\_tag=BN49\_RS20895] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_020956604.1] [location=complement(3980237..3981184)] [gbkey=CDS]

MIEFQGVSKVFAGHPAVKDLTLELREGAFSVLVGTSGSGKSTTLKMINRLLEPDRGTIRFAGEDIRQQPV

LTLRRRMGYAIQSIGLFPHWTVAQNIATVPQLQRWPRARIADRIDELMALLGLEATLRDRYPHQLSGGQQ

QRVGVARALAADPEVLLMDEPFGALDPVTREALQQEMLRIHRLLGRTIVLVTHDIDEALRLADHLVLMDG

GEVVQQGAPLEMLLRPKNSFVQTFFGRSELGVRLLSLREVGDYLRPDERLAGEGLTITMTLREALSQFVA

RRCETLPVVDAEGRPCGTLHFADLLRQEMSHEGAS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043668.1\_3851 [locus\_tag=BN49\_RS20900] [protein=ABC transporter permease] [protein\_id=WP\_046043668.1] [location=complement(3981177..3982334)] [gbkey=CDS]

MTIRCTHRVGLLLTGLLLVTLALPFVTYAPNRLLSGEGRGLWQALPWLAGVQLAAALAGMLLCWLPGRIV

PFLHLLLAELLFPLLIWGCGQAALELSRHGSPLARTSPGSGLWLSLALCLLLASEAIRHLTVRPLWRWLL

NAQVWLLPIILLAIGALDQLSLLKEYANRQEVFDDALRQHLLLLFGTLLPGLLIGLPLGVWLWRRPRWQA

PAFTALNVIQTIPSVALFGLLIAPLAGLARYFPTLGELGVSGTGVAPALIALTLYALLPLVRGVVTGLQQ

VPQDALESATAMGMSAGQRFRQVQLPLAMPVLLRSLRVVSVQTVGMAVVAALIGAGGFGALVFQGLLSSA

LDLVLLGVVPTIALAVVVDALFALWGAWLKGEAND

>lcl|NZ\_FO834906.1\_prot\_WP\_002912823.1\_3852 [locus\_tag=BN49\_RS20905] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_002912823.1] [location=complement(3982342..3983259)] [gbkey=CDS]

MKMATTWSGALALAALISLPLQAAEPVKVGSKIDTEGALLGNMIQQVLESHGVKTINKIQLGTTPVVRGA

IVAGELDIYPEYTGNGAFFFKDENDPAWKNAQQGYEKVKRLDQEKHQLVWLTPAPANNTWTIAVRQDLAE

KNKLTSLADLSRYLKQGGEFKLAASAEFIERPDALPAFEKAYGFNLNQNQLLSLAGGDTAVTIKAAAQQT

SGVNAAMAYGTDGPVAALGLQTLSDPQGVQPIYAPTPVVREAVLKAYPQIADWLQPVFASLDEKTLQQLN

ARIAVEGQDAKRVAADYLQQKGLLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002912825.1\_3853 [gene=bglX] [locus\_tag=BN49\_RS20910] [protein=beta-glucosidase BglX] [protein\_id=WP\_002912825.1] [location=complement(3983396..3985693)] [gbkey=CDS]

MKWLCTVGVAVSLALQPALADELFGNHPLTPQARDAFVTDLLKKMTVDEKIGQLRLISVGPDNPKEAIRE

MIKNGQVGAIFNTVTRPDIRVMQDQVMQLSRLKIPLFFAYDVLHGQRTVFPISLGLASSFNLDAVKTVGR

VSAYEAADDGLNMTWAPMVDVSRDPRWGRASEGFGEDTYLTTMMGQAMVESMQGKSPADRYSVMTSVKHF

AAYGAVEGGKEYNTVDMSPQRLFNDYMPPYKAGLDAGSGAVMVALNSLNGTPATSDSWLLKDVLRDQWGF

KGITVSDHGAIKELIKHGVASDPEDAVRVALKSGINMSMSDEYYSKYLPGLVKSGKVTMAELDDATRHVL

NVKYDMGLFNDPYSHLGPKDSDPQDTNAESRLHRKEAREVARESLVLLKNRLDTLPLKKSGTIAVVGALA

DSKRDMMGSWSAAGVADQSVTVLTGIKEALGDNGKVIYAKGANVTDDKGIVDFLNLYENAVQVDPRSPQE

MIDEAVAAAKQSDVVVAVVGEAQGMAHEASSRTDITLPQSQRNLIAALKATGKPLVLVLMNGRPLALVKE

DQQADALLETWFAGTEGGHAIADVLFGDYNPSGKLPMSFPRSVGQIPTYYSHLNTGRPYNPEKPNKYTSR

YFDEANGPLYPFGYGLSYTTFSVSDVNMSSATMPRDGSVTASVQVTNTGNREGATVIQLYLQDVTASMSR

PVKMLRGFKKVTLKPGETQTVSFPIDVDALKFWNQQMKYVAEPGKFNVFIGVDSARVKQSEFELL

>lcl|NZ\_FO834906.1\_prot\_WP\_002912827.1\_3854 [gene=dld] [locus\_tag=BN49\_RS20915] [protein=D-lactate dehydrogenase] [protein\_id=WP\_002912827.1] [location=3985888..3987633] [gbkey=CDS]

MSSAPTDTHKTFLADLARLVGPSHLLTDPAKTQRYRKGFRSGQGEALAVVFPGTLLELWRVLNACVDADK

IILMQAANTGLTEGSTPNGNDYDREIVIISTLRLDKLHLLDKGEQVLAWPGTTLYSLEKALKPLGREPHS

VIGSSCIGASVIGGICNNSGGSLVQRGPAYTEMSLFAQIDADGKLKLVNHLGIDLGSTPEQILSRLDDER

ISDSDVLHDGRHAHDHDYVTRVRDVDADTPARYNADPDRLFESSGCAGKLAVFAVRLDTFPAEKRQQVFY

IGTNQPQVLTEIRRHILAEFQHLPVAGEYMHRDIYDIAEKYGKDTFLMIDKLGTDKMPFFFTMKGRTDAM

LEKVSLFKPHFTDRFMQKLGHVFPAHLPERMKTWRDKYEHHLLLKMAGDGIEEAQRWLTEYFQQAEGDFF

ACTPEEGSKAFLHRFAAAGAAIRYQAVHADEVEDILALDIALRRNDTEWFEHLPPEIDSQLVHKLYYGHF

MCHVFHQDYIVRKGVDAHALKEKMLELLKARGAQYPAEHNVGHLYEAPESLQQFYRQNDPTNSMNPGIGK

TSKQKYWGEAAPTPASPADPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002912829.1\_3855 [locus\_tag=BN49\_RS20920] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002912829.1] [location=3987719..3988273] [gbkey=CDS]

MPAEAPLLDSDLEIREALPDDAHAIAALYVWHVLNGRASFEEIPPTVDEMRKRIQTVRDNGLPWLVALWR

GAIVGYCYATFYRPRPAYRYTLEESIYVESGMGGRGIGSALLSRLIAECEKGPWRQMLAIIGDGHNNAGS

LAIHKKFGFTVAGQLRSVGYKMGDWRDTLIMQRALGDGDWTLPE

>lcl|NZ\_FO834906.1\_prot\_WP\_004180615.1\_3856 [gene=pbpG] [locus\_tag=BN49\_RS20925] [protein=D-alanyl-D-alanine endopeptidase] [protein\_id=WP\_004180615.1] [location=complement(3988496..3989446)] [gbkey=CDS]

MMPKFRVSLLSLTLLLAVPFAPQALAKTPTAVTASQPEIASGSAMIVDLATKKIIYASQPDLVRPMASIT

KVMTAMVVLDAHLPLDEMLTVDISHTPEMKGIYSRVRLNSQISRRDMLLLALMSSENRAAASLAHHYPGG

YDAFIRAMNAKAQALGMTHTRYVEPTGLSVHNVSTARDLTKLLIASEQYPLIGQLSTTKEETATFAHPAY

SLPFRNTNHLVYRDNWNIQLTKTGFTNAAGHCLIMRTVINQRPVALVVMDAFGKYTHFADASRLRTWIET

GKVMPVPASALSYKKQREAQMAEAMLKGGAQTAQND

>lcl|NZ\_FO834906.1\_prot\_WP\_002912831.1\_3857 [locus\_tag=BN49\_RS20930] [protein=YIP1 family protein] [protein\_id=WP\_002912831.1] [location=complement(3989635..3990222)] [gbkey=CDS]

MNHVWGLFAHPNREMSVIKSENETISHHYTHHVLLMAAVPVICAFIGTTQLGWNFGDGTVIKLSMLTGLA

LAVLFYAVMLAGVAIMGRVIWWMARQYPQQPSLKRCMVFAGYVATPLFLSGIVALYPLVWLCALVGTIAL

FYTGYLLYLGIPTFLSINREEGLSFASSTLAIGVLVLEVLLAITVVLWGYGYRLF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530579.1\_3858 [locus\_tag=BN49\_RS20935] [protein=DedA family protein] [protein\_id=WP\_016530579.1] [location=3990377..3990943] [gbkey=CDS]

MDINHLISQYGYAALIVGSMAEGETITLLGGVAAHQGLLKCPLVVIAVALGGMIGDQLLYLVGRRFGERI

LRRFASQKARIRKAQRMIQHRPWLFVIGTRFMYGFRVIGPLLIGASRLPPRIFLPLNIVGALVWALLFTT

IGYLGGEVVGPWLHHLDAHLKHWIWLILAVVVVAAHWWLRRRESKKKD

>lcl|NZ\_FO834906.1\_prot\_WP\_004149095.1\_3859 [gene=mdtQ] [locus\_tag=BN49\_RS20940] [protein=multidrug resistance outer membrane protein MdtQ] [protein\_id=WP\_004149095.1] [location=complement(3990977..3992416)] [gbkey=CDS]

MKLILNKSVLAALPLAIALAGCAPSHEVANPPQQQIPASHVSMDLPAAVKNGWPQTDWWKDYHDPQLNNL

IQRALANAPDMQIAEQRIRLAEAQARMSQANLGPEMDFSADIERQRMSAEGLMGPFATDTDGNTGPWYTN

GTFGLTAGWDLDLWGKNRALVKARIGELKAQVAEQAQTRELLSGSVARLYWQWQTEAAIKAVLQQVKNEQ

NNIVTVDKALYQRGITNSAEGAENDINVSKTDQQLADVTGTMKEIEARLMALTNSQSQSLNLKPASLPTV

SAQLPDTLGYELLARRPDLQVAHWYIEASLSEVDAAKAAFYPDINLMAFLQQDALHLSDLFRHSAQQMGV

TAGLTLPIFDSGRLNANLDIASAQNSLSIAQYNKAVVDAVNQVAKTASQVETLMAKSQQQQQVEKDAQRV

VDLAQARMAAGILPGSRVSMAKLPALQERITALRLHGQWIDASIQLTSALGGGYHQTVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004149097.1\_3860 [gene=ascB] [locus\_tag=BN49\_RS20950] [protein=6-phospho-beta-glucosidase] [protein\_id=WP\_004149097.1] [location=complement(3992687..3994081)] [gbkey=CDS]

MKTFPTDFLWGGATAANQVEGAYLEDGKGLSTSDVQPHGVFGEVVERVPGDSGIKDVAIDFYHRYPEDIA

LFAEMGFNCLRVSIAWTRIYPNGDDAEPNEAGLAFYDKLFDEMAKHNITPLVTLSHYEMPWALVKNYGGW

GSREVIGFFERYARTVFSRYKNKVKLWLTFNEINMSLHAPMTGVGLPAGSSKGEVYQAIHHQLVASALAV

KACHELVPEGKIGNMLLGGLMYPLSCKPEDVFETLQENRSWQFFGDVQARGAYPGYMQRYFRDNGITLTI

TDADREALKTTVDFISFSYYMTGCVTADEALNQQARGNILSMVPNPHLASSEWGWQIDPLGLRTLLNVLW

DRYQKPLFIVENGLGAKDKVEADGSINDDYRISYLNDHLVQAREAIDDGVELMGFTSWGPIDLVSASKAE

LSKRYGFIYVDRHDDGTGTLARSKKKSFGWYKEVIASRGASLKA

>lcl|NZ\_FO834906.1\_prot\_3861 [gene=bglF] [locus\_tag=BN49\_RS20955] [protein=PTS beta-glucoside transporter subunit IIABC] [pseudo=true] [location=complement(3994097..3996071)] [gbkey=CDS]

MMQAKPERDAHRRGSRVFLFFTTQSPVVCGQRQ\*GKEHGI\*STRAGYSQPRRRQREHCESGSLCDTSAF\*

TEG\*RQSRCRRAEGQSGRDYGGGERRPVSGGDWQPRSRRLAGGAPGGGVKR\*QRTGCRGKSGQRIGVKPA

YRHHLRHLYTVYRRDGGNRSAERPAGAGGDLRLAYAGAGDL\*NLVCRQRRAVLFLPAVSWLYRREEVWRQ

PVYLDGAWRGVNPPADDSGL\*GQPGAGRGGGALSRHSGDLYQLQLVSDPDYSRLMGLLLAGAQEQCAVAV

IDEKLLQPGHLPGGGGPAHLPGDWSGRHLAEPSAGQRLPVYLRVCAMAGGRGTGRHVAGVRYFRPALGAG

AIDDQQHDGTWSRLHAADYSSGGDCPGGRRARYFPRHPRCAPAGAGRFRLLRRAVRHHRAGYLWPDPAAA

PSVYLRLCRRGDWRGDHCL\*QQLCLLVWPAKHLFPGANDPARRD\*RQRLGRAYRHRRGFRARLRADLLRR

PAVR\*RRTRRRDGSPGLGKRYSGADERQRYRPRAGAG\*HLRQRPAG\*RGRHYPGGGPSDCPVPGRSGLPV

SD\*TRHRPAKLQRH\*AADPRRHRHGQTRRRALYRACERGRQGTGRRSAD\*V\*SPGDSGRRLRPGDPDHYQ

QQRRLPGD\*YGGVQHRRSRSAVVVSQPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530631.1\_3862 [gene=bglG] [locus\_tag=BN49\_RS20960] [protein=transcriptional antiterminator BglG] [protein\_id=WP\_016530631.1] [location=complement(3996102..3996935)] [gbkey=CDS]

MQIAKVLNNNVVVVLDEHRREQVVMGRGLAYQKRPGDVLDDSKIEKVFALQSDELVGRLGELLSQIPLEV

MTTCDRIIDLARGRLGKLQESLYITLTDHCHFAIERQKKGIALRNVLLWEIKRLYPKEFALGLEARAIIA

KRLGVELAEDEAGFIALHLVTAQLNSEMPEVMHVTRVMQEILQLVKYQLQLNYDEESLSYQRFVTHLKFF

AQRMLTRTVVEDDDVSLHSAVKDNYAKAWKCAETVATHLQKQYQRSLTTEEIMFLAIHIERVRKEGR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530632.1\_3863 [locus\_tag=BN49\_RS20965] [protein=carbohydrate porin] [protein\_id=WP\_016530632.1] [location=complement(3997091..3998455)] [gbkey=CDS]

MHNKKINQLLIGAMLAAMAPAVSAADIPAWNGSALGFEAGQQGLLGDMLGIRPILEENGFHYNLGYLNEM

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SWGGGSITRLGWLTFARSFDDRRLTWRIGMMNKVQTFDQIIPCDFQLLTQCGGKSANSLTWNNWNIHTWG

TTLEYKLTPTVTLKGGVMEQNPQATARSHAWSWSTKGSKGILLPMEIETRPLINGLPGAYNLGVVWTNAP

QSDLYSGKSGGAGATDPQGYAEHDSTWFMYAGLNQQITRHADDPLRGMSVSLSGSLSDQRSNYIHSAVAA

SMRYRGLFDARPEDWIGFGLTWIDMSSHYARNQRYMNQISGATDYNDPAYQPVAGHSLNGELYYRFRPVS

WLELQPGLQYWHRPGGVAQTQDAWVVEWKTVVTF

>lcl|NZ\_FO834906.1\_prot\_WP\_002912862.1\_3864 [gene=dusC] [locus\_tag=BN49\_RS20970] [protein=tRNA dihydrouridine(16) synthase DusC] [protein\_id=WP\_002912862.1] [location=complement(3998812..3999744)] [gbkey=CDS]

MRVLLAPMEGVLDSLVRELLTEVNDYDLCITEFLRVVDQLLPVKSFYRLCPELHHQSRTPSGTRVRVQLL

GQYPEWLAENAARAVALGSWGVDLNCGCPSKLVNGSGGGATLLKDPELIYRGAKAMREAVPEHLPVTVKV

RLGWDSGERRFEIADAVQQAGASELVVHGRTKEDGYKAERINWQAIGEIRQRLTIPVVANGEIWDWQSAQ

DCMAVTGCDSVMIGRGALNVPNLSRVIKYNEPRMPWPQVVQLLQKYTRLEKQGDTGLYHVARIKQWLGYL

RKEYTEALTLFNEIRALQTSAEIAAAIGRY

>lcl|NZ\_FO834906.1\_prot\_WP\_002912865.1\_3865 [locus\_tag=BN49\_RS20975] [protein=CidA/LrgA family protein] [protein\_id=WP\_002912865.1] [location=4000102..4000500] [gbkey=CDS]

MSKSLTIIWQYLRAFVLIYACLYAGIFIAGLLPITIPGSIIGMLILFVLLALQIMPPQWVNPGCNILIRY

MALLFVPIGVGVMQYWDLLRAQLGPVVISCAISTLVVFVVVSWSSHLVHGERKVIGQKGKEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530141.1\_3866 [locus\_tag=BN49\_RS20980] [protein=CidB/LrgB family autolysis modulator] [protein\_id=WP\_016530141.1] [location=4000497..4001195] [gbkey=CDS]

MMHEIWWSLPLTLIVFFLARKLAARFKFPLLNPLLVAMVVIIPFLLLTGISYERYFAGSKVLNDLLQPAV

VALAFPLYEQLHQIRARWKSIITICFIGSCVAMITGTTVALLMGATPQIAASILPKSVTTPIAMAVSGSI

GGIPAISAVCVIFVGILGAVFGHTLLNLMRIRTKASRGLSMGTASHALGTARCAELDYQEGAFSSLALVL

CGIITSLMAPFLFPLILAVVGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002912869.1\_3867 [gene=cdd] [locus\_tag=BN49\_RS20985] [protein=cytidine deaminase] [protein\_id=WP\_002912869.1] [location=4001320..4002204] [gbkey=CDS]

MHSRFQAALTTLAADLQAAIAPMLADPHFPALLEADQVATLQHATGLDEDALAFALLPLAAACARPDLSH

FNVGAIARGVSGRWYFGGNMEFLGATMQQTVHAEQSAISHAWLRGETSLRAITVNYTPCGHCRQFMNELN

SGLALRIHLPGREAHALEHYLPDAFGPKDLEIKTLLMDEQDHGFPVSGDALTQAAIQAANRCHAPYSHSP

SGVALELKDGTIFSGSYAENAAFNPTLPPLQGALNLLSLNGYDYPAIQRAILAEKADAALIQWDATVATL

KALGCHNIERVLLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002912870.1\_3868 [gene=sanA] [locus\_tag=BN49\_RS20990] [protein=outer membrane permeability protein SanA] [protein\_id=WP\_002912870.1] [location=4002480..4003196] [gbkey=CDS]

MLKRAFYSLLVLLGLLLLTVLGLDRWMSWKTAPYIYDELQDLPYRQVGVVLGTAKYYRTGVINQYYRYRI

QGALNAYNSGKVNYLLLSGDNALQSYNEPMTMRRDLIKGGVDPADIVLDYAGFRTLDSIVRTRKVFDTND

FIIITQRFHCERALFIALHMGIQAQCYAVPSPKDMWSVRLREFGARFGALADLYIFKREPRFLGPLIPIP

AQQHDVPDDAQSYPAVTPEQLLELQKEK

>lcl|NZ\_FO834906.1\_prot\_WP\_002912871.1\_3869 [gene=mglC] [locus\_tag=BN49\_RS20995] [protein=galactose/methyl galactoside ABC transporter permease MglC] [protein\_id=WP\_002912871.1] [location=complement(4003266..4004276)] [gbkey=CDS]

MSALNKKSFLTYLKEGGIYVVLLVLLAIIIFQDPTFLSLLNLSNILTQSSVRIIIALGVAGLIVTQGTDL

SAGRQVGLAAVIAATMLQAVDNANKVFPDMATMPIPLVILLVCAIGAVIGLINGIVIAYLNVTPFITTLG

TMIIVYGINSLYYDFVGASPISGFDSHFSHFAQGFVALGSFRLSYITFYALIAVFFVWILWNKTRFGKNI

FAIGGNPEAAKVSGVNVALNLLMIYALSGVFYAFGGLLEAGRIGSATNNLGFMYELDAIAACVVGGVSFS

GGVGTVFGVVTGVIIFTVINYGLTYIGVNPYWQYIIKGAIIIFAVALDSLKYARKK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530140.1\_3870 [gene=mglA] [locus\_tag=BN49\_RS21000] [protein=galactose/methyl galactoside ABC transporter ATP-binding protein MglA] [protein\_id=WP\_016530140.1] [location=complement(4004292..4005812)] [gbkey=CDS]

MVSNNSERSGEYLLEMSNINKSFPGVKALDNVNLKVRPHSIHALMGENGAGKSTLLKCLFGIYQKDSGSI

LFQGKEIDFHSAKEALENGISMVHQELNLVLQRSVMDNMWLGRYPTKGMFVDQDKMYRDTKAIFDELDID

IDPRARVGTLSVSQMQMIEIAKAFSYDAKIVIMDEPTSSLTEKEVNHLFKIICKLKDRGCGIVYISHKME

EIFQLCDEITILRDGQWIATQPLEGLDMDKIIAMMVGRSLNQRFPDRENTPGEVILQVRNLTSLRQPSIR

DVSFDLHKGEILGIAGLVGAKRTDIVETLFGIREKASGTITLHGKKINNHSANEAINHGFALVTEERRST

GIYAYLDIGFNSLISNIKKYKNSIGLLDNSRMKSDTQWVIDSMRVKTPGQHTQIGSLSGGNQQKVIIGRW

LLTQPEILMLDEPTRGIDVGAKFEIYQLIAELAKKDKGIIIISSEMPELLGITDRILVMSNGLVAGIVET

KTTTQNEILRLASLHL

>lcl|NZ\_FO834906.1\_prot\_WP\_002912878.1\_3871 [gene=mglB] [locus\_tag=BN49\_RS21005] [protein=galactose/glucose ABC transporter substrate-binding protein MglB] [protein\_id=WP\_002912878.1] [location=complement(4005931..4006929)] [gbkey=CDS]

MNKKVFTLSAVMAGLLFGAAAHAADTRIGVTIYKYDDNFMSVVRKAIEKDGKSAPDVQLLMNDSQNDQSK

QNDQIDVLLAKGVKALAINLVDPAAAGTVIEKARGQNIPVVFFNKEPSRKALDSYDKAYYVGTDSKESGI

IQGDLIAKHWKANPNWDLNKDGQIQYVLLKGEPGHPDAEARTTYVIKELNDKGLKTQQLQLDTAMWDTAQ

AKDKMDAWLSGPNANKIEVVIANNDAMAMGAVEALKAHNKSSIPVFGVDALPEALALVKSGAMAGTVLND

ANNQAKATFELAKNLADGKDAAAGTNWKIDNKIVRVPYVGVDKDNLSQFTGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002912919.1\_3872 [gene=galS] [locus\_tag=BN49\_RS21010] [protein=HTH-type transcriptional regulator GalS] [protein\_id=WP\_002912919.1] [location=complement(4007226..4008248)] [gbkey=CDS]

MITIRDVARQAGVSVATVSRVLNNSALVSPDTRDVVMKAVTQLGYRPNANAQALATQVSDTIGVVVMDVS

DAFFGALVKAVDTVAQQHQKYVLIGNSYHEAEKERHAIEVLIRQRCSALIVHSKALSDDELSDFMQHIPG

MVLINRIVPGYAHRCVGLDNVSGALMATRMLLNHGHQRIGYLSSNHGIEDDDMRREGWSKALQEQGIIAP

DSWIGSGSPDMQGGEAAMVELLGRNLGLTAVFAYNDSMAAGALTTLKDNGIVVPQHLSLIGFDDIPISRY

TDPQLTTVRYPVMSMAKLATELALLGAAGKLDREATHCFMPTLVRRHSVAQRQTVGPITN

>lcl|NZ\_FO834906.1\_prot\_WP\_002912921.1\_3873 [locus\_tag=BN49\_RS21015] [protein=DUF418 family protein] [protein\_id=WP\_002912921.1] [location=complement(4008404..4009561)] [gbkey=CDS]

MERNVTLDFVRGVAILGILLLNISAFGLPKAAYLNPAWSGSASLSDAWTWALLDLLAQVKFLTLFALLFG

AGLQLLLPRGKRWIQSRLTLLALLGFIHGLFFWDGDILLAYALVGLVSWRMVREAHHVKSLFNTGVVLYL

TGIAVLVLLGLISGTAANRSWAPDAANLQYEQYWKLHGGMEAVSNRADMLSDNLLALGAQYGWQLAGMML

MGAALMRSGWLKGQFSLRHYRRTGALLVAAGMAVNLPAIFAQWYLAWDYRWCAFLLQAPRELSAPLQAIG

YAALAWGYWPQLCRFRLVGAIACVGRMALTNYLLQTLICTTLFYHLGLFMRFDRLQLLAFVPPIWAVNLL

VSSLWLRRFRQGPVEWLWRQLTLRASGTSLKDTSR

>lcl|NZ\_FO834906.1\_prot\_WP\_004184878.1\_3874 [gene=folE] [locus\_tag=BN49\_RS21020] [protein=GTP cyclohydrolase I FolE] [protein\_id=WP\_004184878.1] [location=complement(4009577..4010245)] [gbkey=CDS]

MSSLSKEAVLVHEALVARGLETPMRAPVQEIDNETRKRLITGHMTEIMQLLNLDLSDDSLMETPHRIAKM

YVDEIFSGLDYSRFPKITVIENKMKVDEMVTVRDITLTSTCEHHFVTIDGKATVAYIPKDSVIGLSKINR

IVQFFAQRPQVQERLTQQILIALQTLLGTNNVAVSIDAVHYCVKARGIRDATSATTTTSLGGLFKSSQNT

RQEFLRAVRHHD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151123.1\_3875 [gene=fghA] [locus\_tag=BN49\_RS21025] [protein=S-formylglutathione hydrolase] [protein\_id=WP\_004151123.1] [location=4010606..4011439] [gbkey=CDS]

MELLEEHRCFDGQQQRWRHHSPVLNCAMTFSIFLPPERETPPPVLYWLSGLTCNDENFTTKAGAQRIAAE

LGIALVMPDTSPRGDEAANDDGYDLGQGAGFYLNATEAPWAAHYRMYDYLRDELPALIRSEFSVGERCAV

SGHSMGGHGALIMALKNPGRYASVSAFAPIVNPSQVPWGKKAFTAYLGADESAWHSWDSCALMQASRPED

AVPTLIDQGDNDPFLAGQLQPAVLAEVARQKAWPLTLRIQPGYDHSYYFIASFIEDHLRFHAQHLFG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530139.1\_3876 [gene=cirA] [locus\_tag=BN49\_RS21030] [protein=catecholate siderophore receptor CirA] [protein\_id=WP\_016530139.1] [location=complement(4011510..4013483)] [gbkey=CDS]

MFRLNPFIRAGLSASVVSLAFPALADVNEETLVVTASATEQNVKDAPASISVITQQDLQRKPVQNLKDVL

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SLYGSDALGGVVNIITKKIGQKWTGTLSADTTIQEHRDRGDTWNGQFFTSGPLIDGVLGMKAYGSLAKRA

KDDPQSSSNATGETPRIEGFTSRDGNVEFAWTPNENHDFTAGYGFDRQDRDSDSLDRNRLERENYSLSHN

GRWDIGNSELKFYGEKVDNKNPGQSGTITSESNAIDGKYVLPLGMINQLVTFGGEWRHDKLKDPVNLSSG

GQSTSASQYALFIEDEWRIIEPLALTTGIRMDDHQTYGDHWSPRAYLVYNATDTVTVKGGWATAFKAPSL

LQLNPDWTTNSCRGSCSIVGNPDLKPETSESFELGLYYRGEEGWLENVEGSITTFQNNVDDMIDVLRTSS

ASEAPGYPNFVGWKTVNGKRVPIFRYFNVNKARIKGVETEVKIPFGDEWKLTLNYTYNDGRDLSNGGDKP

LQTLPFHTANGTLDWKPLDDWSFYVTANYTGQQRAVSATGKTPGGYTLFDVGAAWQVTKNVKLRSGGQNV

GDKDLSRDDYSYTEEGRRYFMAVDYRF

>lcl|NZ\_FO834906.1\_prot\_WP\_002912929.1\_3877 [locus\_tag=BN49\_RS21035] [protein=amino acid permease] [protein\_id=WP\_002912929.1] [location=complement(4013982..4015451)] [gbkey=CDS]

MVSETKTTEAPTLRRELKARHLTMIAIGGSIGTGLFVASGATISQAGPGGALLSYILIGLMVYFLMTSLG

ELAAFMPVSGSFATYGQNYVEEGFGFALGWNYWYNWAVTIAVDLVASQLVMSYWFPDTPGWIWSALFLGI

MFLLNWISVRGFGEAEYWFSLIKVATVIIFIIVGVMMIVGIFKGAQPAGWSNWGIADAPFAGGFSAMIGV

AMIVGFSFQGTELIGIAAGESENPEKNIPRAVRQVFWRILLFYVFAILIISLIIPYTDPSLLRNDVKDIS

VSPFTLVFQHAGLLSAAAIMNAVILTAVLSAGNSGMYASTRMLYTLACDGKAPRIFSKLSRGGVPRNALY

ATTVIAALCFLTSMFGNQTVYLWLLNTSGMTGFIAWLGIAISHYRFRRGYVLQGNDINNLPYRSGFFPLG

PIFAFVLCLIITLGQNYEAFLKDTIDWGGVAATYIGIPLFLVIWFGYKLAKGTRFVRYSEMTFPDRFKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002912932.1\_3878 [locus\_tag=BN49\_RS21040] [protein=DNA-binding transcriptional regulator YeiE] [protein\_id=WP\_002912932.1] [location=complement(4015630..4016496)] [gbkey=CDS]

MHITLRQLEVFAEVHKSGSTTQASQMLALSQSAVSAALTDLEGQLGVQLFDRVGKRLVVNEHGRLLYPRA

LALLERALEIEQLFRGDNGAIRVYASSTIGNYIMPEIIARYRHDFPDLPVELSVGNSLDVINAVADLRVD

FGLIEGPCHAADIIAEPWLEDELVVFAAPNSPLLAGEVTLQQLAEAPWILREHGSGTREIVDYVLLSHLP

AFHLGMELGNSEAIKHAVRHGLGISCLSRRVIAEQLASGTLAELKVPLPRLTRTLWRIHHRQKHISKALQ

RFLHYCQV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530136.1\_3879 [locus\_tag=BN49\_RS21050] [protein=YeiH family protein] [protein\_id=WP\_016530136.1] [location=4016762..4017811] [gbkey=CDS]

MTALTLPTKHRSLWHFVPGLALTAALTGAALWAGSFPAIAGAGFSALTLAILFGMVVGNTVYPKIWQPCD

GGVIFAKQHLLRLGIILYGFRLTFAQIADVGVSGILIDVLTLSSTFFIACFLGQKVFGLDKHTSWLIGAG

SSICGAAAVLATEPVVKAEASKVTVAVATVVIFGTIAIFLYPAMYPLLAHWFTPETYGIYMGSTMHEVAQ

VVAAGHAVSPDAENAAVIAKMLRVMMLAPFLLFLAARVKQLTPAGNGEKSKITIPWFAIMFILVAVFNSF

HLLPKAVVDMLVTLDTVLLAMAMAALGVTTHVSALKKAGAKPLLMALMLFVWLIVGGGVINVAIHSQMA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912937.1\_3880 [gene=nfo] [locus\_tag=BN49\_RS21055] [protein=deoxyribonuclease IV] [protein\_id=WP\_002912937.1] [location=4017883..4018737] [gbkey=CDS]

MKYVGAHVSASGGLANAAIRAAEIEATAFALFTKNQRQWRAAPLSDETIAEFKAACEKYHFGPGQILPHD

SYLINLGHPVEEALEKSRDAFIDEMTRCQQLGLTLLNFHPGSHLQQIPEEECLARIAESINIALAKTEGV

TAVIENTAGQGSNLGFKFEHLAAIIDGVEDKSRVGVCIDTCHAFAAGYDLRSAEACEKTFAAFERIVGFQ

YLRGMHLNDAKSAFGSRVDRHHSLGEGNIGHDCFSWIMQDSRFDGIPLILETINPDIWAEEIAWLRAQQI

AEVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912939.1\_3881 [gene=fruA] [locus\_tag=BN49\_RS21060] [protein=PTS fructose transporter subunit IIBC] [protein\_id=WP\_002912939.1] [location=complement(4018789..4020483)] [gbkey=CDS]

MKTLLIIDAGLGQARAYMAKTLLGAAAPKAHLELIDNPNDAELAIVLGTALPADSALNGKNVYLGDINRA

VAHPELFLGEAKDHAKPYVAPAAVAVPAAAQGQKRIVAVTACPTGVAHTFMAAEAIETEAKKRGWWVKVE

TRGSVGAGNAITPEEVAEADLVIVAADIEVDLAKFAGKPMYRTTTGLALKKTAQELDKAVAEAKPYQPSG

KPQAAAEGKKESAGAYRHLLTGVSYMLPMVVAGGLCIALSFAFGIKAFEVKDTLAAALMQIGGGSAFALM

VPVLAGFIAFSIADRPGLTPGLIGGMLAVSGGSGFIGGIIAGFLAGYVAKAISTKLKLPQSMEALKPILI

IPLVSSLIVGLAMIYLIGKPVAGILAWLTHWLQTMGTANAVLLGAILGAMMCTDMGGPVNKAAYAFGVGL

LSTQTYAPMAAIMAAGMVPPLAMGIATLVARNKFDKGQREGGKAALVLGLCFISEGAIPFAARDPMRVLP

CCIVGGAVTGAISMAVGAKLMAPHGGLFVLLIPGAITPVLGYLLAIVAGTLVAGLAYAVLKRPEAQTAEV

EKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002912941.1\_3882 [gene=fruK] [locus\_tag=BN49\_RS21065] [protein=1-phosphofructokinase] [protein\_id=WP\_002912941.1] [location=complement(4020500..4021438)] [gbkey=CDS]

MSRRVATITLNPAYDLVGFTPEIERGEVNLVRTTGLHAAGKGINVAKVLKDLGIDVTVGGFLGKDNQDGF

QQLFSELGIANRFQVVQGRTRINVKLTEKDGEVTDFNFSGFEVTPGDWERFVNDSLSWLGQFDMVCVSGS

LPSGVSPEAFTDWMTRLRSQCPCIIFDSSREALVAGLKAAPWLVKPNRRELEIWAGRKLPEMKDVIDAAH

ALREQGIAHVVISLGEEGALWVNASGEWIAKPPSVEVVSTVGAGDSMVGGLIYGLLMRESSEHTLRLATA

VAALAVSQSNVGITDRTQLAAMMARVDLQPFN

>lcl|NZ\_FO834906.1\_prot\_WP\_002912947.1\_3883 [gene=fruB] [locus\_tag=BN49\_RS21070] [protein=fused PTS fructose transporter subunit IIA/HPr protein] [protein\_id=WP\_002912947.1] [location=complement(4021439..4022569)] [gbkey=CDS]

MFQLSVQDIHPGQQAGNKEEAIRQVAAALVSAGNVADGYVNGMLAREQQTSTFLGNGIAIPHGTTDTRDQ

VLKTGVQVFQFPQGVTWGEGQTAYVAIGIAASSDEHLGLLRQLTHVLSDDAVAAQLQSATTAEELRALLM

GEKQSEALKLDNETLSLDVAASDLLTLQALNAARLKEVGAVDAAFVSHVINDTPLNLGQGVWLNDSAEGN

LRSAVAVSRAANAFTRDEQPVSLLVTVAMADEQPTAVLNRLSKLLLDKKAEHLLKADAATVLALLTSDDA

IAEDVLSAEFVVRNEHGLHARPGTMLVNTIKQFSSDITVTNLDGSGKPANGRSLMKVVALGVKKGHRLRF

TAQGEDAQQALDAIGEAIAAGLGEGA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151122.1\_3884 [gene=setB] [locus\_tag=BN49\_RS21075] [protein=sugar efflux transporter SetB] [protein\_id=WP\_004151122.1] [location=4022906..4024087] [gbkey=CDS]

MENRSAALPRRGFDVTSSAFLIVAFLTGIAGALQTPTLSLFLTNEVHVRPAMVGFFFTGSAVIGILVSQF

LAGRSDRQGDRKQLIVVCCLLGVLACVLFAWNRNYFILLFIGVFLSSFGSTANPQMFALAREHADRTGRE

AVMFSSILRAQVSLAWVIGPPLAYALAMGFGFTAMYLSAAAAFIVCGIMVWLFLPSMRKAKPVATGRLEA

PRTHRRDALLLFSICTLMWGTNSLYIINMPLFIINELHLPEKLAGLMMGTAAGLEIPTMLIAGYYARRFG

KRFLMRLSAVAGVLFYVGMLTVHTPALLLAMQVLNAIYIGILAGIGMLYFQDLMPGQAGAATTLYTNTTR

VGWIIAGSLAGVVAEIWSYHAVFWIALAMGVVTQACLWRIRDV

>lcl|NZ\_FO834906.1\_prot\_WP\_004175066.1\_3885 [locus\_tag=BN49\_RS21080] [protein=YkgJ family cysteine cluster protein] [protein\_id=WP\_004175066.1] [location=complement(4024127..4024381)] [gbkey=CDS]

MECRTDCGACCIAPSISSPIPGMPQGKPANTRCIQLSERNLCLIFGSPLRPKVCASLQPSPEMCLTHRDE

AITWLLELELATAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002912951.1\_3886 [gene=yeiP] [locus\_tag=BN49\_RS21085] [protein=elongation factor P-like protein YeiP] [protein\_id=WP\_002912951.1] [location=4024529..4025101] [gbkey=CDS]

MPRANEIKKGMVLNYNGKLLIVKNIDIQSPSARGAATLYKMRFSDVRTGLKVEERFKGDDIVDTVTLTRR

FVDFSYVDGNEYVFMDKEDYTPYTFTKEQIEEELQFIPEGGMPDMQVLTWDGQLLALELPQTVDLEIIET

APGIKGASASSRTKPATMSTGLVIQVPEYLTTGEKIRIHIEECRYMGRAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002912952.1\_3887 [gene=uxuA] [locus\_tag=BN49\_RS21090] [protein=mannonate dehydratase] [protein\_id=WP\_002912952.1] [location=complement(4025172..4026362)] [gbkey=CDS]

MEQTWRWYGPNDPVSLDDVRQAGATGVVTALHHIANGQVWPVDEIKARQALLAAKGLTWSVVESIPVHED

IKTHSGQYATWIANYQQSIRNLAACGIDTVCYNFMPILDWTRTDLEYELPDGSRALRFDQIAFAAFELHI

LKRPGAEADYSEEEQRQAEVYFKAMSEADIDKLTRNIIAGLPGAEEGYTLDQFRARLAEYDHIDKAQLRE

NMAYFLRAIVPVCEEVGIRLAVHPDDPPRPILGLPRIVSTIEDMQWLKETVDSINNGFTMCTGSYGVRAD

NDLVKMVETFGDRIHFTHLRSTCREANPKTFHEAAHLSGDVNMVAVVDAILREEQRRKQAGDLRPIPFRP

DHGHQMLDDLRKKTNPGYSAIGRLKGMAEVRGVELALKMTKYPELL

>lcl|NZ\_FO834906.1\_prot\_WP\_004200498.1\_3888 [locus\_tag=BN49\_RS21095] [protein=fructuronate reductase] [protein\_id=WP\_004200498.1] [location=4026570..4028036] [gbkey=CDS]

MTTIATATLPKNVQYPQYDRSQLRSRIVHFGFGAFHRAHQALLTDRVLNNVGGDWGICEISLFSGDTLMS

QLREQDHLFTVLEKGADGNQPIVIGAVHECLNARLDSLAAIIEKFCEPQVAIVSLTITEKGYCIDPATGK

LDPTHPRIIHDLENPTLPQSAPGILVEALARRRERGLPPFTVLSCDNIPDNGHVVKNAVLGMAEKRSPAL

ADWIADNVSFPGTMVDRIVPAATPESLAEIAAVLGVDDPCAISCEPFIQWVVEDHFVAGRPAWETAGVQM

TDDVLPWEQMKLRMLNGSHSFLAWLGYLAGHAHISDCMRDDVFRRAARQLMLDEQAPTLTITGVDLLAYA

DSLIARFSNPALKHRTWQIAMDGSQKLPQRMLDGIRVHLARDSRWPLLALGVAGWMRYVSGTDDAGQTID

VRDPLVDKIRQRVAQSDEQQRVDALLGLEEIFGRDLPHNAQFVAGIRAAWQQLATHGAREAVARALNS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530092.1\_3889 [locus\_tag=BN49\_RS21100] [protein=GTP-binding protein] [protein\_id=WP\_016530092.1] [location=4028157..4029134] [gbkey=CDS]

MTRTNLITGFLGSGKTTSILHLLAQKPADEKWAVLVNEFGEVGIDGALLADSGALLKEIPGGCMCCVNGL

PMQVGLNTLLRQGKPDRLLIEPTGLGHPKQILDILTAAVYEPWIDLRATLCILDPRQLLDERAVSNDNFR

DQLAAADIIVANKSDRETAESARALADWWQRCGGERRKVSAIQGNIDLTLLDEPRRNTAPLPASAEHAHR

HPPTSGLAALSLAEHQRWRRHLNNGQGYQGCGWIFDAETVFDTIGLLEWARLAPVGRVKGVMRIAEGAVR

INRQGEDLHIETLSVAPPDSRIELISANEADWNALQTSLLRLRLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002912965.1\_3890 [locus\_tag=BN49\_RS21105] [protein=phosphatase PAP2 family protein] [protein\_id=WP\_002912965.1] [location=4029172..4029885] [gbkey=CDS]

MAMMKNRIPLILLLNIAGVALFCSWYLPANHGAWLPVDSAIFHFFNHGVSVSHAYAWLLAIINNRAFDAC

SLLAMGCLMLSYWLKAPTAGRRQIAIMGLVMLLAAVIINQLAQHLMPVQRASPSLFFSDITRVSDVVNFP

TKDASKDSFPGDHGMMLLIFASFMWRYFGRRALGVALIIFVVFAFPRVMIGAHWFSDIAVGSLTAVLIGA

PWVLMTPLSDKLIAFFDRYLPSRISAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002912967.1\_3891 [gene=mepS] [locus\_tag=BN49\_RS21110] [protein=bifunctional murein DD-endopeptidase/murein LD-carboxypeptidase] [protein\_id=WP\_002912967.1] [location=4030312..4030881] [gbkey=CDS]

MVKSQPILRYILRVAPAIAVAVLLSACSSTSTARNMHSETHAVGSGDLSSLQASQDEFETMVRNLDVKSR

LMDQYASWKGVRYRLGGSTRKGIDCSAFVQRTFREQFGLELPRSTSEQQETGKSISRAQLRTGDLVLFRA

GSTGRHVGIYLGNNQFVHASTSSGVTISSMDEPYWKKRYNEARRVLSRS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530091.1\_3892 [locus\_tag=BN49\_RS21115] [protein=cyclic di-GMP phosphodiesterase] [protein\_id=WP\_016530091.1] [location=4031070..4032632] [gbkey=CDS]

MLTRYFSPQRKTWLTSLSVGIIVALLAGSIQFMVIYHNRAERFDAIINNVNTYLKSYFHDLRQTIDSLQP

LVDQPCENIDSGLTSHAAFSPNVRAFLLVKNGIAFCSSATGAMNTPLSQLIPAIDISKPVAMAILPGTPM

MPKSAALALWVGKPGDQNSGIFVSINANLTPYILYSARQNDFSGIALAIDHTAISTFSNRLVDPQTLHNA

PIRQAQIEGLPLKVYLYANSWLAENTQFALLLGVVCGLLAGLLCYYVLTIKSDPRKSILLGIKNNQFYIV

YQPVVNAQTLRISGVEVLMRWRHPVVGEIPPDVFINLAETQQMIVPLTHHLLALIASDAAVLKRILPRGV

KLGLNISPAHLQADSFRDDMLRFAAALPADHFHVVLEVTERAMIDKEKSMANFAWLHRQGFEIAIDDFGT

GHSALIYLERYNFDYLKIDRGFVQAIGTETVTSPVLDAVLTLSRRLKLMTVAEGVETQEQAEWLRGQGVH

FLQGYWISRPLSLAGLVAAHDEPANYFTTR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530090.1\_3893 [locus\_tag=BN49\_RS21120] [protein=extracellular solute-binding protein] [protein\_id=WP\_016530090.1] [location=4032701..4034506] [gbkey=CDS]

MYARLFLILLALFSLDAKAQTIQESVAFAIIGEPKYAAGFSHFDYVNPRAPKGGTLTLAAIGTFDNFNRY

ALRGNPAVRTEALYDTLFTTSDDEPGSYYPLIAERARYAEDYSWMEIALNPRARFHDGTPITARDVAFTF

NKFMTEGVPQFRLFYKGTTVKAIAPLTVRIDLAQPGKENMLSLLSLPVMPEAFWRQHKLSDPLSKPPLAS

GPYRISAWRMGQYITYSRVADYWAADLPVNRGRWNFDTLRYDYYLDDNVAFEAFKAGAVDRREETVAKNW

ATRYVGRNFSRGYIIKDEHTNTSAQDTQWLAFNIQRPIFADRRVRQAITLAFDFEWMNKALFYSAYQRAN

SYFQNTEYAARSLPDAAELALLTPMKNELPPELFSQVYQPPVSRGDGFDRANLLKADALLNAAGWTVKNQ

RRVNAATGKPLRFELLLPAGGNDRWVLPFQHNLQRLGIVMDIRQVDNSQYSNRRRSRDYDMMPSLWRAMP

WPGTDLQISLASDYIHSSYNAPGVQSPVVDKLIAQILQWQGNKQKLIPLGRALDRVLTWNNYMLPMWYMA

QDRTAWWNKFSFPATRPIYSSGLDTWWYDVNKAATLPADRR

>lcl|NZ\_FO834906.1\_prot\_WP\_004149130.1\_3894 [locus\_tag=BN49\_RS21125] [protein=microcin C ABC transporter permease YejB] [protein\_id=WP\_004149130.1] [location=4034516..4035610] [gbkey=CDS]

MGSYLIRRLLLVIPTLWAIITINFFIVQIAPGGPVDQAIAAIEFNQRGGMPGAGDGGMGASHARTGAGNI

SEGHYRGGRGLDPEVIAEITHRYGFDKPLHERYLKMLSDYLRFDFGDSLFRSASVLQLIKDSLPVSVSLG

LWSTLIIYLVSIPLGIRKAVSNGSRFDIWSSTLIIIGYAIPAFLFAILLIVIFAGGSYFDLFPLRGLVSP

NFDTLPWYQKILDYLWHITLPVLATVIGGFAALTMLTKNSFLDEIRKQYVVTARAKGVGEKQILWGHVFR

NAMLLVIAGFPATFISMFFTGSLLIEVMFSLNGLGLLGYEATVSRDYPVMFGTLYIFTLIGLLLNIVSDI

SYTLVDPRIDFEGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002912972.1\_3895 [locus\_tag=BN49\_RS21130] [protein=microcin C ABC transporter permease] [protein\_id=WP\_002912972.1] [location=4035610..4036635] [gbkey=CDS]

MSFFSPVNQARWARFRHNRRGYWSLWLFLILFLCSLGAELLANDRPLLVQYRGQLYVPVLKNYTEQTFGG

AFATAADYQDPWLQQQLATHGWALWPPVRFGATTINFASTVPFPSPPSASNWLGTDANGGDVLARILYGT

RISVLFGLLLTLFSSVLGVLAGAIQGYYGGKIDLWGQRFIEVWSGMPTLFLIILLSSVVQPGFWWLLAIT

VLFGWMTLVGVVRAEFLRTRNYDYVRAAQALGVSDRQIILRHMLPNAMVATLTFLPFILCSSITTLTSLD

FLGFGLPLGSPSLGELLLQGKNNLQAPWLGIAAFLSVAVLLTLLIFIGEAVRDAFDPSKAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530087.1\_3896 [gene=yejF] [locus\_tag=BN49\_RS21135] [protein=microcin C ABC transporter ATP-binding protein YejF] [protein\_id=WP\_016530087.1] [location=4036637..4038226] [gbkey=CDS]

MTHPLLAIDNLSIAFRQQGETQTVVHNLSLEVAVGETLALVGESGSGKSISALSVLRLLPTPPASYPSGD

IRFHGQSLLHADEATLRGVRGNRIAMIFQEPMVSLNPLHTLEKQLYEVLSLHRGMRKQAARGEILDCLER

VGIRQAPRRLADYPHQLSGGERQRVMIAMALLTRPELLIADEPTTALDVSVQAQILQLLRELKQELNMGL

LFITHNLSIVRQLADRVAVMQNGRCVEHNDCRALFSAPAHPYTQRLLDSEPDGEPVPLAADAPVLLQADD

LKVAFPVRKGILRRVVDHHRVVNSLSFQLRAGETLGLVGESGSGKSTTGLALLRLIPSGGKITFAGQPIQ

GRNRRQLLPLRRQMQVVFQDPNSSLNPRLTAQQIIEEGLRVHQPTLTAAEREQSVILAMQEVGLDPASRQ

RYPAAFSGGQRQRIAIARALIVKPQLIVLDEPTSSLDKTVQAQILNLLKALQRKHQLAYIFISHDLGVVR

ALCHQVMVLRQGEVVEQGECKSVFSAPRHEYTRQLLALS

>lcl|NZ\_FO834906.1\_prot\_WP\_002912974.1\_3897 [locus\_tag=BN49\_RS21140] [protein=YejG family protein] [protein\_id=WP\_002912974.1] [location=complement(4038230..4038574)] [gbkey=CDS]

MNTQQLSIVHRLPQSYRWLAGFAGSRVEPIPQNGAQNENSLVALKLLSPDGEKAWPVMHKLSQALSDIEV

DCSVLECEGEPCLFVNLQDEFAATCRLKNFGVAIAEPFSGNNPF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530086.1\_3898 [locus\_tag=BN49\_RS21145] [protein=Bcr/CflA family multidrug efflux MFS transporter] [protein\_id=WP\_016530086.1] [location=complement(4038906..4040120)] [gbkey=CDS]

MTLKQNSSLGIVFILGLLAMLMPLSIDMYLPALPVIAAQYNVPDGSAQMTLSTYILGFALGQLLYGPMAD

SLGRKPVILGGTLVFAAAAVACALSQTVDMLIVMRFFHGLAAAAASVVINALMRDIYPKDEFSRMMSFVM

LVTTIAPLVAPMVGGAVLVWFSWHAIFWILALVALVALVALLASLMIGLFVRETLPAERRQPFHLRTTLG

NFATLFRHKRVLSYMLASGFSFAGMFSFLSAGPFVYININHVAPQHFGYYFALNIVFLFLMTMFNSRFVR

QVGALRMFRAGLWIQFAMAVWMVVCALLDVGFWSLVIGVAAFVGCVSMVSSNAMAVILDEFPHMAGTASS

LAGTFRFGIGAIIGALLSMATFTTAWPMLISIAFCATCSIFFSLYASRRRKIAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002912977.1\_3899 [gene=rsuA] [locus\_tag=BN49\_RS21150] [protein=16S rRNA pseudouridine(516) synthase RsuA] [protein\_id=WP\_002912977.1] [location=complement(4040117..4040836)] [gbkey=CDS]

MRLDKFIAQQLGVSRAIAGREIRGSRVTVDGDIVKDASFKLQPEHEVEYDGNTLTQQNGPRYFMLNKPQG

YVCSTDDPDHPTILYFLDEPVAHKLHAAGRLDIDTTGLVLMTDDGQWSHRITSPRHHCEKTYLVALESPL

AEGTAELFAKGVQLHNEKDLTKPALLEVITPTEVRLTISEGRYHQVKRMFAAVGNHVVGLHRERIGDILL

DESLAPGEYRPLTEAEIASVGAPQPRSKT

>lcl|NZ\_FO834906.1\_prot\_WP\_004899509.1\_3900 [locus\_tag=BN49\_RS21155] [protein=DEAD/DEAH box helicase] [protein\_id=WP\_004899509.1] [location=4040984..4042741] [gbkey=CDS]

MTFTLRPYQQEAVDATLAWFRRHTEPAAIVLPTGAGKSLVIAELARLARGRVLVLAHVKELVAQNHAKYC

ALGLEADIFAAGLQRKESHGKVVFGSVQSVARNLDQFRSEFSLLIVDECHRISDDDDSQYQQIIGHLRQV

NPQIRLLGLTATPFRLGKGWIYQFHYHGMVRGDEKALFRDCIYELPLRYMIKHGYLTPPERLDMPVVQYD

FSRLQAQSNGLFSEADLNHELKKQQRITPHIVSQIVEFAENRKGVMIFAATVEHAREVTGLLPVGQAALI

TGETPGPERDRIIEAFKAQAYRYLVNVAVLTTGFDAPHVDLIAILRPTESVSLYQQIVGRGLRLAPGKTD

CLILDYAGNPHDLYAPEVGTPKGKSDNVPVQVFCPACGFANTFWGKTTADGTLIEHFGRRCQGWFEDDDG

HREQCDFRFRFKNCPQCNAENDIAARRCRECDTILVDPDDMLKAALKLKDALVLRCSGMALQHGGDEKGP

WLKITYYDEDGADVSERFRLQTPAQRTAFEQLFIRPHTRPPGVPLRWITPADIVTQQALLRHPDFVVARM

KGQYWQVREKVFDYQGRFRRANELR

>lcl|NZ\_FO834906.1\_prot\_WP\_002912979.1\_3901 [gene=rplY] [locus\_tag=BN49\_RS21160] [protein=50S ribosomal protein L25] [protein\_id=WP\_002912979.1] [location=4042878..4043162] [gbkey=CDS]

MFTINAEVRKEQGKGASRRLRAANKFPAIIYGGEAAPVAIELDHDKVWNMQDKAEFYSEVLTVVVDGKEE

KVKVQAVQRHAFKPKLTHIDFVRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530716.1\_3902 [locus\_tag=BN49\_RS21165] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016530716.1] [location=complement(4043221..4044108)] [gbkey=CDS]

MKTLQYSFAQIEAFATIAETGSLSQAAIRLAKDRTTLRDLLDYLEDALGYRLFSREGRSLTLTAEGEQLF

RQAHLLLRQAQAFESFAQTLPQTAGQALRLVYDPFVPREFLCALADNLARRQIRLSCWSASRREAEQALS

DGVAEMAICQANNRTLGSEMEWRALGTVDLRFYAADSLFHDAPRPLTLLNLSLTPQLVMHRRSDDQIARR

LQISGHTLYMNEITLLRHALEQGRGWGFLPDHLRLGEWQGVSEIATEVGSQGLNVTMVMLWLPGMNKHRM

LSDIVHEAPELWQRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530717.1\_3903 [locus\_tag=BN49\_RS21170] [protein=serine hydrolase] [protein\_id=WP\_016530717.1] [location=4044213..4045499] [gbkey=CDS]

MIRKPLALALILAALPAAAMAQHCGSLTLDVCPTPYDQTLPAAKDMLSWDQTSRVIGFRNDYRNYAGDVF

RHGASTPLERAEKQLTDARYTLNGHTWNLQDYLKRENVSGMLVLKDGKVAWKYLAEGNTDTTLWTSRSVG

KSVVSTLVGIAIQQGKIHSLDDLITVYEPELKGTAWDGVTLKQLIQHTSGVEWNEDYTDPQSHFARLTQC

EAQPGAYTCVRKIVTGLARQHPAGEQWSYSSGGAWLLGDILERATGMSLAAWLEQALWQPAGMAHDGVWH

AYQQGKHDVGAHGFNATLEDWGRFGEFVARDGRLSNGKQLVPAGWFDQAASWTKALNSVSAAHPEGIYGY

QWWNNAIPANAQNVQPTPQEGLKGSLWALGIYGQVIMVNRAEHLVIVQWSTWPQAEPSFNAQPLEAALMY

SAIARELR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530718.1\_3904 [locus\_tag=BN49\_RS21175] [protein=NUDIX domain-containing protein] [protein\_id=WP\_016530718.1] [location=complement(4045518..4046114)] [gbkey=CDS]

MQTHAPHVRHVRETLLSDNWYTLKKYTFELLRRDGRWQELSREAYDRGNGAVILLYNREKRTVVLTRQFR

FPVFTHGHDGYLIEAAAGLLDNASPEARIVAEAEEETGFRVTRVEPVFTVFMSPGSVTEKLYFFIAEYQA

DDRRGDGGGLAAEGEDIEVLEWPLTRALQAIRDGEIMDAKTIILLQYLALNADTLLAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002912986.1\_3905 [locus\_tag=BN49\_RS21180] [protein=DeoR/GlpR family DNA-binding transcription regulator] [protein\_id=WP\_002912986.1] [location=4046197..4046958] [gbkey=CDS]

MLASQRKQQILQILTEEKQVMSGELSQRFNVSEDSIRRDLRELAAEGKLQRVHGGALPVSAAIAPIETRK

SVQIASKQAVARAAAALIQPGQVVIVDGGTTTAAMIGFLPADLSCTVVTHSPGIAVALVDHPRIEVILLG

GRVFKHSVVAVGAETLAGMARINADLFFMGVTGVHPRAGFTTGDYEEAGIKRALTARAAETVVMASREKL

NAASAFAIGELSLASTLIVDGEPDAALRQQLVQSGVEIVPVQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004144267.1\_3906 [gene=yejK] [locus\_tag=BN49\_RS21185] [protein=nucleoid-associated protein YejK] [protein\_id=WP\_004144267.1] [location=complement(4046978..4047985)] [gbkey=CDS]

MSLDIDQIALHQLIKRDEQNLELVLRESLLEPNATVVEMMAELHRVYSAKSKAYGLFNEESELAQALRLQ

RQGEEEFLAFSRAATGRLRDELAKYPFAEGGIVLFCQYRYLAVEYLLVAVLNNLSSMRVNEELDIRSTHY

LDINHADIVARIDLTEWETNPESTRYLTFLKGRVGRKVADFFMDFLGASEGLNAKAQNRGLLQAVDDFAA

DAQLDKSERQNVRQQVYAYCNEQLQAGEEIELESLSKELAGVSEKSFQEFTAEQGYELEESFPADRSTLR

QLTKFAGSGGGLTINFDAMLLGERVFWDPATDTLTIKGTPPNLRDQLQRRTSGGN

>lcl|NZ\_FO834906.1\_prot\_WP\_004195346.1\_3907 [locus\_tag=BN49\_RS21190] [protein=YejL family protein] [protein\_id=WP\_004195346.1] [location=4048172..4048399] [gbkey=CDS]

MPQISRYSDQQVEQLLSELTNVLESHKAPVDLSLMVLGNMVTNLINSSVAPAQRQAIARSFAQALQSSIN

DDPAH

>lcl|NZ\_FO834906.1\_prot\_WP\_002912990.1\_3908 [gene=yejM] [locus\_tag=BN49\_RS21195] [protein=LPS biosynthesis-modulating metalloenzyme YejM] [protein\_id=WP\_002912990.1] [location=4048418..4050178] [gbkey=CDS]

MVTLRQPYREKVSQMVSWGHWFALFNMLLAMVLGSRYLFVADWPTTLAGRLFSYVSLVGHFSFLVFTSYV

LILFPLTFIVVSQRLMRFLSVILATAGMTLLLIDSEVFTRFHLHLNPVVWELVINPDQNEMARDWQLMFI

SVPVIFLIEMLFATWSWQKLRSLTRRRHYARPVAWFFFLSFVSSHLVYIWADANFYRPITMQRANLPLSY

PMTARRFLEKHGLLDAQDYQRRLVEQGAPEAVSVQYPLSNLRYRDLGAGYNVLLITVDNLNYSRFEKTMP

ALAAFAKENVNFTQHMSSGNTADSGLFGLFYGISPGYMDGVLSARIPAALITALNQQGYQLGLFSSDGFS

SPLYRQALLSDFSLPSAKTQSDEQTANQWIGWLDRYAQDENRWFSWISLNGTTLDDTQQQGFVRRYSKAA

GDVDAQIDRVLTALREAGKLDNTVVIITGGHGKPLNAKHDAFDWSREQLQVPLVIHWPGTPAQEIATLTD

NKDVMTTLMQRLLHVSTPANEYSQGEDLFSAARRRNWVTAANGDTLAITTPTITVVLNHNGTYTTWSRDG

EKIKDQKPQLSLLLQVLTDEKRFIAN

>lcl|NZ\_FO834906.1\_prot\_WP\_002912992.1\_3909 [locus\_tag=BN49\_RS21205] [protein=AI-2E family transporter] [protein\_id=WP\_002912992.1] [location=4050516..4051625] [gbkey=CDS]

MRVNGLTKGFFILIVFIVTLAFFDVLSPYYSAILWAAILAVIFNPVKNKIRTRLGERNGLAALMTIVIIC

LIVFTPLAIILSSLAYELNLVYSKLQHNDTQFPTVVASLFAHLPGWARSFLADHNLDSAQQIQQQLSDAA

LKGGQYLAGSAFLIGKGTFGFTVSFGIMLYLLFFLLKDGPYLVLLILESLPLSSYVKQHLFAKFAAVARA

TVKGTVAVALAQGALGGFAFWIAGLDGSILWGALMAFLSLIPAVGSAIIWVPAAIYLFATGQLWQGAFIV

GFFVIVIGLVDNILRPLLVGKDTRMPDYLILIATLGGMEIYGINGFVIGPLIAALFIACWNLLSGREHAG

NTDEIDEEFIEEAKNSRNE

>lcl|NZ\_FO834906.1\_prot\_WP\_004175048.1\_3910 [gene=eco] [locus\_tag=BN49\_RS21210] [protein=serine protease inhibitor ecotin] [protein\_id=WP\_004175048.1] [location=4051800..4052291] [gbkey=CDS]

MKKITTLAVSLLTAACMSAGALAADQPLEKVAPFPKAEKGMKRQVIQLPQQQDESALKVELMIGQTLEVD

CNHHRLGGELESKTLEGWGYDYYVFEKLSGPVSTMMACPDGKKEKKFVTAGLGDDAMLRYNSKLPIVVYT

PSNVDVKYRIWRADETIGNAVVR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530721.1\_3911 [gene=mqo] [locus\_tag=BN49\_RS21215] [protein=malate dehydrogenase (quinone)] [protein\_id=WP\_016530721.1] [location=complement(4052358..4053992)] [gbkey=CDS]

MNKKMAVPRSQAVGPNSTRTNTRHEQETDVLLIGGGIMSATLGTWLQELEPDWSITMVEQMSSVAEESSN

GWNNAGTGHAALMELNYTPQTANGINIDKAVDINEAFHISRQFWAHQVTRGVLNKPKSFINSVPHMSFVW

GEDNVNFLRARYAALQQSELFRGIRYSEDHQQIKAWAPLVMEGRDPLQKVAATRSEVGTDVNYGEITRQL

IAGLQKHDNFSLQLGTVVRRFKRNADKSWTVTLADADNRRQKRVIKAKFIFIGAGGAALTLLQETGIPQA

KEYAGFPVGGQFLVCENPEVVNHHLAKVYGQAEVGAPPMSVPHIDTRIIDGKRVVLFGPFATFSTRFLKN

GSLWDLLASTNTSNILPMLNVGLDNFDLVKYLISQVMQKDKDRLAALCEYYPEARKEDWRLWQAGQRVQI

IKRDAKKGGVLRLGTEVVSDDEGTVAALLGASPGASTAAPIMLQLMEKVFKDKVNSPEWQAKLKAIIPTY

GVRLDGNPAEIEKALAWTSEVLELKYEPAGAVDEVPQAELKPLSGGKPMADIAL

>lcl|NZ\_FO834906.1\_prot\_WP\_129015099.1\_3912 [locus\_tag=BN49\_RS21220] [protein=SulP family inorganic anion transporter] [protein\_id=WP\_129015099.1] [location=4054352..4055512] [gbkey=CDS]

MLAGVLTALALIPEVISFSVIAGIDPQVSLIASVVLCLAMSVFGGRPAMVTAAAGSVALVIGPMVHQHGV

GYILPAVILAGIIQILFGLCGMARLMRFIPPAVMTGFVNALGILIFFAQVPHFWSRQPLIVGLFVLTLLI

VLWAPRVIKAIPAPLIAIVALTLYTATTGQQLPTVGDEGSMSGGLPGFTALTVPLNLTTLQIIWPCALSI

AFVGLMESLLTAKLVDDLTHTSSNKSRESAGLGIANILAGCYGGIAGCAMIGQTIVNVEMGRARSRLSTV

IAGLVLLLLVTALSQVMAKIPMAVLAGVMVIVAVKTFSWHSIRPGELARNPWPETLVMLVTVAATVGTSN

LAIGVLAGIVAMAIIPRRLRAKAQATLETASPDPEK

>lcl|NZ\_FO834906.1\_prot\_WP\_002912996.1\_3913 [gene=mgtE] [locus\_tag=BN49\_RS21225] [protein=magnesium transporter] [protein\_id=WP\_002912996.1] [location=complement(4055475..4056911)] [gbkey=CDS]

MSVLHKKSARLRDEERARLIWLLSTDKAVTSALLGKLTLAERYDEGTLADDLAEVEMLVSHLPPPDLADA

LEALPYDARTALWCLVPDDKRGEVLLEASENVWGDLIDKMSDPELLQAMQPLDIDEQVYLLQHLPRNLTG

RLLATLPAEKRARIRQIMRYADNSVGSIMEFEVITVRPEATLAAVQRYLRRLGKMPENTDKLFVTTRNKL

LLGELELQTILLNDAQKRVGEVMEGDPVTFQPHEEAEKVARTFERDDLLSAAVIDADGKLIGRLTIDEIV

DVVYEETDNDLRRMGGLSDEEDVFAPVSKAVKTRWAWLAVNLCTAFIASRVIDGFEHTISQLVALASLMP

IVAGIGGNTGNQTITMIVRAMALQQIQPGSFTFLILREMGVALINGLVWGGIMGAITWWLYDDPQLGGVM

TLAMMLNLLMAAMMGVIIPMVMVKLGRDPAVGSSVMITAITDTGGFFIFLGLATLFLM

>lcl|NZ\_FO834906.1\_prot\_WP\_004184919.1\_3914 [locus\_tag=BN49\_RS21230] [protein=multidrug ABC transporter permease/ATP-binding protein] [protein\_id=WP\_004184919.1] [location=complement(4057062..4058705)] [gbkey=CDS]

MELLSLVWRQYRWPFLGVIALSLLSAALGIGLIAFINLRLITAVDTSLRVLPEFLGLLGLLMAVTLGSQL

ALTTLGHHFVYRLRGEFVKRILDTQIEQVEKIGSASLLAGLTSDIRNITIAFVRLPELVQGIILTFGSAA

YLAWLSGKMMLVTALWMALTIWGGFVLVSRVYKHMASLRETEDKLYHDYQTVLEGRKELTLNRERAEYVF

NQLYLPDAREYRHHIVRADTFHLSAVNWSNIMMLGAIGLVFWMANSLGWADTAVAATYSLTLLFLRTPLL

SAVGALPTLLSAQVAFNKLRQFSLAPYRADFPRPQAHPDWQTLELRDVTFHYPDQRFAVGPLNLTLKRGE

LVFLIGGNGSGKSTLAMLLTGLYQPISGQILVDGQPLAAERPEEYRKLFSAVFTDVWLFDRLLGPQGEEA

DPALVATWLERLQMAHKLQLENGKIADLRLSKGQKKRVALLLALAESRDIILLDEWAADQDPHFRREFYQ

VLLPLMQQMGKTVFAISHDDHYFQHADRLLEMRAGQLAELTGEEREQASRDAVARTA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530253.1\_3915 [gene=alkB] [locus\_tag=BN49\_RS21235] [protein=DNA oxidative demethylase AlkB] [protein\_id=WP\_016530253.1] [location=complement(4058780..4059433)] [gbkey=CDS]

MLDLFSDTPPWQEPLAPGAVVLRRFARERAPALLQAIADVASQSPFRQMVTPGGYTMSVAMTNCGALGWT

TDRQGYLYAPVDPVTDQTWPPMPAVFHELALAAAAAGGYPEFSPDACLINRYCPGAKLSLHQDKDEQDLR

APIVSVSLGLPAIFQFGGLQRSDPLQRLLLEHGDVVVWGGESRLFYHGIQPLKAGHHPETGDCRYNLTFR

QAGGRQY

>lcl|NZ\_FO834906.1\_prot\_WP\_004211965.1\_3916 [gene=ada] [locus\_tag=BN49\_RS21240] [protein=bifunctional DNA-binding transcriptional regulator/O6-methylguanine-DNA methyltransferase Ada] [protein\_id=WP\_004211965.1] [location=complement(4059433..4060497)] [gbkey=CDS]

MKPIVADTDDRRWQAVCERDTRADGQFVFAVLTTGICCRPSCRSRRARRENVRFFADVAAAVAAGFRPCK

RCQPDKDYPQQQRVDKVAQACRLLEQDAPLTLEALAGQLAMSPFHFHRLFKSVTGMTPKAWQQAWRAQRL

REALEQGIPVTRAALAAGFPDSSSYYRQADAALGMTASQFRRGGAATVVTWTTGDCALGRCLVAQSERGV

CAVLPGDNDAALLDDLRRRFPNAELREGDPDFCQQMAEIFAHLDDSRRPVSLPLDLQGTAFQLQVWQALR

QIPAGETRSYRQVAEHIGQPRAVRAVAGACAANSLAVIVPCHRVVREDGALSGYRWGTARKAQLLAREAQ

HEEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532310.1\_3917 [gene=apbE] [locus\_tag=BN49\_RS21245] [protein=FAD:protein FMN transferase ApbE] [protein\_id=WP\_016532310.1] [location=complement(4060571..4061623)] [gbkey=CDS]

MDMTFFRAALLGACVLLSGCDSATTPATPTATATVLDGKTMGTFWRVSVIGVDEAKAQALRAKVQAQLDA

DDRLLSTWKNDSALMRFNHAATTEPWPVSEAMADIVTLSLRIGAKTHGAMDITVGPLVNLWGFGPDKQPV

TTPDAQAIAAAKARTGLQHLQVINQSGRQFLQKDIPDLFVDLSTVGEGYAADHLARLMEQEGISRYLVSV

GGALVSRGMNGEGKPWRVAIQKPTDRENAVQAIVDINGHGISTSGSYRNYYELDGKRISHVIDPQTGQPI

THKLVSVTVIAPTALEADGWDTGLMVLGPEKAQQVVREEGLAVYMIVKEGEGFKTWMSPQFRTFLVGEKN

>lcl|NZ\_FO834906.1\_prot\_WP\_004180702.1\_3918 [locus\_tag=BN49\_RS21250] [protein=porin OmpC] [protein\_id=WP\_004180702.1] [location=complement(4061727..4062824)] [gbkey=CDS]

MKVKVLSLLVPALLVAGAANAAEIYNKDGNKLDLYGKIDGLHYFSDDKSVDGDQTYMRVGVKGETQINDQ

LTGYGQWEYNVQANNTESSSDQAWTRLAFAGLKFGDAGSFDYGRNYGVVYDVTSWTDVLPEFGGDTYGSD

NFLQSRANGVATYRNSDFFGLVDGLNFALQYQGKNGSVSGEGATNNGRGWSKQNGDGFGTSLTYDIWDGI

SAGFAYSHSKRTDEQNSVPALGRGDNAETYTGGLKYDANNIYLASQYTQTYNATRAGSLGFANKAQNFEV

VAQYQFDFGLRPSVAYLQSKGKDLERGYGDQDILKYVDVGATYYFNKNMSTYVDYKINLLDDNSFTRNAG

ISTDDVVALGLVYQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002913006.1\_3919 [gene=rcsD] [locus\_tag=BN49\_RS21255] [protein=phosphotransferase RcsD] [protein\_id=WP\_002913006.1] [location=4063595..4066252] [gbkey=CDS]

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NIAATSVNTASGGLQETRLKQDVYYLEKPRRKTEALIFGSHDSSTLEMTQKMSDYLDILWGAETIPWSMY

YLNGLDNSLILVSTLPLKDLSSSFKESTISSVVESRRAEMLLQANTLDERETFSPLRHLAWQNAHYFTLR

TTFNQPGHLATVVAFDLPINDLIPPGMTIDSFRIEPDPSQNLATTPDKESADHIGITFNGMQIDIATDIS

TTGMQLLWTVPMSTMLLESMQNILLPLLLNIGLLALALFGFTTFRHYKGRSHSSGAGLPSAANSELRLLR

AINEEIVSLLPLGLLVHDQEANRTVISNPIADHLLPHLNLQNITNMADQHQGVIQATVNNEQYEIRQYRS

QVAPRTQILIIRDQDREVLVNKKLKQAQRLYEKNQQGRAAFMQHIGSALKQPALTLAAEAAALSSTENRT

LAQHADELVKLIDDIQLANLLESDAWKTNQTLFSVQELIDDVVPEVLPAMKRKGLQLLINNALPAGEQRY

GDREALRRTLVLLIQYSVTTTPIGKITLDVCQDESASDRLTFRILDTGNGVSANEIDNMHFPYLNETQSD

LYGKANALTFWLCDRMTRKLGGQLTIKARESLGTRYTLHLKMPASEEAPEAGEHLLDDVIVLLDVTSSEV

RRIVTRQLESWGASCITPDDRATSQAFDLYLTDNPSNLTASGLLLSDDEVGIRKIGPGQLRVNFNISTAM

QEAILQLIEQQLAEEAVQPVTSGNESNAELHASGYYALFADTVPDDVQRLYTEIEAGDFAALAQTAHRLK

GAFAMLNLIPGKQLCETLEHLIREKDAQGIEKYISDIDAYVKSLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913007.1\_3920 [gene=rcsB] [locus\_tag=BN49\_RS21260] [protein=response regulator transcription factor RcsB] [protein\_id=WP\_002913007.1] [location=4066268..4066918] [gbkey=CDS]

MNTMNVIIADDHPIVLFGIRKSLEQIEWVNVVGEFEDSTALINNLPKLDAHVLITDLSMPGDKYGDGITL

IKYIKRHFPDLSIIVLTMNNNPAILSAVLDLDIEGIVLKQGAPTDLPKALAALQKGKKFTPESVSRLLEK

ISASGYGDKRLSPKESEVLRLFAEGFLVTEIAKKLNRSIKTISSQKKSAMMKLGVENDIALLNYLSSVSL

SATDKE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532311.1\_3921 [gene=rcsC] [locus\_tag=BN49\_RS21265] [protein=two-component system sensor histidine kinase RcsC] [protein\_id=WP\_016532311.1] [location=complement(4066964..4069804)] [gbkey=CDS]

MKYLASFHTTLKVSRYLFRALAVLLWLLIAFVSVFYIVNALHEREAEIHQELNLNADQAQRYIQRTADVM

KELKYVAGNRLSAGDAVAQGQNGDMAVPNFEPLYPDSDCSAMSATWRNSLQSLAWFMRYWRDNFTAAYDL

NRIFLIGSDNLCMANFGLRDVPIERDQALKVLHQRIEQYRNAPQNERGNNLFWISQGVRPGVGYFYALTP

VYMANRLQAMLGVEQTIRMESFFTPGSLPMSVTIFDDNGQPLISLAGAEGKIQSEAKWMQERMWFGYSSG

FRELVLKKSLSPSSLSIVYSVSVDQVLERIRMLIINAIVLNILSGAMLFALARMYERRIFIPAENDAQRL

EEHEQFNRKIVASAPVGICILRTADGTNILSNELAHNYLNMLTHEDRQRLTQIICGQQVNFVDVLTSNHT

NLQISFVHSRYRNENVAICVLVDVSARVKMEESLQEMAQAAEQASQSKSMFLATVSHEMRTPLYGIIGNL

DLLQTKALPKGVDRLVTAMNNSSSLLLKIISDILDFSKIESEQLKIEPREFSPREVMNHISANYLPLVVR

KQLGLYCFIEPDVPEQMSGDPMRLQQVISNLLSNAIKFTDTGCIVLHVQCAGDYLQISVRDTGEGIPAKE

VLRLFDPFFQVGTGVQRNFQGTGLGLAICEKLISMMDGDIAVETEPGMGSRFTIRIPLYRVQNTSPVSRD

GFAGKTCWLAIHNTSLAMFVTSLLSYHGLTVRRHAGETPDAEDVLLTDDEALSGWQGRAMVIFCRRHIGI

PQERSAGEWLHSVTTPHELLPLLGRIFHVALASAENSPALMAPEAQAGNNDDMMILVVDDHPINRRLLAD

QLGSLGYQCVTANDGIDALNVLSKQHIDIVLSDVNMPNMDGYRLTQRIRQLGLTLPVIGVTANALAEEKQ

RCLESGMDSCLSKPVTLDVLKQTLTVYAARVRKGRE

>lcl|NZ\_FO834906.1\_prot\_WP\_004140833.1\_3922 [gene=gyrA] [locus\_tag=BN49\_RS21270] [protein=DNA topoisomerase (ATP-hydrolyzing) subunit A] [protein\_id=WP\_004140833.1] [location=complement(4069936..4072569)] [gbkey=CDS]

MSDLAREITPVNIEEELKNSYLDYAMSVIVGRALPDVRDGLKPVHRRVLYAMNVLGNDWNKAYKKSARVV

GDVIGKYHPHGDSAVYDTIVRMAQPFSLRYMLVDGQGNFGSIDGDSAAAMRYTEIRLAKIAHELMADLEK

ETVDFVDNYDGTERIPDVMPTKIPNLLVNGASGIAVGMATNIPPHNLTEVINGCLAYVDDEDISIEGLMA

HIPGPDFPTAAIINGRRGIEEAYRTGRGKVYIRARAEVEVDAKSGRETIIVHEIPYQVNKARLIEKIAEL

VKEKRVEGISALRDESDKDGMRIVIEVKRDAVGEVVLNNLYSQTQLQVSFGINMVALHHGQPKIMNLKDI

IAAFVRHRREVVTRRTIFELRKARDRAHILEALAVALANIDPIIELIRRAPTPAEAKTALVAQAWDLGNV

AAMLERAGDDAARPEWLEPEFGVRDGKYYLTEQQAQAILDLRLQKLTGLEHEKLLDEYKELLEQIAELLH

ILGSADRLMEVIREELELIRDQFGDERRTEITANSADINIEDLINQEDVVVTLSHQGYVKYQPLTDYEAQ

RRGGKGKSAARIKEEDFIDRLLVANTHDTILCFSSRGRLYWMKVYQLPEASRGARGRPIVNLLPLEADER

ITAILPVREYEEGVNVFMATASGTVKKTALTEFSRPRSAGIIAVNLNEGDELIGVDLTSGQDEVMLFSAA

GKVVRFKEDAVRAMGRTATGVRGIKLAENDSVVSLIIPRGEGAILTVTQNGYGKRTAAAEYPTKSRATQG

VISIKVTERNGSVVGAVQVDDCDQIMMITDAGTLVRTRVSEVSIVGRNTQGVILIRTAEDENVVGLQRVA

EPVDDEELDAIDGSAAEGDDDIAPEADTDDDIAEDEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913014.1\_3923 [locus\_tag=BN49\_RS21275] [protein=bifunctional 3-demethylubiquinone 3-O-methyltransferase/2-octaprenyl-6-hydroxy phenol methylase] [protein\_id=WP\_002913014.1] [location=4072716..4073444] [gbkey=CDS]

MNAEKTSVAPNVDHAEIAKFEAVASRWWDLEGEFKPLHRINPLRLGYIAERSGGLFGKKVLDVGCGGGIL

AESMAREGATVTGLDMGAEPLQVARLHALESGIQVDYVQETVEEHAAKHPQQYDVVTCMEMLEHVPDPQS

VVHACARLVKPGGQVFFSTINRNGKAWLMAVVGAEYVMKMVPKGTHDVKKFIKPAELLGWVDQTTLKEQH

IIGLHYNPLTNTFKLAPGVDVNYMLHTTAKQD

>lcl|NZ\_FO834906.1\_prot\_WP\_009307388.1\_3924 [gene=nrdA] [locus\_tag=BN49\_RS21280] [protein=ribonucleoside-diphosphate reductase subunit alpha] [protein\_id=WP\_009307388.1] [location=4073789..4076074] [gbkey=CDS]

MNQSLLVTKRDGTTERINLDKIHRVLDWAAEGLNNVSISQVELRSHIQFYDGIKTADIHETIIKAAADLI

SRDAPDYQYLAARLAIFHLRKKAFGQFEPPALYDHVVKMVEKGKYDHHLLEDYTEEEFQQMDGFLDHWRD

MNFSYAAVKQLEGKYLVQNRVTGEIYESAQFLYILVAACLFSNYPRETRLDYIKRFYDAVSTFKISLPTP

IMSGVRTPTRQFSSCVLIECGDSLDSINATSSAIVKYVSQRAGIGINAGRIRALGSPIRGGEAFHTGCIP

FYKHFQTAVKSCSQGGVRGGAATLFYPMWHLEVESLLVLKNNRGTDANRVRHMDYGVQINKLMYTRLLKG

GDITLFSPSDVPGLYDAFFADQDEFERLYTQYEQDDTIRKQRIKAVELFSLMMQERASTGRIYIQNVDHC

NTHSPFDPVVAPVRQSNLCLEIALPTKPLEDVNDENGEIALCTLSAFNLGAIDSLDELEELAVLAVRALD

ALLDYQDYPIPAAKRGAMGRRTLGIGVINFAYYLAKHGKRYSDGSANNLTHKTFEAIQYYLLKASNELAI

EQGACPWFNETTYAQGILPIDTYKKDLDGIVSEPLHYDWEALRESIKTHGLRNSTLSALMPSETSSQISN

ATNGIEPPRGHVSIKASKDGILRQVVPDYENLQNAYELLWEMPNNDGYLQLVGIMQKFIDQSISANTNYD

PTRFPSGKVPMQQLLKDLLNAYKFGVKTLYYHNTRDGAEDAQDDLAPSIQDDGCESGACKI

>lcl|NZ\_FO834906.1\_prot\_WP\_004140835.1\_3925 [gene=nrdB] [locus\_tag=BN49\_RS21285] [protein=ribonucleotide-diphosphate reductase subunit beta] [protein\_id=WP\_004140835.1] [location=4076176..4077306] [gbkey=CDS]

MAYTTFSQTKNDQLLEPMFFGQPVNVARYDQQKYDIFEKLIEKQLSFFWRPEEVDVSRDRIDYQALPEHE

KHIFISNLKYQTLLDSIQGRSPNVALLPLISIPELETWVETWAFSETIHSRSYTHIIRNIVNDPATVFDD

IVTNEQIQKRAEGISHYYDSLIEMTSYWHLLGEGTHTVNGKTVTVNLRELKKKLYLCLMSVNALEAIRFY

VSFACSFAFAERKLMEGNAKIIRLIARDEALHLTGTQHMLNLLRSGSDDPEMAEIAEECKQECYDLFVLA

AQQEKEWADYLFRDGSMIGLNKDILCQYVEYITNIRMQAVGLDLPFQTRSNPIPWINTWLVSDNVQVAPQ

EVEVSSYLVGQIDSEVDADDLSNFQL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530376.1\_3926 [gene=yfaE] [locus\_tag=BN49\_RS21290] [protein=class I ribonucleotide reductase maintenance protein YfaE] [protein\_id=WP\_016530376.1] [location=4077306..4077560] [gbkey=CDS]

MKRIFLKISDARLECQDEHPSLLAALESHNINVEYQCREGYCGSCRTRLVSGQVDWLTEPLAFIQPGEIL

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>lcl|NZ\_FO834906.1\_prot\_WP\_014907172.1\_3927 [gene=glpQ] [locus\_tag=BN49\_RS21295] [protein=glycerophosphodiester phosphodiesterase] [protein\_id=WP\_014907172.1] [location=complement(4078022..4079092)] [gbkey=CDS]

MKMKLTALMSGMILSSSALCFSATAADKMVIAHRGASGYLPEHTLPAKAMAYAQGADYLEQDLVMTKDDR

LVVLHDHYLDRVTDVAQRFPQRARKDGRFYAIDFTLDEIKSLKFTEGFEPKNGKNVQTYPGRFPMGKSDF

RIHTFEEEIEFVQGLNHSTGKNIGIYPEIKAPWFHHQEGKDIAASTLKVLKEYGYTSKQDKVYLQCFDAN

ELKRIKNELEPKMGMDLNLVQLIAYTDWNETQQKQADGKWVNYSYDWMFKPGAMAQIAQYADGIGPDYHM

LVAEGSKPGAVKLTAMVKEAHASHLQVHPYTVRADQLPEYATNVNQLYDVLYNQAGVDGLFTDFPDKAVQ

FLDAKH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913019.1\_3928 [gene=glpT] [locus\_tag=BN49\_RS21300] [protein=glycerol-3-phosphate transporter] [protein\_id=WP\_002913019.1] [location=complement(4079102..4080448)] [gbkey=CDS]

MLSIFKPAAHKARLPAAEIDPLYRRLRWQIFIGIFFGYAAYYLVRKNFALAMPYLIEQGFSRGDLGFALS

GISIAYGFSKFIMGSVSDRSNPRIFLPAGLILAALVMLVMGFVPWATSSIMIMFVLLFLCGWFQGMGWPP

CGRTMVHWWSQKERGGIVSVWNCAHNVGGGIPPLLFLLGMAWFNDWHAALYMPAFGAILLAIFAFAMMRD

TPQSCGLPPIEEYKNDYPDDYSEKHEEELTAKQIFMQYILPNKLLWYIAIANVFVYLLRYGILDWSPTYL

KEVKHFALDKSSWAYFLYEYAGIPGTLLCGWMSDKVFKGNRGATGVFFMTLVTIATVVYWLNPPGNPGVD

MACMIIIGFLIYGPVMLIGLHALELAPKKAAGTAAGFTGLFGYLGGSVAASAIVGYTVDFFGWDGGFMVM

IGGSVLAVILLVIVMLGERRHHQQLKQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913020.1\_3929 [gene=glpA] [locus\_tag=BN49\_RS21305] [protein=anaerobic glycerol-3-phosphate dehydrogenase subunit A] [protein\_id=WP\_002913020.1] [location=4080720..4082342] [gbkey=CDS]

MTGRLDSEVIIIGGGATGAGIARDCARRGLRTLLIERHDIATGATGRNHGLLHSGARYAVTDNESARECI

SENRILRRIARHCIEPTNGLFITLPEDDLAWQQTFIDACQQAGIEATPLSPQEALRREPAVNPTLLGAVQ

VPDGTIDPFRLTAANMLDAREHGAQILTGCEVTGLLRRGDRVCGVQVYDRQLHQARTLYAGMVVNAAGIW

GQRIAEYADLRITMFPAKGSLLILDHRINNLVINRCRKPADADILVPGDTISLIGTTSMHIPYDEIDDNR

VTAAEVDTLLREGEKLAPVMGRTRILRAYSGVRPLVASDNDPSGRSVSRGIVLLDHAQRDGMEGFITITG

GKLMTYRLMAEWATDAVCRKLGNTTPCTTAEAPLPGSQEPTESTLQKIISLPTPLRGSAVYRHGDRTPSW

LGDSRQHRSLVCECEAVTAGEVKYAVENLAVNTLLDLRRRTRIGMGTCQGELCACRAAGLLQRFNVTTPA

QSLTQLSEFLNERWKGVQPIAWGDALRESEFTRWVYLGLCGLPQEHRDEV

>lcl|NZ\_FO834906.1\_prot\_WP\_023280376.1\_3930 [gene=glpB] [locus\_tag=BN49\_RS21310] [protein=glycerol-3-phosphate dehydrogenase subunit GlpB] [protein\_id=WP\_023280376.1] [location=4082332..4083591] [gbkey=CDS]

MKFDCAIIGGGLAGLLCGLALNQHGLRSVIISRGQSALHFSSASLDLLSALPNGDNVTDVAQGLQQLAEQ

LPEHPYSRLGAEAVLEYATQTEALLAACGAVMQGDARRPHRRVTPLGTLRPAWLSPLEVPVAPLPSQGAC

LVGISGFADFQPHLAAAALGQHGVTAAAVEIELPLLDVLRDNPTEFRAANIARVLDDENMWPALHAALLP

LAQQYDLLIMPACFGLADDRLYHWLQARLPCPLRLLPTLPPSVPGMRLHSQLQRQFIREGGAWLAGDEVV

KISHRQDAVEAVWTRNHGDIALRPRFTVLASGSFFSNGLVATRDSVREPILGLDLHQALPRESWYQRDFF

ASQPWQRFGVKTDALLRPLLGGQPFHNLFAIGSLLGGFDAIQLGCGGGVCAVTALHAARQIHALAGGRP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529919.1\_3931 [gene=glpC] [locus\_tag=BN49\_RS21315] [protein=anaerobic glycerol-3-phosphate dehydrogenase subunit GlpC] [protein\_id=WP\_016529919.1] [location=4083588..4084766] [gbkey=CDS]

MNDTRFESCIKCTVCTTTCPVSRVNPRYPGPKQAGPDGERLRLKDGALYDEALKYCINCKRCEVACPSDV

KIGDIIQRARAQYGQQKPTLRDAILSHTDLMGTLSTPFAPLVNAATGLKPVRRLLDATLNIDHRRTLPKY

GFGTFRRTYRQLAARQKQYSEQVAFFHGCYVNYNHPQLGKDLIRVVNALGTGVQLLSKEKCCGVPLIANG

FFDKARKQAQSNVAAMRENTLPIIATSSTCAFTLRDEYPHLLDVDNSDLRDRVELATRWIWKQLAAGRTL

PLRPLPLKVVYHTPCHMEKMGWSLYTLELLRLIPGLQLEVLDSQCCGIAGTYGFKTENYAVSQAIGAPLF

RQIEESGADLVVTDCETCKWQIEMSTSKRCEHPLTVLAQALV

>lcl|NZ\_FO834906.1\_prot\_WP\_002913043.1\_3932 [gene=yfaU] [locus\_tag=BN49\_RS21320] [protein=2-keto-3-deoxy-L-rhamnonate aldolase] [protein\_id=WP\_002913043.1] [location=complement(4084788..4085591)] [gbkey=CDS]

MNALLSNPFKRGLLRGETQIGLWLSSTSSYMAEIAATSGYDWLLIDGEHAPNTIQDLYHQLQAIAPYASQ

PVIRPVEGNRSLIKQVLDIGARTLLVPMVDTAEQAREVVSATRYPPIGSRGVGAGVARAARWGRVENYMA

EANDELCLLIQVESRTALENLDAILEVDGIDGVFIGPADLSASLGYPDDAGHPDVQRVIEQSIRRIRAAG

KAAGFLAVDPAMAEKCLAWGANFVAVGVDTMLYTQALDRRLAMFKSASAQPQEKTSY

>lcl|NZ\_FO834906.1\_prot\_WP\_002913045.1\_3933 [locus\_tag=BN49\_RS21325] [protein=MFS transporter] [protein\_id=WP\_002913045.1] [location=complement(4085606..4086895)] [gbkey=CDS]

MSNTLLESVVKKNRARLIPFMLALYVLAFLDRSNIGFAKETYQLDTGLSNEAYALGAGIFFVVYAFLGVP

ANLLMRKFGARRWIGCTTLLWGVLSAAMAWADTEAKFLLVRTLLGAAEAGFFPGMIYLTSQWFPQQNRAS

IMGLFYMGAPLALTLGSPLSGALLEMHGFMGHPGWFWMFVIEGLLAVAAGAFTFFWLDDSPQHARFLSAA

EKQALISELAREEEKKIASRLSDALRNGRVWQLALIYLTIQVAVYGLIFFLPTQVAALLGTKVGFVASVV

TAIPWVAALFGTWLIPRYSDRTGERRNIAALTLLAAAVGIAVSGLVAPVLAIIALCVAAVGVIAVQPVFW

TMPTQLLSGTALAAGIGFVNLFGAIGGFLAPIVRVQAETLFASSAAGLLTLAGVAIVGVVIIFSLSLTRA

VPQRGSVQH

>lcl|NZ\_FO834906.1\_prot\_WP\_004175029.1\_3934 [gene=rhmD] [locus\_tag=BN49\_RS21330] [protein=L-rhamnonate dehydratase] [protein\_id=WP\_004175029.1] [location=complement(4086938..4088143)] [gbkey=CDS]

MTLPKIKHVRAWFIGGATAEQGAGGGDYHDQGANHWIDDHIATPMSKYKQYEQSRQSFGINVLGTLIVEV

EADNGQTGFAVSTAGEMGCFIVEKHLNRFIEGKCVSDIKLIHDQMLNATLYYAGSGGLVMNTISCVDLAL

WDLFGKVVGLPVYKLLGGAVRDEIQFYATGARPDLAQEMGFIGGKMPTHWGPHDGDAGIRKDVAMVADMR

EKCGPDFWLMLDCWMSQDVNYATKLAHACAPYNLKWIEECLPPQQYEGYRELKRQAPAGMMVTSGEHHGT

LQSFRTLSETGIDIMQPDVGWCGGLTTLVEIAAIAKARGQLVVPHGSSVYSHHAVITFTNTPFSEFLMTS

PDCATLRPQFDPILLGEPVPERGRIHKSVLDKPGFGVELNRDCNLKRPYQH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913046.1\_3935 [locus\_tag=BN49\_RS21335] [protein=IclR family transcriptional regulator] [protein\_id=WP\_002913046.1] [location=complement(4088154..4088939)] [gbkey=CDS]

MLESTKVPALTRAIEILNLIGRIGPCSAATIIAELGIPKSTVYLLLGELKKQRFISMDNQDNYCLWTKLV

ELAGQALSKMDLRELARPRLTRLMDECGLLCHLGIIDQGNAYYILKIESPATISVRSHEGKSLSLYRSGI

GKCLLAWQPASVQASIIEDLQWERATPTTITDAQQLREELGRIRARGWSFDNGEDYPDVRCVAAPVFNAN

NDLTAAISVVGTRLQINEDNRDYLAGKAIACAKDISRLLGWKSPFEQLASS

>lcl|NZ\_FO834906.1\_prot\_WP\_004151110.1\_3936 [locus\_tag=BN49\_RS21340] [protein=nicotinamide mononucleotide deamidase-related protein YfaY] [protein\_id=WP\_004151110.1] [location=complement(4089144..4090340)] [gbkey=CDS]

MLNVEMLSTGDEVLHGQIIDTNAAWLADFFFNQGLPLTRRNTVGDDLDALVAILRERSEQADVLIVNGGL

GPTSDDLSALAAATAKGEGLILHPEWLETMTRFFAERGRPMAESNRKQAEIPASAEMINNPVGTACGFAI

QLNRCLMFFTPGVPSEFKVMVEQEILPRLRQRFTLPDPPVCLRLTTFGRSESELAQSLNPLTLPPGVVMG

YRSSMPIIELKLTGPANQRDAMLALWPEVRKVAGDSLIFEGTEGLPAQIARCLQERQLSLTLSEQFTSGL

LALQLSRAGAPLLASEVVPAQEETLAQAARWAAERRINHFAGLALAVSGQENDHLNVALATPDGTFALRV

KFSATRHSLAVRQEVCAMMALNMLRRWLNGQPLASEHGWINVVDSLSL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913070.1\_3937 [locus\_tag=BN49\_RS21345] [protein=YfaZ family outer membrane protein] [protein\_id=WP\_002913070.1] [location=complement(4090443..4090985)] [gbkey=CDS]

MKKSIFMALAGVMMVSSAAHAISVTGEAGEHYTNLGVGFGTESTGLAVSGNWLHSDNDGDAAGLGLGLNI

PLGPFLATVGGKGIYTNPKQGDEGYAAAVGGGLQWKIGDSFRLYGDYYYSPDSLSSGIDSYQEANVGASW

TIMRPLSIQAGYRYLNLAGKDGNRDNTIADGPYIGASASF

>lcl|NZ\_FO834906.1\_prot\_WP\_004180717.1\_3938 [locus\_tag=BN49\_RS21355] [protein=Rpn family recombination-promoting nuclease/putative transposase] [protein\_id=WP\_004180717.1] [location=complement(4091260..4092201)] [gbkey=CDS]

MERATNSPHDAVFKHLLSHRATARDFLDIHLPAPLRALCNLNTLRLESGSFIDDELRASHSDILYSLQTQ

AGEGYIYLLIEHQSSADRHMAFRLMRYAIAAMQRHLDKGHTQLPLVIPLLFYHGRVSPWPYPMCWLAGFA

DPDIARRIYGEDFPLIDITSTPDDEIMRHRRVAMLELLQKHIRQRDLMDLHEQLVRLLALGYTSRRQLKT

LLHYLLQAGNAADPVAFLRHLAQNVPRRPHKETLMNIAQFLEQRGHQQGLKQGLEQGLQQGIEQGEQQTA

ERIARAMLANGLDLSLVAKLTGLAPECLARLQH

>lcl|NZ\_FO834906.1\_prot\_WP\_004184975.1\_3939 [gene=nudI] [locus\_tag=BN49\_RS21360] [protein=nucleoside triphosphatase NudI] [protein\_id=WP\_004184975.1] [location=4092339..4092764] [gbkey=CDS]

MRHRTIVCPLIENEGHYLLCKMAADRGVFPGQWALSGGGVEPGERIEEALRREIREELGEKLILTHIAPW

CFRDDTRVKTYPDGHQETIYMIYLIFDCVSANRDVTINEEFDDYAWVKAEDLKNYDLNAATRVTLSLKGL

L

>lcl|NZ\_FO834906.1\_prot\_WP\_029602056.1\_3940 [gene=menE] [locus\_tag=BN49\_RS21365] [protein=o-succinylbenzoate--CoA ligase] [protein\_id=WP\_029602056.1] [location=complement(4092820..4094196)] [gbkey=CDS]

MTFNDWPWRHWRQRRGEALALRLNNQPLTWRELCARVDALASGFAAQGVMEGQGVALRAYNQPETLLAWL

ALLQCGARVLPLNPQLPAVLLQALLPALTMQHQLVLNGDVLPGNLPMLTLQLVEGEHAACWHGDRLVSMT

LTSGSTGLPKAAVHSANAHLASAAGVLALMPFAAGDDWLLSLPLFHVSGQGIVWRWLLAGARLTVRDKQP

LAQMLHGCTHASLVPTQLWRLLNDDAAVSLKAVLLGGASIPVELTERARKQGIRSFCGYGLTEFASTVCA

KEADGAADVGEALPGREVKIVAGEIWLRASSMAAGYWRDGQLLSLTNNEGWFATRDRGALHNGRLTVVGR

LDNLFFSGGEGIQPEEVERVILAHPQVQQVFIVPLDDAEYGQRPVAVVECDDGCELSALAAWSAERLARF

QQPVRWLRLPETLKNGGIKISRRALCEWVRQQTHATVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004214603.1\_3941 [gene=menC] [locus\_tag=BN49\_RS21370] [protein=o-succinylbenzoate synthase] [protein\_id=WP\_004214603.1] [location=complement(4094193..4095158)] [gbkey=CDS]

MRVSQVYRWQIPMDAGVVLRERRLKTRDGLFIRLQEGEREGWGEISPLPGFSVETLEEAQMALLAWAQAW

RDGAEPPLPTQPSVAFGISCAQAELGGELPQAADYRAAPLCSGDPDELFARLAAMPGEKVAKVKVGLWEA

VRDGMVVNLLLEAIPDLQLRLDANRAWTPLKAQQFAKYVNPAYRQRIAFLEEPCKTREDSRAFSRETGIA

IAWDESLREADFRFVAEPGVRAVVIKPTLTGSLQKVQQQVAAAHALGLSVVISSSIESSLGLTQLARVAA

WLTPQTIPGLDTLALMGAQLVRPWPESALPVLNIDALEPLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913098.1\_3942 [gene=menB] [locus\_tag=BN49\_RS21375] [protein=1,4-dihydroxy-2-naphthoyl-CoA synthase] [protein\_id=WP\_002913098.1] [location=complement(4095158..4096015)] [gbkey=CDS]

MISLDEAMLYAPVEWHDCSEGYTDIRYHKSTDGIAKITINRPQVRNAFRPLTVKEMIQALADARYDDNIG

VIVLTGEGEKAFCAGGDQKVRGDYGGYQDDSGVHHLNVLDFQRQIRTCPKPVVAMVAGYSIGGGHVLHMM

CDLTIAAENAIFGQTGPKVGSFDGGWGASYMARIVGQKKAREIWFLCRQYDAQQALDMGLVNTVVPLADL

EKETVRWCREMLQNSPMALRCLKAALNADCDGQAGLQELAGNATMLFYMTEEGQEGRNAFNQKRQPDFSK

FKRNP

>lcl|NZ\_FO834906.1\_prot\_WP\_009307384.1\_3943 [gene=menH] [locus\_tag=BN49\_RS21380] [protein=2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase] [protein\_id=WP\_009307384.1] [location=complement(4096030..4096788)] [gbkey=CDS]

MILSAAVDNGQPGYPWLVFLHGFSGDRNEWRKVGDAFPAWPRLYLDLPGHGGSADIAVQDFAGVNTLLQS

MFNSYNIHKYWLIGYSLGGRVAMNFASQPRAGMRGLIVEGGHPGLQDVEARQVRRSNDRAWAERFHREPL

EQVFADWYQQPVFASLNAAQRESLVALRSRNNGATLAAMLQATSLAAQADLRASLQARDFPFHYLCGERD

AKFRAIAQTLAADLHLIHHAGHNAHRDNPAAVIACLAQILAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002913103.1\_3944 [gene=menD] [locus\_tag=BN49\_RS21385] [protein=2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylic-acid synthase] [protein\_id=WP\_002913103.1] [location=complement(4096785..4098455)] [gbkey=CDS]

MSVSAFNRRWAAVILEALTRHGVQHICIAPGSRSTPLTLAAAENRAFIHHTHFDERGLGHLALGLAKASR

QPVAVIVTSGTATANLYPALIEAGLTGEKLILLTADRPPELIDCGANQAIRQPGMFASHPAQTISLPRPS

QDIPARWLVSTIDQALGALHAGGVHINCPFAEPLYGDMDETGVEWQQQLGNWWQSDKPWLRQALQLESEK

QRDWFFWRQKRGVVVAGRMSAAEGKKVAEWAQTLGWPLIGDVLSQTGQPLPCADLWLGNGKAVSELAQAQ

IVVQLGSSLTGKRVLQWQATCEPDEYWLVDNLPGRLDPAQHRGRRLLSSVERWLELHPAEKRQPWATVIP

QLAGQAWQAAVASNEPFGEAQLAQRIRGYLPEQGQLFVGNSLVVRLIDALAQLPAGYPVYSNRGASGIDG

LIATAAGVQRASARPTLAIVGDLSALYDLNSLALLRQASAPLVLIVVNNNGGQIFSMLPTPQDERRQFYL

MPQDVDFSHAAAMFGLAYHRPDDWPSLDEALAGAWRRAGATVIELAVNETDGAQTLQQLLAQVSRL

>lcl|NZ\_FO834906.1\_prot\_3945 [gene=menF] [locus\_tag=BN49\_RS21390] [protein=isochorismate synthase MenF] [pseudo=true] [location=complement(4098538..4099823)] [gbkey=CDS]

MLSVSTALARLQDGLGESFPDSPGTRIIDVAFPLNDAFDPLLWCGQQAQWPQFYWQQRNGDEELATLGAV

KTFTSLDAANRFLRQAGRICVSAA\*MRLNRSRAAWRCRVWSGAGAAAGPCCGWCCIVISPCVRMPRRPAR

FSPA\*QPLRRLPAPYRRC\*ASATHPTILNGRQ\*LRGRLRRSAPVKWIK\*CWRGQPTCSLPPRWTP\*ASWR

LAGAAILTVFIS\*WRSMPGRHFSAPRRNGCGAGAARCCAPKRWRGPSRTIRKTRRRSNWPTG\*\*KTTKTS

GKTCWW\*RISASACRVRPRRWTSCRRRW\*GCVRCSISDAASGPSWRRLTTAAVCCSCSPPPRWPACRAGR

RWRSFSVMNRFPANGTPGPPGICHWRKASFAWRCVRRK\*TTTPCGCMPGRGSSAALMHSRSGRRLTTKRP

GCARCCVH

>lcl|NZ\_FO834906.1\_prot\_WP\_004184987.1\_3946 [locus\_tag=BN49\_RS21395] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004184987.1] [location=complement(4099959..4100420)] [gbkey=CDS]

MMTWQDLHHSELTVPQLYALLKLRSEVFVVEQQCVYQDVDGDDLVGENRHLLGWRDGELVAYARILKSEE

EFAPVVIGRVIVSPAARGAKLGYQLMEQALASCQQHWPQKAIYLGAQAHLQSFYAHFGFTPVTEVYDEDG

IPHIGMAREKRAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004214593.1\_3947 [gene=rnz] [locus\_tag=BN49\_RS21400] [protein=ribonuclease Z] [protein\_id=WP\_004214593.1] [location=4100478..4101398] [gbkey=CDS]

MELTFLGTSAGVPTRTRNMTSIILNLQQPTRAEMWLFDCGEGTQHQFLHTPYHPGKLNKIFITHLHGDHL

FGLPGLLCSRSMQGNSLPLTLYGPKGLKEFVETALRLSGSWTDYPLTIIEVGPGLVFDEEGYRVTAYPLS

HPVECYGYRIAQHDKPGTLDAAQLIADGVPPGPLFHQLKRGQRVELADGRVIDGSRYLGPATPGKTLAIF

GDTAPCPQALEMARGADVMVHETTLEQAMAEKANSRGHSSSQQTAALAKEAGVGTLIATHFSSRYDAEGC

LRMLAECREIFPNTLLAEDFMVYKMA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043682.1\_3948 [gene=nuoN] [locus\_tag=BN49\_RS21405] [protein=NADH-quinone oxidoreductase subunit NuoN] [protein\_id=WP\_046043682.1] [location=complement(4101453..4102910)] [gbkey=CDS]

MTITPQQLIALLPLLIVGLTVVVVMLSIAWRRNHFLNATLSVLGLNAALVSLWFVGQNGAMDVTPLIRVD

GYAMLYTGLVLLASLATCTFAYPWLEGYKDNKEEFYLLVLIAALGGILLAGANHLAALFLGIELISLPLF

GLVGYAFRQKRSLEASIKYTILSAAASSFLLFGMALVYANSGNLSFLALGKSLADNMLHEPLLLAGLGLM

IVGLGFKLSLVPFHLWTPDVYQGAPAPVSTFLATASKIAIFGVVMRLFLSMPVGNSEAVRVVLGLIAFAS

IIFGNLMALSQTNIKRLLGYSSISHLGYLLVALIALQSGEMSMEAVGVYLAGYLFSSLGAFGVVSLMSSP

YRGPDADSLFSYRGLFWHRPILSAVMTVMMLSLAGIPMTLGFIGKFYVLAVGVHAHLWWLVAAVVVGSAI

GLYYYLRVAVSLYLSAPEQLNRDAPSNWQYSAGGIVVLISALLVLVLGIWPQPLISIVQLATPLM

>lcl|NZ\_FO834906.1\_prot\_WP\_002913146.1\_3949 [gene=nuoM] [locus\_tag=BN49\_RS21410] [protein=NADH-quinone oxidoreductase subunit M] [protein\_id=WP\_002913146.1] [location=complement(4102917..4104446)] [gbkey=CDS]

MLLPWLILIPFIGGFLCWQTERFGVKVPRWIALITMGLTLVLGLQLWMQGGYSLTQSAGIPQWQSEFVLP

WIPRFGISIHLAIDGLSLLMVVLTGLLGVLAVLCSWREIEKYQGFFHLNLMWILGGVIGVFLAIDMFLFF

FFWEMMLVPMYFLIALWGHKASDGKTRITAATKFFIYTQASGLVMLIAILALAFVHFNATGVWTFNYEDL

LKTPMSHGVEYLLMLGFFIAFAVKMPVVPLHGWLPDAHSQAPTAGSVDLAGILLKTAAYGLLRFALPLFP

NASAEFAPIAMWLGVIGIFYGAWMAFAQTDIKRLIAYTSVSHMGFVLIAIYTGSQLAYQGAVIQMIAHGL

SAAGLFILCGQLYERLHTRDMRQMGGLWSKIKWLPAMSMFFAVATLGMPGTGNFVGEFMILFGSYKVVPT

ITVISTFGLVFASVYSLSMLHRAYFGKAKSEVAAKELPGMSLRELSIILLLVVLLVLLGFFPQPILDTSH

AAMSNIQQWFVNSVSTTRP

>lcl|NZ\_FO834906.1\_prot\_WP\_032103507.1\_3950 [gene=nuoL] [locus\_tag=BN49\_RS21415] [protein=NADH-quinone oxidoreductase subunit L] [protein\_id=WP\_032103507.1] [location=complement(4104616..4106457)] [gbkey=CDS]

MNMLALTILLPLIGFVLLAFSRGRWSENLSAAVGMGSVGLAALVTAYVGVDFFANGKQAVSVPLWTWMSV

GDFNIGFNLVLDGLSLTMLSVVTGVGFLIHMFASWYMRGEEGYSRFFAYTNLFIASMVVLVLADNLLLMY

LGWEGVGLCSYLLIGFYYTDPKNGAAAMKAFVVTRVGDVFLAFALFILYNELGTLNFREMVELAPQHFAN

GSTTLQWATLMLLGGAVGKSAQLPLQTWLADAMAGPTPVSALIHAATMVTAGVYLIARTHGLFLMTPEVL

HLVGIVGAVTLVLAGFAALVQTDIKRVLAYSTMSQIGYMFLALGVQAWDAAIFHLMTHAFFKALLFLSSG

SVILACHHEQNIFKMGGLRKSIPLVYVCFLVGGAALSALPLITAGFFSKDEILAGAMANGHINLMVAGLV

GAFMTSLYTFRMIFIVFHGKEQIHAHAGKGITHHLPLIVLLVLSTFVGALIVPPLEGVLPQTTELAHGSV

MMLEIASGIIAIAGILIAAWLWLGKRTLVTSIANSAPGRFFGTWWFHAWGFDWLYDKVFVKPFLGIAWLL

KRDPLNSLMNIPAILSRFAGKGLLVSENGYLRWYVASMSIGAVVVLALLMVLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913148.1\_3951 [gene=nuoK] [locus\_tag=BN49\_RS21420] [protein=NADH-quinone oxidoreductase subunit NuoK] [protein\_id=WP\_002913148.1] [location=complement(4106454..4106756)] [gbkey=CDS]

MIPLTHGLILAAILFVLGLTGLVIRRNLLFMLISLEIMINAAALAFVVAGSYWGQADGQIMYILAISLAA

AEASIGLALLLQLHRRRQNLNIDSVSELRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002913150.1\_3952 [gene=nuoJ] [locus\_tag=BN49\_RS21425] [protein=NADH-quinone oxidoreductase subunit J] [protein\_id=WP\_002913150.1] [location=complement(4106753..4107307)] [gbkey=CDS]

MEFAFYICGLIAILATLRVVTHTNPVHALLYLIISLLAIAGVFFSLGAYFAGALEIIVYAGAIMVLFVFV

VMMLNLGGTEIEQERKWLQPGIWIGPAILSAVLLVVIVYAILGINDQGIDGAAINAKEVGIALFGPYVLA

VELASMLLLAGLVVAFHIGREERAGEVLSNRLNDSDKRKTEEHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913152.1\_3953 [gene=nuoI] [locus\_tag=BN49\_RS21430] [protein=NADH-quinone oxidoreductase subunit NuoI] [protein\_id=WP\_002913152.1] [location=complement(4107319..4107861)] [gbkey=CDS]

MTLKELLVGFGTQVRSIWMIGLHAFAKRETRMYPEEPVYLPPRYRGRIVLTRDPDGAERCVACNLCAVAC

PVGCISLQKAETVDGRWYPEFFRINFSRCIFCGLCEEACPTTAIQLTPDFELGEYKRQDLVYEKEDLLIS

GPGKYPEYNFYRMAGMAIDGKDKGEAENEAKPIDVKSLLP

>lcl|NZ\_FO834906.1\_prot\_WP\_002913156.1\_3954 [gene=nuoH] [locus\_tag=BN49\_RS21435] [protein=NADH-quinone oxidoreductase subunit NuoH] [protein\_id=WP\_002913156.1] [location=complement(4107876..4108853)] [gbkey=CDS]

MSWLTPDLIDILLSILKAVVILLVVVTCGAFMSFGERRLLGLFQNRYGPNRVGWGGSLQLVADMIKMFFK

EDWIPRFSDRVIFTLAPVIAFTSLLLAFAIVPVSPTWVVADLNIGILFFLMMAGLAVYAVLFAGWSSNNK

YSLLGAMRASAQTLSYEVFLGLSLMGVVAQAGSFNMTDIVNNQAHLWNVIPQFFGFVTFAIAGVAVCHRH

PFDQPEAEQELADGYHIEYSGMKFGLFFVGEYIGIVTVSALIVTLFFGGWNGPWLPPFIWFALKTAFFMM

MFILIRASLPRPRYDQVMSFGWKVCLPLTLVNLLVTAAVILWQAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529916.1\_3955 [gene=nuoG] [locus\_tag=BN49\_RS21440] [protein=NADH-quinone oxidoreductase subunit NuoG] [protein\_id=WP\_016529916.1] [location=complement(4108850..4111576)] [gbkey=CDS]

MATIHVDGKEYEVNGADNLLEACLSLGLDIPYFCWHPALGSVGACRQCAVKQYQNAEDTRGRLVMSCMTP

ASDGTFISIDDSEAKQFRESVVEWLMTNHPHDCPVCEEGGNCHLQDMTVMTGHSFRRYRFTKRTHRNQDL

GPFISHEMNRCIACYRCVRYYKDYADGTDLGVYGAHDNVYFGRPEDGTLESEFSGNLVEVCPTGVFTDKT

HSERYNRKWDMQFAPSICQQCSIGCNISPGERYGELRRIENRYNGTVNRYFLCDRGRFGYGYVNLKDRPR

QPVQRRGDDLITLNAEQAMQGAADILRQSKKVIGIGSPRASIESNFALRELVGADNFYTGIAKGEQARLQ

MMLKVLREGGIHTPSLRDIESYDAVLVLGEDITQTGARVALAVRQAVKGKAREMAAAQKVADWQIAAILN

IGQRAKHPLFVTNVDDTRLDDIAAWTYRAPVEDQARLGFAIAHALDDSAPAVDGLSQDLQGKVDVIVQAL

AGAKKPLIISGTNAGSMEILQAAANVAKALKGRGADVGVTMVARAVNSVGLGMIGGGSLEEALDELESGA

ADAVIVLENDLHRHASTARVDAALAKAPLVMVVDHQRTAIMDKAHLVLSAASFAESDGTVVNNEGRAQRF

FQVYDPAYYDAKTVMLESWRWLHSLHSTVNNRQVDWTQLDHVIDAAIAALPQLAGIKDAAPDATFRIRGQ

KLAREPHRYSGRTAMRANISVHEPRQPQDKDTMFAFSMEGNNQPSAPRSQIPFAWAPGWNSPQAWNKFQD

EVGGKLRHGDPGVRLFEASASGLEYFTAVPASFQAEEGKWRIAPYYHLFGSDELSQRAPVFQSRMPEPYI

KLNPADAAKLGVNPGAMLSFSVEGQTLRLPLVISEGLTAGQVGLPMGMPGIAPVLTGSRIDSLQEAKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913158.1\_3956 [gene=nuoF] [locus\_tag=BN49\_RS21445] [protein=NADH-quinone oxidoreductase subunit NuoF] [protein\_id=WP\_002913158.1] [location=complement(4111609..4112946)] [gbkey=CDS]

MKTVIRTAETHPLTWRLRDDKQPVWLDEYRSKNGYEGARKALTGMAPDEIVTAVKDAGLKGRGGAGFSTG

LKWSLMPKDESMNIRYLLCNADEMEPGTYKDRLLMEQLPHLLVEGMLISAFALKAYRGYIFLRGEYIEAA

QHLRRAIAEATEAGLLGKNILGTGFDFELFVHTGAGRYICGEETALINSLEGRRANPRSKPPFPASSGVW

GKPTCVNNVETLCNVPAILANGVEWYQNISTSKDAGTKLMGFSGRVKNPGVWELPFGTTAREILEDYAGG

MRDGLKFKAWQPGGAGTDFLTEAHLDLPMEFESIGKAGSRLGTSLAMAVDHEINMVSLVRNLEEFFARES

CGWCTPCRDGLPWSVKILRALERGEGQPGDIETLEQLCRFLGPGKTFCAHAPGAVEPLQSAIKYFREEFE

AGIKQQFSNTHAINGIQPNLLKTRW

>lcl|NZ\_FO834906.1\_prot\_WP\_002913160.1\_3957 [gene=nuoE] [locus\_tag=BN49\_RS21450] [protein=NADH-quinone oxidoreductase subunit NuoE] [protein\_id=WP\_002913160.1] [location=complement(4112943..4113443)] [gbkey=CDS]

MHENQQPQTEAFELSAAEREAIEHEKHHYEDPRAASIEALKIVQKQRGWVPDGAIYAIADVLGIPASDVE

GVATFYSQIFRQPVGRHVIRYCDSVVCHITGYQGIQAAIEKKLNIKPGQTTFDGRFTLLPTCCLGNCDKG

PTMMIDEDTHSHLTPEAIPDLLEQYK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529915.1\_3958 [gene=nuoC] [locus\_tag=BN49\_RS21455] [protein=NADH-quinone oxidoreductase subunit C/D] [protein\_id=WP\_016529915.1] [location=complement(4113446..4115254)] [gbkey=CDS]

MVNNMTDLTAHDAAPAWQTRDHLDDPVIGELRNHFGPDAFTVQPTRTGVPVVWVKREQLLEVGDFLKKLP

KPYVMLFDLHGMDERLRTHRDGLPAADFSVFYHLISIDRNRDIMLKVALSENDLHLPTFTKLFPNANWYE

RETWEMFGITFDGHPNLRRIMMPPTWEGHPLRKDYPARATEFDPFELTKAKQDLEMEALTFKPEEWGMKR

GTDNEDFMFLNLGPNHPSAHGAFRIILQLDGEEIVDCVPDIGYHHRGAEKMGERQSWHSYIPYTDRIEYL

GGCVNEMPYVLAVEKLAGITVPDRVNVIRVMLSELFRINSHLLYISTFIQDVGAMTPVFFAFTDRQKIYD

LVEAITGFRMHPAWFRIGGVAHDLPRGWDRLLREFLEWMPKRLDSYEKAALRNTILKGRSVGVAAYTAKE

ALEWGTTGAGLRATGIDFDVRKWRPYSGYENFDFEVPTGGGVSDCYTRVMLKVEELRQSLRILQQCLDNM

PEGPFKADHPLTTPPPKERTLQHIETLITHFLQVSWGPVMPANESFQMIEATKGINSYYLTSDGSTMSYR

TRVRTPSFAHLQQIPSAIRGSLVSDLIVYLGSIDFVMSDVDR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913178.1\_3959 [gene=nuoB] [locus\_tag=BN49\_RS21460] [protein=NADH-quinone oxidoreductase subunit NuoB] [protein\_id=WP\_002913178.1] [location=complement(4115341..4116015)] [gbkey=CDS]

MDYTLTRIDPNGENDRYPLQKQEIVTDPLEQEVNKSVYMGKLEHALHDMVNWGRKNSIWPYNFGLSCCYV

EMVTSFTAVHDVARFGAEVLRASPRQADLMVVAGTCFTKMAPVIQRLYDQMLEPKWVISMGACANSGGMY

DIYSVVQGVDKFIPVDVYIPGCPPRPEAYMQALMLLQESIGKERRPLSWVVGDQGVYRANMQSERERKRG

ERIAVTNLRTPDEI

>lcl|NZ\_FO834906.1\_prot\_WP\_002913181.1\_3960 [gene=nuoA] [locus\_tag=BN49\_RS21465] [protein=NADH-quinone oxidoreductase subunit NuoA] [protein\_id=WP\_002913181.1] [location=complement(4116031..4116477)] [gbkey=CDS]

MRMSTSTEVIAHHWAFAIFLIIAIGLCCLMLVGGWYLGGRARARSKNTPFESGIDSVGSARLRLSAKFYL

VAMFFVIFDVEALYLYAWSTSIRESGWVGFVEAAIFILVLLAGLVYLVRIGALDWTPARSRRTLVNPETD

SPTNRHMQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002913183.1\_3961 [locus\_tag=BN49\_RS21475] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002913183.1] [location=complement(4117129..4118055)] [gbkey=CDS]

MINTTRPILNLDLDLLRTFVAVADLNTFAAAAAAVCRTQSAVSQQMQRLEQLVGKELFARHGRNKLLTEQ

GIQLLGYARKILRFNDEACMSLMYGSLQGALSIGASEETADTILPFLLNRIGCFYPRMTLEIKVHPHAAI

MEMLAEGLVDLALTTHQPPGFTSFTLRTSPTLWYCAAEYVLAKGESIPLILLEEPSPFRQDIIAALETAR

VSWHLAHGASSLSGVKAAVKAGLGVTARPVEMMSPDLRVAGISEGLPALPDTRYVVSCNPRTVSELPQAI

FQSLSQEIHPWETGTALTPEEGGNTLVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913185.1\_3962 [gene=alaA] [locus\_tag=BN49\_RS21480] [protein=alanine transaminase AlaA] [protein\_id=WP\_002913185.1] [location=4118928..4120145] [gbkey=CDS]

MSPIEKSSKLENVCYDIRGPVLKEAKRLEEEGNKVLKLNIGNPAPFGFEAPDEILVDVIRNLPTAQGYCD

SKGLYSARKAIMQHYQARGMRDVTVEDIYIGNGVSELIVQAMQALLNSGDEMLVPAPDYPLWTAAVSLSS

GKAVHYLCDESSDWFPDLDDIRAKITPRTRGIVIINPNNPTGAVYSKELLQEIVEIARQHNLIIFADEIY

DKILYDEAQHHSIAALAPDLLTVTFNGLSKTYRVAGFRQGWMVLNGPKKHAKGYIEGLEMLASMRLCANV

PAQHAIQTALGGYQSISEFIIPGGRLYEQRNRAWELINDIPGVSCVKPKGALYMFPKIDAKRFNIHDDQK

MVLDFLLQEKVLLVQGTAFNWPWPDHVRIVTLPREDDLEMAISRFGRFLSGYHQL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913188.1\_3963 [gene=yfbR] [locus\_tag=BN49\_RS21485] [protein=5'-deoxynucleotidase] [protein\_id=WP\_002913188.1] [location=4120227..4120826] [gbkey=CDS]

MSQSHFFAHLSRLKLINRWPLMRNVRTENVSEHSLQVAMVAHALAAIKNRKFGGQVNAERIALLAMYHDA

SEVLTGDLPTPVKYFNSQIAQEYKAIEKIAQQKLVDMVPDELRDIFEPLIDEHHYSEEEQSIVKQADALC

AYLKCLEELSAGNNEFLLAKGRLEKTLASRRSAEMDYFMQVFVPSFQLSLDEISQDSPL

>lcl|NZ\_FO834906.1\_prot\_WP\_004180741.1\_3964 [locus\_tag=BN49\_RS21490] [protein=SLC13 family permease] [protein\_id=WP\_004180741.1] [location=complement(4120871..4122703)] [gbkey=CDS]

MNGELIWVLSLLAIAVVLFATGKVRMDAIALMVIVAFVLSGTLTLNEAFSGFSDPNVILIAALFIIGDGL

VRTGVATKMGAWLVSVAGNSETKMLIYLMLTVAGLGAFMSSTGVVAIFIPVVLSVSARMNTSPSRLMMPL

SFAGLISGMMTLVATPPNLVVNSELLREGLHGFSFFSVTPIGLVVLILGIVYMLAVRFMLKTDNGDSARD

GRKRSTFRDLIREYHLTGRARRLAIRPGSPMIGQRLDDLKLRERYCANVIGVERWRRFRRVIVNVNGVSE

FRARDVLLIDMSASDVDLRQFCGEQMLEPMVLRGEYFADQALDVGMAEVALIPDSEMIGKTVREIAFRTR

FGLNIVGMKRDGKAMDGSVVDEPLQLGDILLVVGNWRQIALLAKRGRDFVVLNMPVEVDDASPAHSQAPH

AIFCLVLMVALMLTDEIPNPIAAIIACLLMGKFRCINAESAYKAIHWPSIILIVGMMPFALALQKTGGVD

LVVKGLMDVAGGEGPYLMLGCLFVMCAAIGLFISNTATAVLMAPIALAAAKSMGVSPYPFAMVVAMAASA

AFMTPVSSPVNTLVLGPGKYSFSDFVKIGVPFTILVMVVCVLLIPVLFPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004174996.1\_3965 [locus\_tag=BN49\_RS21495] [protein=sugar phosphatase] [protein\_id=WP\_004174996.1] [location=complement(4122780..4123439)] [gbkey=CDS]

MQCKGFLFDLDGTLVDSLPVVERSWCKWGDRFAIDHDEILSFIHGKQAITSIRHFMPGRSEEDIQAEFRY

LEQIEATDIEGIVALPGALALLNTLNEAGIPWAIVTSGSIPVAHARHRAAGLPMPEVFVTAEQVKHGKPA

PDAYLLGAERLGLPAGECAVVEDAPAGLLSGLAAGCRTIAVNVPADAPRLDEADLVLSSLEDLVVERQTD

GVVNVRLKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913193.1\_3966 [locus\_tag=BN49\_RS21500] [protein=YfbU family protein] [protein\_id=WP\_002913193.1] [location=complement(4123451..4123945)] [gbkey=CDS]

MEMTNAQRLILSNQYKMMTMLDPDNAERYRRLQTIIERGYGLQMRELDREFGQLTEETCRTVIDIMEMYH

ALHVSWTNLKDAAGIDERRVTFLGFDAATEARYLGYVRFMVNVEGRYSHFDAGTHGFNSQTPMWEKYQRM

LSVWHACPRQYHLSSNEINQIINA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913194.1\_3967 [locus\_tag=BN49\_RS21505] [protein=DUF412 domain-containing protein] [protein\_id=WP\_002913194.1] [location=complement(4124033..4124488)] [gbkey=CDS]

MSTPEKRPVSFFSLFNRGQHYAKTWPLDKRLAPVFIENRIIRATRYAIRIMPPIAIFTLCWQIALGGQLG

PAVATALFALSLPMQGLWWLGKRSVTPLPPSILNWFYEVRGKLQEAGQALAPVEGKPDYQALADTLKRAF

KQLDKTFLDDL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529145.1\_3968 [gene=ackA] [locus\_tag=BN49\_RS21510] [protein=acetate kinase] [protein\_id=WP\_016529145.1] [location=4124826..4126028] [gbkey=CDS]

MSSKLVLVLNCGSSSLKFAILDAVNGDEYLSGLAECFHLPEARIKWKMDGSKQEAELGAGAAHSEALNFI

VNTILAQKPELSAQLTAIGHRIVHGGEKYTSSVVIDESVIQGIKDAASFAPLHNPAHLIGIAEALKSFPQ

LKDKNVAVFDTAFHQTMPEESYLYALPYSLYKEHGVRRYGAHGTSHFYVTQEAAKILNKPVEELNIITCH

LGNGGSVSAIRNGKCVDTSMGLTPLEGLVMGTRSGDIDPAIIFHLHDTLGMSVDAINKMLTKESGLLGLT

EVTSDCRYVEDNYQEKADAKRAMDVYCHRLAKYIGSYTALMDGRLDAVIFTGGIGENAAMVRELSLGKLG

VLGFEVDHERNLAARFGKSGFINKEGTRPAVVIPTNEELVIAQDASRLTA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529144.1\_3969 [gene=pta] [locus\_tag=BN49\_RS21515] [protein=phosphate acetyltransferase] [protein\_id=WP\_016529144.1] [location=4126229..4128376] [gbkey=CDS]

MSRTIMLIPTGTSVGLTSVSLGVIRAMERKGVRLSVFKPIAQPRSGGDAPDQTTTIVRASSSTTAAAEPL

KMSHVESLLSSNQKDVLMEEIIANYHANTQDAEVVLVEGLVPTRKHQFAQALNFEIAKTLNAEIVFVMSQ

GTDTPEQLNERIELTRNSFGGAKNTSITGVIVNKLNAPVDDQGRTRPDLSEIFDDSSKAKIVKIDPAQLQ

KGSTLPVLGAVPWSFDLIATRAIDMAHHLNATIINEGDINTRRVKSVTFCARSIPHMLEHFRPGSLLVTS

ADRPDVLVAACLAAMNGVEIGAILLTGGYEMDARISKLCERAFATGLPVFMVNTNTWQTSLSLQSFNLEV

PVDDHERIEKVQEYVANYINADWIESLTATSERSRRLSPPAFRYQLTELARKAGKRVVLPEGDEPRTVKA

AAICAERGIATCVLLGNPDEINRVAAAQGVELGAGIEIVDPEVVRESYVGRLVELRKNKGMTEAVAREQL

EDNVVLGTLMLEQDEVDGLVSGAVHTTANTIRPPLQLIKTAPGSSLVSSVFFMLLPEQVYVYGDCAINPD

PTAEQLAEIAIQSAESAIAFGIEPRVAMLSYSTGTSGAGSDVEKVREATRLAQEKRPDLMIDGPLQYDAA

VMADVAKSKAPNSPVAGRATVFIFPDLNTGNTTYKAVQRSADLISIGPMLQGMRKPVNDLSRGALVDDIV

YTIALTAIQSAQQQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913197.1\_3970 [gene=yfcD] [locus\_tag=BN49\_RS21520] [protein=NUDIX hydrolase YfcD] [protein\_id=WP\_002913197.1] [location=complement(4128469..4129020)] [gbkey=CDS]

MAEQNHLASTEWVDIVNENNEVIAQSSREQMRAQCLRHRATYIVVHDGMGKILVQRRTETKDFHPGMLDA

TAGGVVQADEQLLESARREAEEELGIAGVPFADHGQFYYEDKFCRVWGSLFSCVSHGPFALQEEEVSEVC

WLTPEEITARCDEFTPDSLKALALWMTRNAGNEYDDAEESERE

>lcl|NZ\_FO834906.1\_prot\_WP\_004174991.1\_3971 [gene=yfcE] [locus\_tag=BN49\_RS21525] [protein=phosphodiesterase] [protein\_id=WP\_004174991.1] [location=complement(4129078..4129629)] [gbkey=CDS]

MKLMFASDIHGSLPATERVLERFAQSGARWLIILGDVLNHGPRNALPEGYAPGEVAERLNSVAERIVAVR

GNCDSEVDQMLLRFPMTAPWQQVLSERYRLFLTHGHLYSPDNLPPLAAGDVLAYGHTHIPVAEKRGAIYL

FNPGSVSIPKGGYSASYGLLDQGRLQVLALNDNQVIAEVAIYP

>lcl|NZ\_FO834906.1\_prot\_WP\_009307378.1\_3972 [gene=yfcF] [locus\_tag=BN49\_RS21530] [protein=glutathione transferase] [protein\_id=WP\_009307378.1] [location=complement(4129692..4130330)] [gbkey=CDS]

MSQPVITLWSDADFFSPYVMSVYVALQEKSLPFTLKTVDLNRGEHLQAGWTGYAATRRVPLLEVDDFALS

ESSAITEYLDERFAPPEWERIYPHDLQKRARARQIQAWLRSDLMPIREERSTAVVFGGAKMPDLSEAGRQ

SAEKLFATATMLLAHGGQNLFGEWSIADADLALMLNRLVLNGDKVPEALADYASFQWQRASIQRYVALSA

KR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529143.1\_3973 [gene=yfcG] [locus\_tag=BN49\_RS21535] [protein=GSH-dependent disulfide bond oxidoreductase] [protein\_id=WP\_016529143.1] [location=4130511..4131140] [gbkey=CDS]

MIDLYYAPTPNGHKITLFLEEAELAYRLIRVDIGKGEQFHPQFLAISPNNKVPAIVDHMPADGGAQLSVF

ESGAILLYLAEKSGKLLSGELRERYVTLQWLYWQVGGLGPMLGQNQHFSHSAPQTVPYAIERFQVETQRL

YGVLNQRLGCSPWLGGDHYSIADIAAWPWVNCHVRQRIDLANYPAVHNWYERIKQRPATAEAMLKIQLY

>lcl|NZ\_FO834906.1\_prot\_WP\_002913200.1\_3974 [gene=folX] [locus\_tag=BN49\_RS21540] [protein=dihydroneopterin triphosphate 2'-epimerase] [protein\_id=WP\_002913200.1] [location=4131206..4131568] [gbkey=CDS]

MSQPDAIIRIKNLRLRTFIGIKEEEIANRQDVVVNVAIHYPADKARDSEDINDALNYRTITKRIISHLEN

GRFSLLEKLTQDVLNIACEHHWVTYAEVEIDKLHALRYADSVSMTMSWRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913203.1\_3975 [locus\_tag=BN49\_RS21545] [protein=TIGR01777 family oxidoreductase] [protein\_id=WP\_002913203.1] [location=4131587..4132480] [gbkey=CDS]

MKILLTGGTGLIGRHLIPRLLELGHSVTVSTRHPDTARARLDPRVTLWRDFEGHHHLNDIDAVINLAGEP

IADKRWTAEQKQRLCHSRWDLTQRLVGLIHASDTPPSVLISGSAIGYYGDLGEVVVTEEEPPHNEFTHKL

CARWEQIACEAQSERTRVCLLRTGVVLAPRGGILGKMTPAFKLGLGGPIGNGRQYLAWIHIDDMVNGILW

LLDNDLRGPFNMVSPYPVHNEQFAHALGHALHRPAIFRVPAAAIRLLMGESAVLVLGGQRALPKRLEAAG

FAFRWYDLDEALKDVLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004217247.1\_3976 [locus\_tag=BN49\_RS31175] [protein=hypothetical protein] [protein\_id=WP\_004217247.1] [location=complement(4132460..4132576)] [gbkey=CDS]

MAMLQRQGEAIQAWSMSQQNGIRGANAPLCQPLTQHIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004140943.1\_3977 [locus\_tag=BN49\_RS21555] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004140943.1] [location=4132696..4133223] [gbkey=CDS]

MTTITTPRLSLTRFVTDDWPFFLRLRQDPQVMRFMGEVLSEEALRSVFVSRCADPGVFVLRDKFGEALGD

IGLRISPKNPHEADVGYALLPQAQGKGYASEALRAVCEYGFTTLGVQAINAWVLGENRGSSRLLEKQGFV

RTQVLEKAYHLNGVDYDDWIYRLEREAHPASADAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529142.1\_3978 [gene=hisP] [locus\_tag=BN49\_RS21560] [protein=histidine ABC transporter ATP-binding protein HisP] [protein\_id=WP\_016529142.1] [location=complement(4133229..4134002)] [gbkey=CDS]

MSDNKLNVIDLHKRYGEHEVLKGVSLQAKAGDVISIIGSSGSGKSTFLRCINFLEKPSEGTIVVSGQNIG

LVRDKDGQLKVADKNQLRLLRTRLTMVFQHFNLWSHMTVLENVMEAPIQVLGLNKQEARERAVKYLAKVG

IDERQQAKYPVHLSGGQQQRVSIARALAMEPEVLLFDEPTSALDPELVGEVLRIMQQLAEEGKTMVVVTH

EMGFARHVSSHVIFLHQGKIEEEGHPDALFGAPKSPRLQQFLKGSLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913207.1\_3979 [gene=hisM] [locus\_tag=BN49\_RS21565] [protein=histidine ABC transporter permease HisM] [protein\_id=WP\_002913207.1] [location=complement(4134010..4134726)] [gbkey=CDS]

MIEIIQEYWKSLLWTDGYRFTGVAITLWLLISSVVMGGILAVFLAIGRVSSNKFIQFPIWLFTYIFRGTP

LYVQLLVFYSGMYTLEIVKGTELLNAFFRSGLNCTVLALTLNTCAYTTEIFAGAIRSVPAGEIEAARAYG

FSSVKLYRCIILPSALRIALPAYSNEVILMLHSTALAFTATVPDLLKIARDINSATYQPFTAFGIAAVLY

LIISYVLISLFRKAEKRWLQHIKPSSTH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913208.1\_3980 [locus\_tag=BN49\_RS21570] [protein=histidine ABC transporter permease HisQ] [protein\_id=WP\_002913208.1] [location=complement(4134723..4135409)] [gbkey=CDS]

MLYGFSQVILQGALVTLELALSSVVLAVLIGLAGAGAKLSSNRPLALVFEGYTTLIRGVPDLVLMLLIFY

GLQIALNSVTDALGMAQFDIDPMIAGIITLGFIYGAYFTETFRGAYLAVPKGHIEAATAFGFSGGQTFRR

ILFPAMMRYALPGIGNNWQVILKATALVSLLGLEDVVKATQLAGKSTWQPFYFAIVCGLIYLVFTTVSNG

VLLLLERRYTVGVKRADL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913209.1\_3981 [gene=hisJ] [locus\_tag=BN49\_RS21575] [protein=histidine ABC transporter substrate-binding protein HisJ] [protein\_id=WP\_002913209.1] [location=complement(4135474..4136256)] [gbkey=CDS]

MKKLALSLSLALALSSVSTVFAAIPQKIRIGTDPTYAPFESKNAQGELVGFDIDLAKELCKRINTQCTFV

ENPLDALIPSLKAKKIDAIMSSLSITEKRQQEIAFTDKLYAADSRLVVKKGSPVTPDLATLKGKRVGVLQ

GTTQETYGNEHWAPKGIEIVSYQGQDNIYSDLTAGRIDAAFQDEVAASEGFLKQPIGKDYQFGGPSIKDE

KLFGVGTGMGLRKEDNELREALNKAFAEMRKDGTYDKLAKKYFDFNVYGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913210.1\_3982 [gene=argT] [locus\_tag=BN49\_RS21580] [protein=lysine/arginine/ornithine ABC transporter substrate-binding protein ArgT] [protein\_id=WP\_002913210.1] [location=complement(4136524..4137306)] [gbkey=CDS]

MKKTILALSLLVGMSSTASVFAALPQSIRIGTDATYAPFSSKDAKGDFVGFDIDLGNELCSRIKVKCTWV

GSDFDSLIPSLKAKKIDAIISSLSITEKRQQEIAFSDKLYAADSRLIAAKGSPIQPTLEALKGKHVGVLQ

GSTQEAYANDRWRSQGVDVVAYQNQDLIYSDLAAGRLDAALQDEVAASEGFLKQPAGKDFAFAGPSVKDK

KYFGDGTGIGLRKDDAELKAAFDKALGEMRKDGTYDKMAKKYFDFNVYGD

>lcl|NZ\_FO834906.1\_prot\_WP\_004140952.1\_3983 [locus\_tag=BN49\_RS31180] [protein=hypothetical protein] [protein\_id=WP\_004140952.1] [location=4137347..4137508] [gbkey=CDS]

MVIADQSCSFCAIFPVRAGNRVKFVKIKLQDCLKREDTSITGETAAPERKKTK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913212.1\_3984 [locus\_tag=BN49\_RS21590] [protein=UbiX family flavin prenyltransferase] [protein\_id=WP\_002913212.1] [location=complement(4137589..4138158)] [gbkey=CDS]

MKRLIIGISGASGAIYGVRMLQVLRDVPDIETHLILSQAARQTLAMETDYSVREVQALADVVHDARDIAA

SISSGSFKTAGMVILPCSMKTLSGIVHSYTDGLLTRAADVVLKERRPLVLCVRETPFHLGHLRLLVQAAE

LGAVIMPPVPAFYHRPQSLDDVINQTVNRVLDQFDISLEHDLFTRWQGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913213.1\_3985 [gene=purF] [locus\_tag=BN49\_RS21595] [protein=amidophosphoribosyltransferase] [protein\_id=WP\_002913213.1] [location=complement(4138294..4139811)] [gbkey=CDS]

MCGIVGIAGVMPVNQSIYDALTVLQHRGQDAAGIITIDANNCFRLRKANGLVSDVFEARHMQRMQGNMGI

GHVRYPTAGSSSASEAQPFYVNSPYGITLAHNGNLTNAHELRKKLFEEKRRHINTTSDSEILLNIFASEL

DNFRHYPLEADNIFAAIAATNRLIRGAYACVAMIIGHGMVAFRDPNGIRPLVLGKRDVGDGRTEYMVASE

SVALDTLGFEFLRDVAPGEAVYITEKGQLYTRQCADNPVSNPCLFEYVYFARPDSFIDKISVYSARVNMG

TKLGEKIAREWEDLDIDVVIPIPETSCDIALEIARILDKPYRQGFVKNRYVGRTFIMPGQQLRRKSVRRK

LNANRAEFRDKNVLLVDDSIVRGTTSEQIIEMAREAGAKKVYLASAAPEIRFPNVYGIDMPTANELIAHG

REVDEIRQIIGADGLIFQDLNDLIDAVRAENPDIQQFECSVFNGVYVTRDVDQQYLDYLDSLRNDDAKAV

QLQNEVENLEMHNEG

>lcl|NZ\_FO834906.1\_prot\_WP\_002913214.1\_3986 [gene=cvpA] [locus\_tag=BN49\_RS21600] [protein=colicin V production protein] [protein\_id=WP\_002913214.1] [location=complement(4139845..4140333)] [gbkey=CDS]

MVWIDYAIMAVLGLSCLVSLIRGFVREALSLVTWGCAFYVASHYYADLSVWFTGFEDERVRNGIAIAALF

IVTLIVGAIVNYVIGQLVEKTGLSGTDRVLGICFGALRGVLIIAAILFFLDTFTGMAKSDDWHQSQFIPY

FTPVIRWFFEYLQSSSSFLPKV

>lcl|NZ\_FO834906.1\_prot\_WP\_004214089.1\_3987 [gene=dedD] [locus\_tag=BN49\_RS21605] [protein=cell division protein DedD] [protein\_id=WP\_004214089.1] [location=complement(4140550..4141239)] [gbkey=CDS]

MASKFQNRLVGTIVLVALGVIILPGLLDGQKKHYQDEFAAIPLVPKPGDRDEPDMLPAATQALPSQPPEG

AAEEVRAGDAAAPSLDPSRIPVNSNSFDDVQEPVVAAKPQPKPQPKPQPQQQAATPTPPPAKPQQQQPPQ

QQAALPAPTGKAYVVQLGALKNADKVNEIVGKLRASGFKVYTSPSTPVQGKITRILVGPDASKDKLKGQL

GDLQQISGLSGVVMGFTPN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529577.1\_3988 [gene=folC] [locus\_tag=BN49\_RS21610] [protein=bifunctional tetrahydrofolate synthase/dihydrofolate synthase] [protein\_id=WP\_016529577.1] [location=complement(4141229..4142497)] [gbkey=CDS]

MEKDPIPQATSPLATWLSYLEHLHSKTIDLGLARVSEVARQMDIVKPAPFVFTVAGTNGKGTTCRTLETV

LMAAGYKVGVYSSPHLVRYTERVRIQGAELPEAAHTASFAEIEAARGDISLTYFEYGTLSALWLFKQAQL

DVVILEVGLGGRLDATNIVDADVAVVTSIALDHTDWLGPDRESIGREKAGIFRAGKPAIVGEPDMPHTIA

DVASEKGALLQRRGVDWRYEVEGETWSFRDAAGALSRLPLPQVPLPNAATAVAALRASGIAVDDAILRAG

IRDAMLPGRFQIISDAPRVILDVAHNPHAAAYLAGRLKTLAKTGRVLAVIGMLHDKDIAGTLANLAPEVD

AWYCAPLEGPRGATAEQLVEHLRGGTVYSSVAQAWRAAMADAKVEDTVLVCGSFHTVAQVMEEIDAGRIG

GE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913220.1\_3989 [gene=accD] [locus\_tag=BN49\_RS21615] [protein=acetyl-CoA carboxylase, carboxyltransferase subunit beta] [protein\_id=WP\_002913220.1] [location=complement(4142573..4143493)] [gbkey=CDS]

MSWIERIKSNITPTRKASIPEGVWTKCDSCGQVLYRAELERNLEVCPKCDHHMRMSARNRLHSLLDEGSL

VELGSELEPKDVLKFRDSKKYKDRLASAQKETGEKDALVVMKGTLYAMPVVAAAFEFSFMGGSMGSVVGA

RFVRAVEQALEDNCPLICFSASGGARMQEALMSLMQMAKTSAALAKMQERGLPYISVLTDPTMGGVSASF

AMLGDLNIAEPKALIGFAGPRVIEQTVREKLPPGFQRSEFLIEKGAIDMIVRRPEMRLKLASILAKLMNL

PAPVAVSEAPHEGVVVPPAPDQEPEA

>lcl|NZ\_FO834906.1\_prot\_WP\_008803926.1\_3990 [locus\_tag=BN49\_RS21620] [protein=DedA family protein] [protein\_id=WP\_008803926.1] [location=complement(4143679..4144338)] [gbkey=CDS]

MDLIHFLIDFILHIDVHLAELVAQYGVWVYAILFLILFCETGLVVTPFLPGDSLLFVAGALSALPTNDLN

VHLMVLLMVIAAIVGDAVNYTIGRLFGEKLFSNPNSKIFRRSYLDKTHSFYERHGGKTIILARFVPIVRT

FAPFVAGMGHMSYRHFAAYNVVGALLWVLLFTYAGYLFGDLPVVQENLKLLIVAIIVLSVLPGVIEIIRH

KRAASKQAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913226.1\_3991 [gene=truA] [locus\_tag=BN49\_RS21625] [protein=tRNA pseudouridine(38-40) synthase TruA] [protein\_id=WP\_002913226.1] [location=complement(4144365..4145177)] [gbkey=CDS]

MSEMEQQPICKIALGIEYDGSKYYGWQRQNEVRSVQEKLEKALSQVANEPITVFCAGRTDAGVHGTGQVV

HFETRAQRKDAAWTLGVNANLPGDIAVRWVKHVPADFHARFSATARRYRYVIYNHRLRPAVLSHGVTHFH

QPLDAERMQRAAQCLLGENDFTSFRAVQCQSRTPWRNVMHINVTRYGAYVVVDIKANAFVHHMVRNIVGS

LMEVGAGNQPESWMAELLAAKDRTLAAATAKAEGLYLVSVDYPAHYDLPVLPMGPLFLAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002913227.1\_3992 [locus\_tag=BN49\_RS21630] [protein=aspartate-semialdehyde dehydrogenase] [protein\_id=WP\_002913227.1] [location=complement(4145177..4146190)] [gbkey=CDS]

MSEGWNIAVLGATGAVGEALLETLAERQFPVGEIFALARNDSAGEHLRFGGKSVIVKDAAEFDWTQAQLA

FFAAGVEASAAYVEEATNAGCLVIDLSGLFALEPDVPLVVPDVNPFVLGDYRNRNLIAVPNSLTSQLLTA

LKPLIDQGGLSRISVTNLLSASGQGKKAVDALAGQSAKLLNGIPIDEDDFFGRQLAFNMLPLLPDREGSV

REERRIVDEARKILQDDGLMISASVVQSPVFYGHAQMVSFEAMRPLAAEEARDAFTRGEDIELSEEGEFP

TQVGDASGNARLSIGCVHNDYGMPEQIQFWSVADNVRFGGALMAVKIAEKLIEEYLY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529576.1\_3993 [gene=pdxB] [locus\_tag=BN49\_RS21635] [protein=4-phosphoerythronate dehydrogenase PdxB] [protein\_id=WP\_016529576.1] [location=complement(4146254..4147390)] [gbkey=CDS]

MKILVDENMPYARELFSRLGDVQAIPGRPVPADALTDADALMVRSVTRVNEALLAGKAIKFVGTATAGTD

HVDQAWLQQAGIGFSAAPGCNAIAVVEYVFSSLLMLAERDGFALRDRTVGIVGVGNVGGRLQKRLEALGI

KTLLCDPPRAHRGDEGDFRSLEALVQEADVITFHTPLYKEGQYKTLHLADEALISRLKPGTILINACRGP

VVDNAALLKRLEAGQPLSVVLDVWEPEPDLNVELLKRVDIGTAHIAGYTLEGKARGTTQVFEAYSAFIGH

PQQVALDTLLPAPEFGRITLHGPLDQPTLKRLVHLVYDVRRDDAPLRKVAGVAGEFDKLRKNYQERREWS

SLYVQCSDEQAATLLRLLGFNAVHHPVR

>lcl|NZ\_FO834906.1\_prot\_WP\_042940786.1\_3994 [gene=flk] [locus\_tag=BN49\_RS21640] [protein=flagella biosynthesis regulator Flk] [protein\_id=WP\_042940786.1] [location=4147501..4148478] [gbkey=CDS]

MTHPLADMPDRPPGRGPSGTAATGEPSLSMQQRTVLERLITRLVALTSQQNAEVWACVKHDLGLKGDSPL

LACHFSAAEASLNQRLAAAQDNHHHRQTLAQLSDLLGQGNNRQAVRDYIRQHYGQTALHALSQTQLETIL

HLLQHGQLSIPQPQQRPPTLRPLLPAEHNTLNQLVTKLAAATGEPSKLIWQSMLELCGVKSGELIPATHF

LPLSYWLQARQTLSAQSAPTLTSLQGALKQPLEAAEWQKIVDFASRSWQVTPQTTLSPAQILALLNKVFV

LRVARAQETLAIPQEEPVARRTWSAKPWQLALGAVVLLLVLWLLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004149211.1\_3995 [locus\_tag=BN49\_RS21645] [protein=MFS transporter] [protein\_id=WP\_004149211.1] [location=complement(4148565..4149740)] [gbkey=CDS]

MSAVTETTSNSSANFSLFRITFAVFLTYMTVGLPLPVIPLFVHQELGFGNTVVGVAVGIQFLATVLTRGY

AGRLADQYGAKRSVLQGMLACALAGAAWLAAALLPLPVLARLGLLLLGRLILGFGESQLLTGNLSWGMGL

VGPARSGKVMSWNGMAMYGSLAVGAPLGLLIYSHFGVAVLACVTMGLPLVAWLINGTVRKVAAHGGERPS

LWSVIGMIWRPGIGLGLQGVGFAVIGTFVSLYFASHSWPMAGFTLTAFGGAFVLMRVLFGWMPDRFGGVK

VAMVSLLIEAVGLTLLGLAPNAWLALAGAALTGCGCSLIFPSLGVEVVKRVPAQVRGTALGGYAAFQDIS

YGLTGPLTGLLATSLGYSSVFLAGALCAALGILVTLISFRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913291.1\_3996 [gene=fabB] [locus\_tag=BN49\_RS21650] [protein=beta-ketoacyl-ACP synthase I] [protein\_id=WP\_002913291.1] [location=complement(4149950..4151170)] [gbkey=CDS]

MKRAVITGLGIVSSIGNNQQEVLASLREGRSGITFSQELKDSGMRSHVWGNVKLDTTGLIDRKVVRFMSD

ASIYAYLSMEQAVADAGLAPEAYQNNPRVGLIAGSGGGSPKFQVFGADAMRSPRGLKAVGPYVVTKAMAS

GVSACLATPFKIHGVNYSISSACATSAHCIGNAVEQIQLGKQDIVFAGGGEELCWEMACEFDAMGALSTK

YNDTPEKASRTYDANRDGFVIAGGGGMVVVEELEHALARGAHIYAEIVGYGATSDGADMVAPSGEGAVRC

MQMAMHGVDTPIDYLNSHGTSTPVGDVKELGAIREVFGDNSPAISATKAMTGHSLGAAGVQEAIYSLLML

EHGFIAPSINVEELDEQAAGLNIVTKPTDAKLTTVMSNSFGFGGTNATLVMRKYNA

>lcl|NZ\_FO834906.1\_prot\_WP\_046044057.1\_3997 [gene=mnmC] [locus\_tag=BN49\_RS21655] [protein=bifunctional tRNA (5-methylaminomethyl-2-thiouridine)(34)-methyltransferase MnmD/FAD-dependent 5-carboxymethylaminomethyl-2-thiouridine(34) oxidoreductase MnmC] [protein\_id=WP\_046044057.1] [location=4151329..4153317] [gbkey=CDS]

MKQNAIQPANLEFNAEGTPVSRDFDDVYFSNDNGLEETRYVFLGGNRLPERFPSHPRPLMIVAESGFGTG

LNFLTLWQAFDVFVRDNPDVTLQRLHFISFEKYPLKAEDLRLAHQRWPELAPWAQQLQAQWPSAFGGCHR

LLLDGGRVTLDLWFGDINELTRELDDSLNQQVDAWFLDGFAPAKNPDMWTQDLFSAMARLARPGGTLATF

TSAGFVRRGLQEAGFTMRKSKGFGRKREMLTGEMAQTLSFPARVPWFARSSSDAREAAIIGGGIASALLS

LALLRRGWQVTLYCADEAPAQGASGNRQGALYPLLSQHDPALARFFPAAFTFARRMYDALPVMFDHQWCG

VTQLGWDEKSAHKIAQMLALNLPPDIACAVTAEQVAGLTGVDTGCGGITYPAGGWLCPQQLTAELLALAA

TRGLHVHYGYPVETLSAEGDGWLLNQQRYHQAVVLANGHRITGFAQTAQLPVYPVGGQVSHIPTTPRLAA

LRQVLCYDGYLTPQNPQNQQHCIGASYHRGKTDTTFSEEDQQHNRQRLIDCFPGAEWPQDVDISANDARC

GVRCATRDHLPMVGNVPDYAATLTQYASLHAQPDIADSAPVCRNLFMLGALGSRGLCTAPLSAELLAAQM

SAEPLPLDSDTLAALNPNRLWVRKLLKGKAVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913338.1\_3998 [locus\_tag=BN49\_RS21660] [protein=YfcL family protein] [protein\_id=WP\_002913338.1] [location=complement(4153379..4153660)] [gbkey=CDS]

MIAEFESRILALIDNMVDHASDDELFAGGYLRGHLTLAVAELEGEGEHSADAVHSRVSQSLEKAISAGEL

SPPDQILVQGMWHNLYQQAKNQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174962.1\_3999 [locus\_tag=BN49\_RS21665] [protein=elongation factor P hydroxylase] [protein\_id=WP\_004174962.1] [location=complement(4153692..4154240)] [gbkey=CDS]

MQQQHHYQQLIDLFDSCFAEEFNTRLIKGDDEPIYLPADDETPYHRIVFAHGFFASALHEISHWCVAGKA

RREQVDFGYWYCPDGRDAMTQSQFEDVEVKPQAFEWLFCVAAGFPFNVSCDNLEGDVEPDRIAFQRRVHA

RVMALLEQGIPERPARFIRALQHYYQTPPLTAEHFPWPEDLH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913340.1\_4000 [locus\_tag=BN49\_RS21670] [protein=sulfite exporter TauE/SafE family protein] [protein\_id=WP\_002913340.1] [location=complement(4154240..4155049)] [gbkey=CDS]

MDSFIELFAVSPLVLVVLFFVAILAGFIDSLAGGGGLLTVPALMAAGMPPAQALATNKLQACGGSLSATL

YFVRRKVVNLADQKLNILMTFIGSTAGALLVQHVQSDILKQILPLLVIGIGLYFLLMPKLGEADRQRRLY

GLPFALVAGGSVGFYDGFFGPGAGSFYALAFVTLAGFNLAKSTAHAKLLNATSNVGGLLLFIIGGKVIWA

TGFVMMAGQFIGARAGSRLVLSKGQSLIRPMIVIVSAVMSAKLLYDSHGAEILQWLGIH

>lcl|NZ\_FO834906.1\_prot\_WP\_004174960.1\_4001 [gene=mepA] [locus\_tag=BN49\_RS21675] [protein=penicillin-insensitive murein endopeptidase] [protein\_id=WP\_004174960.1] [location=complement(4155049..4155873)] [gbkey=CDS]

MKNTVIALLALLASAGSLAATPWQKITQPIGGSAQSIGAFSNGCIVGAEALPLSAPGYQVMRTDQRRYFG

HPDLVQFIQRLSNQVHNKGMGTVLIGDMGMPAGGRFNGGHASHQTGLDVDIFLQLPQTRWTSSQLLKPQA

LDLVASDGKHVVPSLWSPQISQLIKLAAEDSEVTRIFVNPAIKQQLCLDAGSDRQWLRKVRPWFQHRAHM

HVRLRCPAGSLECEDQAPPPPGDGCGAELQSWFEPPKPGSTPPVKKTPPPLPPSCQALLDEHVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913342.1\_4002 [gene=aroC] [locus\_tag=BN49\_RS21680] [protein=chorismate synthase] [protein\_id=WP\_002913342.1] [location=complement(4155876..4156961)] [gbkey=CDS]

MAGNTIGQLFRVTTFGESHGLALGCIVDGVPPGIPLTEADLQHDLDRRRPGTSRYTTQRREPDQVKILSG

VFEGVTTGTSIGLLIENTDQRSQDYGAIKDLFRPGHADYTYEQKYGLRDYRGGGRSSARETAMRVAAGAI

AKKYLAAKFGIVIRGCLTQMGDIPLAIKDWDQVEQNPFFCPDPDKIDALDELMRGLKKEGDSIGAKVTVV

ADGVPPGLGEPVFDRLDADIAHALMSINAVKGVEIGDGFEVVKLRGSENRDEITKAGFQSNHAGGILGGI

SSGQQIVANIALKPTSSITVPGHTINRFGEEVEMITKGRHDPCVGIRAVPIAEAMLAIVLMDHFMRQRAQ

NGDVTTTIPRW

>lcl|NZ\_FO834906.1\_prot\_WP\_002913346.1\_4003 [gene=prmB] [locus\_tag=BN49\_RS21685] [protein=50S ribosomal protein L3 N(5)-glutamine methyltransferase] [protein\_id=WP\_002913346.1] [location=complement(4157003..4157935)] [gbkey=CDS]

MDKIFVDEAVNELHTIQDMLRWAVSRFSAANIWYGHGTDNPWDEAVQLVLPSLYLPLDIPEDMRTARLTS

SEKHRIVERVIRRVNERIPVAYLTNKAWFCGHEFYVDERVLVPRSPIGELINNQFAGLINHKPQHILDMC

TGSGCIAIACAYAFPEAEVDAVDISPDALAVAEHNVESHGLIHHVTPIRSDLFRDLPKLQYDLIVTNPPY

VDEEDMADLPEEYEHEPVLGLASGSDGLKLTRRILGNAPDYLSDDGILICEVGNSMVHLMEQYPDVPFTW

LEFDNGGDGVFMLTKQQLIDARAHFGIYKD

>lcl|NZ\_FO834906.1\_prot\_WP\_002913348.1\_4004 [gene=smrB] [locus\_tag=BN49\_RS21690] [protein=endonuclease SmrB] [protein\_id=WP\_002913348.1] [location=4158103..4158654] [gbkey=CDS]

MKKKTSLSEEDQALFRQLMTGTRKIKQDTIVHRPQRKKITEVAPKRLLQEQVDNSHYFSDEFQPLLNTEG

STKYVRPDVSHFELKKLRRGDYSPELFLDLHGLTQQQAKQELGALIAACRREHVFCACVMHGHGKHILKQ

QTPLWLAQHPHIMAFHQAPKEYGGDAALLILIEVEEWQPPELP

>lcl|NZ\_FO834906.1\_prot\_WP\_002913355.1\_4005 [gene=sixA] [locus\_tag=BN49\_RS21695] [protein=phosphohistidine phosphatase SixA] [protein\_id=WP\_002913355.1] [location=complement(4158675..4159160)] [gbkey=CDS]

MQVFIMRHGDAALDAASDSVRPLTVCGCDESRQMATWLKGQKVDIERVLVSPYLRAEQTLDIVGECMNLP

KHVDVMPELTPCGDVGMVSAYLQALANEGVATALVVSHLPLVGYLVSELCPGETPPMFTTSAIACVTLDA

DGKGEFLWQKSPCNLKMANAI

>lcl|NZ\_FO834906.1\_prot\_WP\_004174952.1\_4006 [gene=fadJ] [locus\_tag=BN49\_RS21700] [protein=fatty acid oxidation complex subunit alpha FadJ] [protein\_id=WP\_004174952.1] [location=complement(4159370..4161514)] [gbkey=CDS]

MDTVSAFKLEVRADKIAVITIDAPGEKMNTLKAEFGSQVRGLIRQLRDDKSVRGVVFISAKADNFIAGAD

INMIARCRSAQEAEALARQGQQIMAEIHGLSIPVIAAIHGACLGGGLELALACHGRICSDDEKTRLGLPE

VQLGLLPGSGGTQRLPRLIGVSTALDMMLTGKQLRPRQALKAGLVDEVVPQAILLQAAVELALKGRPTSR

EVPVRERVLAGPLGRHLLFQFVGKQTQRKTQGNYPAVKRILQVVENGLAHGCSSGYAEEARAFGELAMSP

QSQALRSIFFASTDLKKDPGAEAGPGPLRSVAVLGGGLMGGGIAYVTACKGGLPVRIKDIQPRGINHALK

YSWDLLNKQVRQRRLRPVERDRQMALISGTTDYQGFAHRDVVIEAVFEDLALKQRMVSEVEQYGGPQTIF

ASNTSSLPIGDIAAHASRPGQVIGLHFFSPVEKMPLVEVIPHKGTDPQTIATVVQLAKRQGKTPIVVADK

AGFYVNRILAPYINEAMRLLVEGEPIEVIDNALVKFGFPVGPIQLLDEVGIDTGTKIIPVLEGAFGERFS

PPANIIDAILKDDRKGRKNNRGFYLYETKGRKSKKRPDPAVYPLLGIGRPQSRLSAQQVAERCVMMMLNE

AARCFDEQIIRSARDGDIGAVFGIGFPPFLGGPFRYMDTIGAGEVAAILQRLAAQFGPRFTPCDTLLRMA

EQGTTFWPADERLT

>lcl|NZ\_FO834906.1\_prot\_WP\_021313703.1\_4007 [gene=fadI] [locus\_tag=BN49\_RS21705] [protein=acetyl-CoA C-acyltransferase FadI] [protein\_id=WP\_021313703.1] [location=complement(4161514..4162824)] [gbkey=CDS]

MSQALPLITRQGDRIAIVTGLRTPFARQATAFHGVPAIDLGKMVVGEMLARSDIPAEVIEQLVFGQVVQM

PEAPNIAREIVLGTGMSVHTDAYSVSRACATSFQAVANVAESLMAGTIRAGIAGGADSSSVLPIGVSKTL

ARTLVDANKARTLSQKLKLFSRLRPRDLLPVPPAVAEYSTGLRMGDTAEQMAKSWGISREEQDALAHRSH

QLAAKAWEEGKLSAEVMTAYAPPFREPLEQDNNIRKNSTLADYQKLRPAFDRKHGTVTAANSTPLTDGAA

AVILMTESRAKELGLRPLGYLRSYAFTAIDVWQDMLLGPAWSTPLALERAGLTLADLTLIDMHEAFAAQT

LANLQCLASDRFAREVLGRSQATGEVDESKFNVLGGSIAYGHPFAATGARMITQTLHELRRRGGGFGLVT

ACAAGGLGAAMIVEAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913359.1\_4008 [locus\_tag=BN49\_RS21710] [protein=YfcZ/YiiS family protein] [protein\_id=WP\_002913359.1] [location=complement(4162984..4163268)] [gbkey=CDS]

MSKCSADETPVCCCMDVGTIVDNTDCTASYSRVFANRAEAEQTLAALSEKARNVESEPCQINPTFTDVDG

GVQLDIDFVFSCEAESLIFQLGLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913360.1\_4009 [gene=fadL] [locus\_tag=BN49\_RS21715] [protein=long-chain fatty acid transporter FadL] [protein\_id=WP\_002913360.1] [location=4163642..4164964] [gbkey=CDS]

MSQKTRFTQSALAVAVALVSTQAWSAGFQLNEFSASGLGRAYSGEGAIADDAGNASRNPALIMMFDRPTM

SAGAVFVDPGVNVSGTSPTGKSLKADNIAPTAWVPNFHFVAPINDQFGWGASITSNYGLATEYNDDYAAG

SMGGKTDLTTANFNLSGAYRLDSNWSFGLGFDAVYAKAKIERYAGDLGQIVAGSGALPPALAGQVAKIPA

DTQIAHLNGNAWGFGWNAGILYELDKNNRYGLTYRSEVKIDFDGNYRSSLPAAYNQILGNFGLPAGTSGQ

TTNGSLTLNLPEMWELSGYNRVAPQWAVHYSLTYTSWSQFQELKATGSNGQTLFYKEEGFKDAYRLALGT

TYYYDDNWTFRTGIAFDDSPVPANNRSISIPDQDRLWLSAGTTYAFNKDASVDVGVSYMHGQHVEIKEGP

YTFRSEGTAWLYGANFNYRF

>lcl|NZ\_FO834906.1\_prot\_WP\_002913362.1\_4010 [gene=mlaA] [locus\_tag=BN49\_RS21720] [protein=phospholipid-binding lipoprotein MlaA] [protein\_id=WP\_002913362.1] [location=complement(4165026..4165787)] [gbkey=CDS]

MNYRLSALALGATLLVGCASSSSGDRPQGRSDPLEGFNRTMFNFNFNVVDPYVLRPVAVAWRDYVPQPAR

NGLSNFTSNLEEPAVMVNYFLQGDPYKGMVHFTRFFLNTILGMGGLIDVAGMANPQLQRVEPHRFGSTLG

HYGVGYGPYVQLPFYGSFTLRDEGGDMADGLYPVLSWLTWPMSIGKWAVEGIETRAQLLDSDGLLRQSSD

PYILMREAYFQRHDFIANGGKLTPADNPNAQAIQDELKDIDSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004149224.1\_4011 [locus\_tag=BN49\_RS21725] [protein=formate/nitrite transporter family protein] [protein\_id=WP\_004149224.1] [location=4166077..4167006] [gbkey=CDS]

MDELDNNKLKAEDDEREVESEENQRGEEIEVNEDRLPSRAMAIHEHIRQEGEKEMERDALALLWSAIAAG

LSMGASLLAKGIFHVKLEGIPGGFLLENLGYTFGFIIVIMARQQLFTENTVTAVLPVMHNPTLGNVGLLM

RLWSVVLAGNLIGTAVAAWAFNYMPIFDEPTRQAFVSIAEDVMKNSPTEMFANAIISGWLVATMVWMFPV

AGAAKIVVIILMTWLIALADTTHIVVGSVEILYLVFNGNLPWSDFIWPFALPTLAGNICGGTFIFALLSH

AQIRNDMSSKRKAEARAQAAEKGKKADRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004174945.1\_4012 [locus\_tag=BN49\_RS21735] [protein=WbuC family cupin fold metalloprotein] [protein\_id=WP\_004174945.1] [location=4167419..4167901] [gbkey=CDS]

MKQITLSDMQQQSEAAASAPRLRAHRNFHPELSDPIQRLAIAMEPGTYIRPHRHRHTFELLLPLKGRFVV

LNFDDHGVVTNRVVLGETCTALEMEAGTWHTVLSLDAGGMVFEVKQGAYQPLAEMDTMAWAPAEGQPGTA

EMMAWYAIAQPGDRFLSMPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004149226.1\_4013 [locus\_tag=BN49\_RS21740] [protein=hypothetical protein] [protein\_id=WP\_004149226.1] [location=4168269..4169150] [gbkey=CDS]

MNITERNIWKLNNLPPMEYCSLARAQKLLNCELEDILHWHDIGAINLCLKLNPTPGILKIAVLSHQEKEV

TSAFNPFTSVEAGETVWSHHSHIRSILRLEGDIPTMETLRGNTVTQFNVKVFASGLWHPHCRNLMALLEA

PDDILFENRLSMMLPDKPFVYCHFIPEEDERPSISLNRIYITSQAIEKIYAHSISARPMDVTKNPLLDQT

RYIQQELTVLPQSEVLLEFIHYLVQSHTVFNEKLQNMAEPDKTQLFHHVLERLKEEGMLIENAQPDEGDI

GSEASRESQFAGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004149227.1\_4014 [gene=cynR] [locus\_tag=BN49\_RS21745] [protein=transcriptional regulator CynR] [protein\_id=WP\_004149227.1] [location=complement(4169160..4170068)] [gbkey=CDS]

MLLRQLSYFIAVAEHCGFSRAAAALHVSQPALSQQIRQLEAMLEVQLFDRSGRRIRLTDAGEIWLEYARR

ALRELEEGRRALHDAEDLQHGKLRIAMTPTFTTYMLGPLMEAYYRRYPGVKVLIQEMNQERMEAMLLEDE

LDVGIAFDDSRSQEIVVQPLLTETLALVVSRAHPLAGERDLQLQALDAQPLILLSSEFATREQIDRYCRL

HRLEPDVRMEANSIGAVLSVIRSTTLATLLPAAIAGQFDDVVAIELRPALLQRTACLLQRQGAWQSAAAR

EFITLARENAITIEQENRQSLA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530540.1\_4015 [locus\_tag=BN49\_RS21750] [protein=nucleoside deaminase] [protein\_id=WP\_016530540.1] [location=4170201..4170659] [gbkey=CDS]

MSAHDRYLQRALVLAKQNIADGGRPFGAVLVRNDEIVAESVNTFHLSGDPTAHAELNAVRDLAARLGSAV

LRECVIYASGQPCPMCLSALYLTGVREVFFANSNQDGEPFQLSTAAIYQQLQQPLTQQTLPIHHRPQPEG

TELYQRWAERQS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043693.1\_4016 [locus\_tag=BN49\_RS21755] [protein=CynX/NimT family MFS transporter] [protein\_id=WP\_046043693.1] [location=4170656..4171852] [gbkey=CDS]

MTPALRQNLTLAVLVLTGINMRPLLTSIGPLLPDIRAASGMSYTLAALLTALPVIAMGVLALAAGWVDRY

IGQKRSIALSLLIIAAGALLREIAPNSGLLLTSALAGGIGIGIIQAAIPAVIKHLFPRRTPLVMGLWSAA

LMGGGGLGAAFTPWLASHSAAWHDALAWWALPALLALFSWLAICRQLPRAPHHASASPRVAIIGQRRAWT

LGLYFGLINAGYASLIAWLPPYYIQLGDSAQYSGSLLALLTVGQTAGALLLPALARQEDRRQLLLLALAL

QLIGFCGFIWLPEHFSALWAIACGVGLGGAFPLCLVLALDHAGQPAVAGRLVAFMQGIGFIIAGLSPWLS

GLLRSLSGNYTLDWSWHAICVLLLMALTLRFIPAHYPAEWRQRASDLP

>lcl|NZ\_FO834906.1\_prot\_WP\_099119320.1\_4017 [gene=ypdK] [locus\_tag=BN49\_RS30570] [protein=membrane protein YpdK] [protein\_id=WP\_099119320.1] [location=4172191..4172262] [gbkey=CDS]

MKYFFMGLSFMVIVWAGTFALMI

>lcl|NZ\_FO834906.1\_prot\_WP\_016529619.1\_4018 [gene=alaC] [locus\_tag=BN49\_RS21760] [protein=alanine transaminase] [protein\_id=WP\_016529619.1] [location=complement(4172333..4173547)] [gbkey=CDS]

MAESSPERRFTRIDRLPPYVFNITAELKMAARRRGEDIIDFSMGNPDGATPPHIVEKLCTVAQRPDTHGY

STSRGIPRLRRAISRWYEERYNVDIDPESEAIVTIGSKEGLAHLMLATLDHGDTVLVPNPSYPIHIYGAV

IAGAQVRSVPLVEGGDFFNELERAIRESYPKPKMMILGFPSNPTAQCVELDFFEKVVALAKQYDILVVHD

LAYADIVYDGWKAPSIMQVPGARDVAVEFFTLSKSYNMAGWRIGFMVGNKTLVNALARIKSYHDYGTFTP

LQVAAIAALEGDQQCVRDIAEQYKRRRDVLVKGLHEAGWMVECPKASMYVWAKIPEPYAAMGSLEFAKKL

LNEAKVCVSPGIGFGDYGDTHVRFALIENRDRTRQAIRGIKAMFRADGQLASAS

>lcl|NZ\_FO834906.1\_prot\_WP\_009486222.1\_4019 [locus\_tag=BN49\_RS21765] [protein=hypothetical protein] [protein\_id=WP\_009486222.1] [location=4173636..4173821] [gbkey=CDS]

MLSRGPLKNIPWHIKRVSTALNAAVHGRNNPGLYKSGNTLISFLTQNIIVNGEDRRYRDAF

>lcl|NZ\_FO834906.1\_prot\_WP\_004153200.1\_4020 [locus\_tag=BN49\_RS31185] [protein=hypothetical protein] [protein\_id=WP\_004153200.1] [location=complement(4173818..4173931)] [gbkey=CDS]

MGAPRQWPERDMIKNLTAEDQPWNHKAEKSHFLKGIN

>lcl|NZ\_FO834906.1\_prot\_WP\_032418581.1\_4021 [locus\_tag=BN49\_RS21775] [protein=sensor histidine kinase] [protein\_id=WP\_032418581.1] [location=4173930..4175627] [gbkey=CDS]

MHEIFTMMLAVYDRAALMLICLFFLIRLRLFRELLHKSAHTPKELLAVTAIFSLFALFSTWSGVPVEGSL

VNVRIIAVMSGGILFGPWVGAIVGAIAGVHRYLIDIDGVTAVPCFITSIVAGLLSGLINRKVAREQRWKI

GILAGMICETLTMILVVVWAPSLSLGVDIVSKIGIPMILGSVCIGFIVLLVQSVEGEKEASAARQAKLAL

DIANKTLPLFRHVNSDSLRQVCEIIRRDITADAVAITNTEHVLAYVGVGEANYQRHDDMISPTTRQAIRY

GKIIIKNNDEAHRTPEIHSLMVIPLWEKGVVTGTLKIYYCHAHRITSTLQEMAIGLSQIISTQLEVSRAE

QLREMANKAELRALQSKINPHFLFNALNAISSSIRLNPDTARQLIFNLSRYLRYNIELKDDEQIDIKREL

YQIKDYIAIEQARFGDKLTVIYDIDDDVSCVIPSLLIQPLVENAIVHGIQPCKGKGVVTIGINECGNRVR

ISVRDTGNGIDPAVVARVEADEMPGNKIGLLNVHHRVKLLYGEGLHIRNLTPGTEIAFYVPNNSTPQALT

ESLLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002913374.1\_4022 [locus\_tag=BN49\_RS21780] [protein=LytTR family DNA-binding domain-containing protein] [protein\_id=WP\_002913374.1] [location=4175639..4176376] [gbkey=CDS]

MKVIIVEDEFLAQQELSWLINTHSQMEIVGSFDDGLDVLKFLQHNKVDAIFLDINIPSLDGVLLAQNISQ

FAHKPFIVFITAWKEHAVEAFELEAFDYILKPYQESRIINMLQKLTTAWQQQNNAASGLASAAPRENDTI

NLIKDERIIVTSIHDIYYAEAHEKMTFVYTRRESFVMPMNITEFCSKLPTAHFFRCHRSYCVNLSKIREI

EPWFNNTYVLRLRDLEFQVPVSRSKVKEFRQLMNL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913377.1\_4023 [gene=glk] [locus\_tag=BN49\_RS21785] [protein=glucokinase] [protein\_id=WP\_002913377.1] [location=complement(4176430..4177395)] [gbkey=CDS]

MTKFALVGDVGGTNARLALCDLASGEISRAKTYSGLDYPSLEAVVRVYLEEHQVTVNEGCIAIACPITGD

WVAMTNHTWAFSIAEMKRNLGFAHLEIINDFTAVSMAIPMLKAEHLIQFGGSAPVAGKPIAVYGAGTGLG

VAHLVHVDKRWVSLPGEGGHVDFAPNSEEEGIILEELRAELGHVSAERVLSGPGLVNLYRAIVKSDGRLP

ENLQPREVTERALADSCTDCRRALSLFCVIMGRFGGNLALTLGTFGGVYIAGGIVPRFLEFFKASGFRGG

FEDKGRFKAYVQDIPVYLIVHDNPGLLGSGAHLRQTLGQVL

>lcl|NZ\_FO834906.1\_prot\_WP\_004154521.1\_4024 [locus\_tag=BN49\_RS21790] [protein=ion channel protein] [protein\_id=WP\_004154521.1] [location=4177659..4178894] [gbkey=CDS]

MLHPRARTMLILSVPAILIGIACSLILIVAMKVAALLQRVLWSNLPAQLGVSADSPLWIIAMLTATGIAV

GLVIRYSPGHAGPDPATESLIGAPIATGALPGLLAALILGLAGGVSLGPEHPIMVVNIALAVAVGSRLFP

RVSSLDWTILAASGTIGALFGTPVAAALIFSQTLNSSNDTPLWDRLFAPLLAAAAGALTTGLFFHPHFSL

PIPHYGQMRFVDILSGIIVALIAIAVGMVAVWCLPRLHALMHRLKNPILTLGIGGLLLGIVGTIGGPLTL

FKGLDEMQQLAFSQTLTAADFLLIALVKLAALVLASASGFRGGRIFPAVFVGVALGLMLHAHVDAVPAAI

TVSCAILGMVLVVTRDGWLSLFMAAVVVPDTTLLPLLCMVMLPAWLLLAGRPLMIAKRHTD

>lcl|NZ\_FO834906.1\_prot\_WP\_004159719.1\_4025 [locus\_tag=BN49\_RS21795] [protein=thiamine pyrophosphate-binding protein] [protein\_id=WP\_004159719.1] [location=complement(4178891..4180552)] [gbkey=CDS]

MQPTYTIGDYLLDRLVDCGIDRLFGVPGDYNLQFLDRVIAHSALGWVGCANELNAAYAADGYARIKGAGA

LLTTYGVGELSALNGIAGSYAEHIPVLHIVGAPSTGAQQRGELLHHTLGDGDFRHFARMSEQITCSQALL

TAGNACHEIDRVLRDMLTHHRPGYLMLPADVARAAAIAPAQRLLVEPAPADENQLAGFCEHASRLLRGSR

RISLLADFLAQRYGLQKTLREWVAKTPVAHATMLMGKGLFDEQQSGFVGTYSGIASAPQTREAIENADTI

ICIGTRFTDTITAGFTQHLAREKTIEIQPFAVRVGDHWFSGVPMDKALAALMTLSAPLAAEWATPQVVAP

EAEEGAEGELTQKNFWATVQGALRPGDIILADQGTAAFGIAALKLPSEASLIVQPLWGSIGFTLPAAYGA

QTAAAERRVVLIVGDGAAQLTIQEMGSMLRDKQKPLILLLNNEGYTVERAIHGPEQRYNDIALWDWQRLP

EAFAPDVASRCRRVTQTSELREAMTESITSDTLTLVEVMLPKMDIPDFLRAVTQALEERNSRV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174934.1\_4026 [gene=mgrA] [locus\_tag=BN49\_RS21800] [protein=L-glyceraldehyde 3-phosphate reductase] [protein\_id=WP\_004174934.1] [location=4180733..4181725] [gbkey=CDS]

MVYQASTTRYQTMEYRRCGRSGLQLPAISLGLWHNFGDETRVETSRQMLLHAFDLGITHFDLANNYGPPP

GSAESNFGRILKESLLPYRDELIISTKAGYTMWDGPYGDWGSRKYLVASLNQSLKRMGLEYVDIFYHHRP

DPQTPLMETMRALDHLVRQGKALYVGISNYPLAQAREAVKILNDLGTPCIIHQPRYSMFERGVEEGLLDF

LQTEGIGSIAFSPLAGGQLTDRYLNGIPADSRAASSSRFLQPEQLTPARLEKIRQLNRQAEARGQKLSQM

ALAWVLREEKVTSVLIGASKTAQLDDAVGMLQNRHFTTEECAAIDAILAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913419.1\_4027 [locus\_tag=BN49\_RS21805] [protein=DUF2502 domain-containing protein] [protein\_id=WP\_002913419.1] [location=4181856..4182215] [gbkey=CDS]

MFRSLILAAVLLAAGPLVANAGEITLLPSVKLQIGDRDNYGNYWDGGSWRDRDYWRRHYEWRDNRWHRHD

NGWHKGWYKGRDKAWERGYRAGWNDRDDHRGGWGRGPGGRGHGHGHGHH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530286.1\_4028 [locus\_tag=BN49\_RS21810] [protein=Nramp family divalent metal transporter] [protein\_id=WP\_016530286.1] [location=complement(4182273..4183514)] [gbkey=CDS]

MTSSRVENSSSRAARKVKLALMGPAFVAAIGYIDPGNFATNIQAGVSFGYQLLWVVVWANLMAMLIQVLS

AKLGIATGKNLAEQIRDHYPRPVVWFYWVQAEIIAMATDLAEFIGAAIGFKLVLGVSLLQGAVLTGVATF

LILMLQRRGQKPLEKVIGGLLLFVAVAYVVELIFSQPALAPLTKGLVIPTLPNGEAVFLAAGVLGATIMP

HVIYLHSSLTQHLHGGTRKERYNATRWDVAIAMTIAGFVNLAMMATAAAAFHFNGHTGVADLDQAYMTLE

PLLSHAAATIFGLSLIAAGLSSTVVGTLAGQVVMQGFIRFHIPLWFRRAITMLPSFVVILLGLDPTRILV

MSQVLLSFGIALALVPLLIFTSNAKLMGDLVNTRWVRGIGWAIVAIVVSLNGWLIVGSLLGVD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530285.1\_4029 [gene=nupC] [locus\_tag=BN49\_RS21815] [protein=nucleoside permease NupC] [protein\_id=WP\_016530285.1] [location=4183861..4185063] [gbkey=CDS]

MDRVLHFVLAIVVVAILALLVSHDRQKIRIRYVVQLLVIEVLLAWFFLNSDIGLGFVKGFSEMFEKLLGF

ANEGTNFVFGGMNDKGLAFFFLKVLCPIVFISALIGILQHIRILPIVIRAIGTVLSKVNGMGKLESFNAV

SSLILGQSENFIAYKDILGKMSRNRMYTMAATAMSTVSMSIVGAYMTMLQPKYVVAALVLNMFSTFIVLS

LINPYRVEESEENLQMSNLHEGQSFFEMLGEYILAGFKVAIIVAAMLIGFIALISALNALFATVTGWFGY

SISFQGILGYIFYPIAWVMGVPASEALQVGSIMATKLVSNEFVAMMDLQKIASTLSPRAEGIISIFLVSF

ANFSSIGIIAGAIKGLNEEQGNVVSRFGLKLVYGSTLVSVLSASIAALVL

>lcl|NZ\_FO834906.1\_prot\_WP\_004151096.1\_4030 [locus\_tag=BN49\_RS21820] [protein=EAL domain-containing protein] [protein\_id=WP\_004151096.1] [location=complement(4185112..4187283)] [gbkey=CDS]

MLDKININIKKTLLAFIICLVAIPLARFISPQTIIDGNLIYIAWLPISVMFSVIFIFGRYAIAPLILAFA

ITNSFLIKLTLPQAFILLFCQLFAVFVSCAILRLLVGKRWRCGPTAKHMGARIFWGGFFAPVLLKITMYL

AGQYFAFPLAITSYFGSMPLIYTVIDIQSLISAALIFTTFLYYPMRMIISPRYARRFWQQECLPWLAPQY

RSFTLYWFIALAVILTLLCAPYQSEFIAGYLVPVIFIVYFIGISRIGHALLRISWSVSAFLLVVYNKNFL

QGVQSEYSLSFVLSVLISFTICLFYMADIYARSDRNKRRWRSQAEEDPLTGLPNLRALESHLQSCPQQAI

CSLRIDNLDFLSRHYGLMMGVDCKRQIIRALQPLLGAADKVFQVPGSELILVLDGPEPSSRLNHMVAVLN

HKKFSWHNQPLDLEFGAAWGRDDGQGEGLYQMLGQLSWLSEQAGSERRVLALDEEQDLVVDQTTEQVRLL

MRVKQVLKDRALMLYAQPIQNPEGEGYHEILTRMRCGDSVIMPDRFIPLIVQFNLSQRFDMLVLETLFSM

LHKHPGQRFSVNLLPATLMQKNSAGQIIALFQRYSVSPELITIEVTEEQAFSNADTSRQNLEALRAFGCA

IAIDDFGTGYANYERLKHLQADIIKIDGCFVRDILTDPLDAIMVKSIVEMARAKQMSVVAEYVESEPQKA

RLLELGVNYLQGYLIGKPQPLGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913434.1\_4031 [locus\_tag=BN49\_RS21835] [protein=putative DNA-binding transcriptional regulator] [protein\_id=WP\_002913434.1] [location=4187905..4188258] [gbkey=CDS]

MLKERMTPEEIAHLTGYSRQTINKWVRKEGWQTSPRPGVQGGKARLVHVNEQVREFIRSAQRVAETPGIY

SPHDSDLESLLLTLSKELTPSEQKQLMSLLLREGITGLLLRLGIRDR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913435.1\_4032 [locus\_tag=BN49\_RS21840] [protein=putative DNA-binding transcriptional regulator] [protein\_id=WP\_002913435.1] [location=4188262..4188654] [gbkey=CDS]

MMKLKDKMTPAELADCLGLARQTINRWVREKQWRTEAIPGVKGGRARLVVIDQPVREFLTNIPARRHLLT

DNHLAESPGAYLVNEADAIWRQITETLQLMTPAEQLQLRDLLAREGISGFLARLGIASPE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530971.1\_4033 [gene=gltX] [locus\_tag=BN49\_RS21845] [protein=glutamate--tRNA ligase] [protein\_id=WP\_016530971.1] [location=complement(4188706..4190124)] [gbkey=CDS]

MKIKTRFAPSPTGYLHVGGARTALYSWLFARNHGGEFVLRIEDTDLERSTPEAIEAIMDGMNWLNLQWDE

GPYFQTKRFERYNNVIDEMLEAGTAYKCYCSKERLEALREEQMAKGEKPRYDGRCRHSHEHHADDEPCVV

RFANPQEGSVIFDDQIRGPIEFSNQELDDLIIRRTDGSPTYNFCVVVDDWDMAITHVIRGEDHINNTPRQ

INILKALNAPVPVYAHVSMINGDDGKKLSKRHGAVSVMQYRDDGYLPEALLNYLVRLGWSHGDQEIFTRE

EMIEFFSLGAVSKSASAFNTDKLLWLNHHYINTLPAEYVATHLQWHIEQENIDTRNGPQLAELVKLLGER

CKTLKEMAQSCRYFYEEFAEFDADAAKKHLRPVARQPLEVVRDKLAAISDWTAENVHHAIQATADELEVG

MGKVGMPLRVAVTGAGQSPALDVTVHAIGKSRSVDRINKALAFIAEREGQAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002913438.1\_4034 [locus\_tag=BN49\_RS21870] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002913438.1] [location=complement(4190867..4191793)] [gbkey=CDS]

MNYSLRQLKVFVTVARARSFSRAGEMIGLSQSAVSHSVKELEHQTGVRLLDRTTREVVLTEAGQQLAGRL

ERLLDELTITLRDAGRVGQQLSGTVKVAASQTISAHLIPQCIAHSNRRYPDIDFVLHDRPQQWVLESIRQ

GEVDFGIVIDPGPAADLQCEVVLAEPFLLLCREDHPFASLTEVPWQALQDERLILQDYASGSRPLIDAAL

SRLAIRANIVQEIGHPATLFPMVESGIGISVLPALALPLPQGSHLTVKRLTPVMERQLMLACRKNRSLST

AAQALWEIVREEGENLTAARVEDPLYQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913439.1\_4035 [locus\_tag=BN49\_RS21875] [protein=bile acid:sodium symporter] [protein\_id=WP\_002913439.1] [location=4191882..4192880] [gbkey=CDS]

MKLFRILDPFTATLITVVLLASFFPARGAFVPFFEHLTTAAIALLFFMHGAKLSREAIIAGGSHWRLHLW

VMCSTFILFPLLGVLFAWWAPVNVDPMLYSGFIYLCILPATVQSAIAFTSLAGGNVAAAVCSASASSLLG

IFVSPLLVGVLMNLHGAGGSLEQVGKIMLQLLLPFVLGHLSRPWIGDWVAKHKKWIGKTDQTSILLVVYS

AFSEAVVNGIWHKVGLGSLLFIVVVSLVLLAIVIAVNVFVARRCGFNKADEITIVFCGSKKSLANGIPMA

NILFPTSILGIMVLPLMIFHQIQLMVCAVLARRYKQQTDARLAEEKANAAKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913440.1\_4036 [locus\_tag=BN49\_RS21880] [protein=DUF3820 family protein] [protein\_id=WP\_002913440.1] [location=complement(4192877..4193095)] [gbkey=CDS]

MDKAQLVEIANTEMPFGKYKGRRLIDVPEEYLLWFARKDQFPAGHLGELMALTLLIKTEGLSDLVQPLKK

AR

>lcl|NZ\_FO834906.1\_prot\_WP\_004180820.1\_4037 [gene=ligA] [locus\_tag=BN49\_RS21885] [protein=NAD-dependent DNA ligase LigA] [protein\_id=WP\_004180820.1] [location=complement(4193097..4195112)] [gbkey=CDS]

MEPIEQQLTELRTTLRHHEYLYHVMDAPEVPDAEYDRLMRKLRELESQHPELITPDSPTQRVGAAPLTAF

SQIRHEVPMLSLDNVFDEESFLAFNKRVQDRLKSTDHLTYCCELKLDGLAVSILYENGVLVQAATRGDGT

TGEDITSNVRTIRAIPLKLHGENIPARLEVRGEVFLPQAGFEKINEEARRTGGKVFANPRNAAAGSLRQL

DPRITAKRPLTFFCYGVGVLEGGELPASHSARLLQFKAWGLPVSDRVTLCHTPEEVLTYYRKVEEERPHL

GFDIDGVVIKVDSLALQEQLGFVARAPRWAVAFKFPAQEQMTFVRDVEFQVGRTGAITPVARLEPVHVAG

VLVSNATLHNADEIERLGLKIGDKVVIRRAGDVIPQVVNVVLSERPADARDVVFPTHCPVCQSDVERVEG

EAVARCTGGLICGAQRKESLKHFVSRRALDVDGMGDKIIDQLVEKEYVHTPADLFRLTAGKLTGLDRMGP

KSAQNVVNALEKAKETTFARFLYALGIREVGEATAAGLAAHFGTLEALEQASIEELQKVPDVGIVVATHT

FNFFAEESNRDVIAQLLAEGVRWPAPVVVKAEEIDSPFAGKTVVLTGSLSQLSRDDAKARLVALGAKVAG

SVSKKTDLVIAGEAAGSKLAKAQELGIEVIDEAEMMRLLGE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532018.1\_4038 [gene=zipA] [locus\_tag=BN49\_RS21890] [protein=cell division protein ZipA] [protein\_id=WP\_016532018.1] [location=complement(4195182..4196243)] [gbkey=CDS]

MMQDLRLILIIVGAIAIIALLVHGFWTSRKERSSMFRDRPLKRMKSRDDESENDDFDDNVEGVGEVRVHP

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QPQPAQPPGQPQHQPQPVVQQPVAPQPVTPTVAQPQPAAPQQPAPQPVAASQPAVAEPQPVEPQQPAAPQ

PKERKETVIVMNVAAHHGAQLNGEVLINSIQQAGFKFGEMNIFHRHLSPDGSGPVLFSLANMVKPGTFNP

DSMADMMTPGVTIFMQVPSYGDELQNFKLMLQSAQYIADEVGGVVLDDQRRMMTPQKLREYQDRIREVKD

ANA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532019.1\_4039 [gene=cysZ] [locus\_tag=BN49\_RS21900] [protein=sulfate transporter CysZ] [protein\_id=WP\_016532019.1] [location=4196474..4197235] [gbkey=CDS]

MVSSSAPTPHSGVYYFSQGWKLIGLPGIRRYVFLPLLVNVLLMGAAFWWLFTRLGSWIPSLMSHVPDWLQ

WLNYLLWPVVVLSILLVFGYFFSTIANWIAAPFSGLLAEQLEARLTGATPPDVGVFGIMKDIPRIMKREW

QKLAWYLPRAIVLLLLYFIPGVGQTVAPVLWFLFSAWMLAIQYCDYPFDNHKVPFKTMREALRSRKVMNM

QFGALTSLFTVIPVLNLVILPVAICGATAMWVDCYRDRHASWK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532020.1\_4040 [gene=cysK] [locus\_tag=BN49\_RS21905] [protein=cysteine synthase A] [protein\_id=WP\_016532020.1] [location=4197412..4198383] [gbkey=CDS]

MSKIFEDNSLTIGHTPLVRLNRIGNGRILAKVESRNPSFSVKCRIGANMIWDAEKRGVLKPGMELVEPTS

GNTGIALAYVAAARGYKLTLTMPETMSIERRKLLKALGANLVLTEGAKGMKGAIQKAEEIVASNPEQFLL

LQQFSNPANPEIHEKTTGPEIWEDTDGQVDVFISGVGTGGTLTGVSRYIKNTKGKKDLITVAVEPTDSPV

IAQALAGEELKPGPHKIQGIGAGFIPGNLDLKLVDKVIGITNEEAISTARRLMEEEGILAGISSGAAVAA

ALKLQEDEAFTNKNIVVILPSSGERYLSTALFADLFTEKELQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002913505.1\_4041 [gene=ptsH] [locus\_tag=BN49\_RS21915] [protein=phosphocarrier protein Hpr] [protein\_id=WP\_002913505.1] [location=4198764..4199021] [gbkey=CDS]

MFQQEVTITAPNGLHTRPAAQFVKEAKGFTSEITVTSNGKSASAKSLFKLQTLGLTQGTVVTLSAEGEDE

QKAVEHLVKLMAELE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913506.1\_4042 [gene=ptsI] [locus\_tag=BN49\_RS21920] [protein=phosphoenolpyruvate-protein phosphotransferase PtsI] [protein\_id=WP\_002913506.1] [location=4199066..4200793] [gbkey=CDS]

MISGILASPGIAFGKALLLKEDEIVIDRKKISADKVDQEVERFLSGRAKASAQLEVIKTKAGETFGEEKE

AIFEGHIMLLEDEELEQEIIALIKDKHMTADAAANEVIDGQATALEELDDEYLKERAADVRDIGKRLLRN

ILGLAIIDLSAIQDEVILVAADLTPSETAQLNLKKVLGFITDAGGRTSHTSIMARSLELPAIVGTGSITA

QVKNGDYLILDAVNNQVLINPSNEQIEALRSLQAQVAEEKAELAKLKDLPAITLDGHQVEVCANIGTVRD

VEGAERNGAEGVGLYRTEFLFMDRDALPTEEEQFAAYKAVAEACGSQAVIVRTMDIGGDKELPYMNFPKE

ENPFLGWRAVRIAMDRKEILRDQVRAILRASAFGKLRIMFPMIISVEEVRALKKEIEIYKQELRDEGKAF

DESIEIGVMVETPAAATIARHLAKEVDFFSIGTNDLTQYTLAVDRGNDMISHLYQPMSPSVLNLIKQVID

ASHAEGKWTGMCGELAGDERATLLLLGMGLDEFSMSAISIPRIKKIIRNTNFEDAKVLAEQALAQPTTDE

LMTLVNKFIEEKTIC

>lcl|NZ\_FO834906.1\_prot\_WP\_000522253.1\_4043 [gene=crr] [locus\_tag=BN49\_RS21925] [protein=PTS glucose transporter subunit IIA] [protein\_id=WP\_000522253.1] [location=4200836..4201345] [gbkey=CDS]

MGLFDKLKSLVSDDKKDTGTIEIVAPLSGEIVNIEDVPDVVFAEKIVGDGIAIKPTGNKMVAPVDGTIGK

IFETNHAFSIESDSGIELFVHFGIDTVELKGEGFKRIAEEGQRVKVGDPVIEFDLPLLEEKAKSTLTPVV

ISNMDEIKELIKLSGSVTVGETPVIRIKK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532021.1\_4044 [locus\_tag=BN49\_RS21930] [protein=hypothetical protein] [protein\_id=WP\_016532021.1] [location=complement(4201386..4201625)] [gbkey=CDS]

MKSYRLVIRQQGRIVGHFDTTGEAAQEDACVARSLFGLAGGYQCELLVADSERRILESTPEGLRVLSREK

CYRPVTCAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174917.1\_4045 [gene=pdxK] [locus\_tag=BN49\_RS21935] [protein=pyridoxine/pyridoxal/pyridoxamine kinase] [protein\_id=WP\_004174917.1] [location=complement(4201622..4202488)] [gbkey=CDS]

MGQQDDIQSVLFHDKSRASEVDIVAVQSQVVYGSVGNSIAVPAIKQHGLRVLAVPTVLFSNTPHYETFYG

GIIPEEWFVGYLQALEERDALRELRAVTTGYMGSAVQIERLAQWLTRVRARHPGLCILVDPVIGDVDSGI

YVKAEIPDAYRQHLLPLAQGITPNLFELETLSGQRCRDRQEAVAAARSLLSDTLKWVVITSAPGEADSTI

NVLVVTADAVEVVVHPRVETDLKGTGDLFCAELVSGLLSGLALGAATQAAAQRVLEVMNWTAAQGCDELI

LPPLEQSR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043703.1\_4046 [gene=ptsJ] [locus\_tag=BN49\_RS21940] [protein=transcriptional regulator PtsJ] [protein\_id=WP\_046043703.1] [location=4202571..4203869] [gbkey=CDS]

MLAGKTASEIFDNIRHLVQSGGLQPGEVLPPVRELASQLAVNRNTVAAAYKRLVTSGLAVSQGRNGTAIK

ARDTLPALEGGDPTTPLNDISSGNPDPARLPDLPRYLGQIARTPRLYGDAPIEPRLGQWAEAWFAREIAV

PFAVNLASGAIDALERLLCALLLPGDGVVVEDPCFLSSINMVRYAGFTPCPVAVDAEGMDPDGLEEALRN

GARAVILTPRAHNPTGCSLTETRAHALREVLARYPQVLAIVDDHFALLSATPWHSPLPASTQRWALVRSM

SKTLGPDLRLAFIASDAATSAALRLRLNAGNQWVSHLLQDLTLACLTDEAFIASMTETRRHYRQQNEKLA

AALARHGFSHATPGDGLNFWLPLTAASQPYALRLARAGWLVREGEVFGIRTPSHGLRLSLGRLSDAEISR

LAADIAQALDAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004145609.1\_4047 [locus\_tag=BN49\_RS21945] [protein=DUF4440 domain-containing protein] [protein\_id=WP\_004145609.1] [location=4204010..4204405] [gbkey=CDS]

MHHPDLALKAVIEACDRAISQEDYDTLMSYYAEDAALVVKPGMVVRGKENIRKAFIAIADYFQHRLVVTQ

GKMEVIEGGGNALVIMETRLDIPTADGISQVTRRATYVFQKQGERWLCTVDNSYGTDLLDD

>lcl|NZ\_FO834906.1\_prot\_WP\_016532026.1\_4048 [gene=cysM] [locus\_tag=BN49\_RS21950] [protein=cysteine synthase CysM] [protein\_id=WP\_016532026.1] [location=complement(4204402..4205313)] [gbkey=CDS]

MNTLEQTIGNTPLVKLQRLGPDNGSEVWVKLEGNNPAGSVKDRAALSMIVEAEMRGEIQPGDVLIEATSG

NTGIALAMIAALKGYRMKLLMPDNMSQERRAAMRAYGAELILVSKEQGMEGARDLALEMAQRGEGKLLDQ

FNNPDNPYAHYTTTGPEIWQQTAGRITHFVSSMGTTGTITGVSRFLREQSKPVTIVGLQPEEGSSIPGIR

RWPAEYMPGIFNASLVDTVLDIHQQDAENTMRQLAVREGIFCGVSSGGAVAGALRIARENPGAVVVAIVC

DRGDRYLSTGVFGEEHFSQGAGI

>lcl|NZ\_FO834906.1\_prot\_WP\_002913623.1\_4049 [gene=cysA] [locus\_tag=BN49\_RS21955] [protein=sulfate/thiosulfate ABC transporter ATP-binding protein CysA] [protein\_id=WP\_002913623.1] [location=complement(4205432..4206526)] [gbkey=CDS]

MSIEIANIKKSFGRTQVLNDISLDIPSGQMVALLGPSGSGKTTLLRIIAGLEHQTSGHIRFHGTDVSRMH

ARDRKVGFVFQHYALFRHMTVFDNIAFGLTVLPRRERPNAAAIKAKVTKLLEMVQLAHLADRYPAQLSGG

QKQRVALARALAVEPQILLLDEPFGALDAQVRKELRRWLRQLHEELKFTSVFVTHDQEEAMEVADRVVVM

SQGNIEQADAPERVWREPSTRFVLEFMGEVNRLQGVIRGGQFHVGAHRWPLGYTPAYQGPVDLFLRPWEV

DISRRTSLDSPLPVQVLEASPKGHYTQLVVQPLGWYDEPLSVVLTGDEAPSRGERLFVGLQNARLYNGTE

RIEPRGELALAESA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913625.1\_4050 [gene=cysW] [locus\_tag=BN49\_RS21960] [protein=sulfate/thiosulfate ABC transporter permease CysW] [protein\_id=WP\_002913625.1] [location=complement(4206516..4207391)] [gbkey=CDS]

MAEVTQLKRYDAPRINWGKWFLIGVGMLVSAFILVVPMLYIFIQAFSKGLMPVLENLANPDMLHAIWLTV

MIALITVPVNLVFGTLLAWLVTRFTFPGRQLLLTLLDIPFAVSPVVAGLVYLLFYGSNGPLGGWLDAHNL

QIMFAWPGMVLATIFVTCPFVVRELVPVMMSQGSHEDEAAVLLGASGWQMFRRVTLPNIRWALLYGVVLT

NARAIGEFGAVSVVSGSIRGETLSLPLQIELLEQDYNTVGSFTAAALLTLMAILTLFLKSMLQWRLANQK

ERAQQEGNHEH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913626.1\_4051 [gene=cysT] [locus\_tag=BN49\_RS21965] [protein=sulfate/thiosulfate ABC transporter permease CysT] [protein\_id=WP\_002913626.1] [location=complement(4207391..4208224)] [gbkey=CDS]

MFAVSSKRVLPGFTLSLGTSLLFVCLILLLPLSALVMQLAQMSWAQYWDVITNPQVVAAYKVTLLSAFVA

SIFNGVFGLLMAWILTRYRFPGRTLLDALMDLPFALPTAVAGLTLASLFSVNGIYGEWLAKFDIKVTYTW

LGIAVAMAFTSIPFVVRTVQPVLEELGPEYEEAAETLGATRWQSFRKVVLPELSPALLAGIALSFTRSLG

EFGAVIFIAGNIAWKTEVTSLMIFIRLQEFDYPAASAIASVILAASLLLLFSINTLQSRFGRRVVGH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913628.1\_4052 [gene=cysP] [locus\_tag=BN49\_RS21970] [protein=thiosulfate/sulfate ABC transporter substrate-binding protein CysP] [protein\_id=WP\_002913628.1] [location=complement(4208224..4209240)] [gbkey=CDS]

MAVKSLKKGYLALAASMLLVAQAQATELLNSSYDVSRELFAALNPPFEQQWAKDNGGDKLTIKQSHAGSS

KQALAILQGLKADVVTYNQVTDVQILHDKGNLIPADWQSRLPNNSSPFYSTMGFLVRKGNPKNIHDWNDL

VRSDVKLIFPNPKTSGNARYTYLAAWGAADKADGGDKAKTEQFMTQFLKNVEVFDTGGRGATTTFAERGL

GDVLISFESEVNNIRKQYEAQGFEVVIPKTNILAEFPVAWVDKNVKANGTEKAAKAYLNWLYTPQAQTII

TDYYYRVNNPKVMDALKDKFPQTELFRVEDKFGSWPEVMKTHFASGGELDKLLAAGRK

>lcl|NZ\_FO834906.1\_prot\_4053 [locus\_tag=BN49\_RS29460] [protein=DUF559 domain-containing protein] [pseudo=true] [location=4209441..4209784] [gbkey=CDS]

MKNTQIFARQLRRSLTPAERRPGYLLGNRRFASDTFRRQRPVGPYILDFACCAIRLAIELDGGQHDDAAP

AGNRARDGVFYASGIMSLKSMKMR\*WRRYLKHLSRQCPHPSPLT

>lcl|NZ\_FO834906.1\_prot\_WP\_004145614.1\_4054 [locus\_tag=BN49\_RS21985] [protein=Dyp-type peroxidase] [protein\_id=WP\_004145614.1] [location=complement(4209880..4210779)] [gbkey=CDS]

MSQVQSGILPEHCRAAIWIEANLKGDVNALREASKIFVDNVATFQAKFPDAKLGAVVAFGNNVWRQLSGG

EGADELKDFPVYGKGLAPSTQYDLLIHILSARHEVNFSVAQAALAAFGDAIDVKEEIHGFRWVEERDLSG

FVDGTENPAGEETRREVAVIKDGVDAGGSYVFVQRWEHNLKQLNRMSVPDQEMMIGRTKDANEEIDGDER

PVTSHLSRVDLKEDGKGLKIVRQSLPYGTASGTHGLYFCAYCARLYNIEQQLLSMFGDTDGKRDAMLRFT

KPVTGGYYFAPSLERIQAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913630.1\_4055 [locus\_tag=BN49\_RS21990] [protein=RpoE-regulated lipoprotein] [protein\_id=WP\_002913630.1] [location=complement(4210874..4211449)] [gbkey=CDS]

MKSLRVMLCALPLALTGCSTMSAVNWSAAYPWNWFGASTEVTEQGVGKLTASTPLNEQAISDALGSDYRL

RSGMKTDKGNIVHYFEALKNNSVALTINGDNGAISRIDVRDADIKTASGVKIGTPFSDLYSKAFGNCQKG

SHDNGAVVECQAEGSQHISYAFTGHWSGPDELMPSDDTLKNWKVSKIIWRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913635.1\_4056 [locus\_tag=BN49\_RS21995] [protein=DUF2919 domain-containing protein] [protein\_id=WP\_002913635.1] [location=complement(4211511..4211960)] [gbkey=CDS]

MKNTEFIPADFDAHGRLRLPLLFWCVLLLQARTWVLFLMAGASRQQGDAILNLFYPDHERFWLGLLPGVP

AVLAFLLSGYRQRLPRLWRAMRWLLVLSQVLLLLWQPMLWLSGESPSSLTIALLVADGYALWWLLTSRRL

GACFHQTTF

>lcl|NZ\_FO834906.1\_prot\_WP\_002913637.1\_4057 [locus\_tag=BN49\_RS22000] [protein=GNAT family acetyltransferase] [protein\_id=WP\_002913637.1] [location=complement(4211947..4212372)] [gbkey=CDS]

MEIRVFRQQDFEEVVTLWERCDLLRPWNDPEMDIERKLNHDVSLFLVAEVNGEVVGTVMGGYDGHRGSAY

YLGVHPEYRGRGIANALLNRLEKKLIARGCPKINIMVREDNDVVQGMYERLGYEYADVLTLGKRLIEDEE

Y

>lcl|NZ\_FO834906.1\_prot\_WP\_002913639.1\_4058 [gene=amiA] [locus\_tag=BN49\_RS22005] [protein=N-acetylmuramoyl-L-alanine amidase AmiA] [protein\_id=WP\_002913639.1] [location=4212584..4213456] [gbkey=CDS]

MSTFKPLKILASRRQVLKAGLAAMTLSGVASQVSAKEQPLKTSNGHSKPAAKKAGGRRIVMLDPGHGGID

TGAIGHNGSKEKHVVLAIAKNVRSILRSNGIDARLTRTGDTFIPLYDRVEIAHQHGADLFMSIHADGFTN

PSAAGASVFALSNRGASSAMAKYLSDRENRADEVAGKKATDKDHLLQQVLFDLVQTDTIKNSLTLGSHIL

KKIKPVHKLHSRNTEQAAFVVLKSPSIPSVLVETSFITNPNEEKLLGTTAFRQKIATAIANGIISYFHWF

DNQKAHSKRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913641.1\_4059 [gene=hemF] [locus\_tag=BN49\_RS22010] [protein=oxygen-dependent coproporphyrinogen oxidase] [protein\_id=WP\_002913641.1] [location=4213456..4214355] [gbkey=CDS]

MKPDAAQVKTFLLQLQDNLCQQLSAVDGAPFIEDAWQREGGGGGRSRVLREGRVFEQAGVNFSHVHGDAM

PASATAHRPELAGRSFEAMGVSLVVHPLNPYVPTSHANVRFFIAEKPGADPVWWFGGGFDLTPYYGFEED

AVHWHRTARDLCLPFGEEVYPRYKKWCDDYFYLKHRQEQRGIGGLFFDDLNTPDFDHCFAFMQAVGNGYA

DAYLPIVERRKATPYGERERHFQLYRRGRYVEFNLVWDRGTLFGLQTGGRTESILMSMPPLVRWEYDYQP

EPGSPEAALSEFIQVRDWL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913642.1\_4060 [gene=eutR] [locus\_tag=BN49\_RS22015] [protein=HTH-type transcriptional regulator EutR] [protein\_id=WP\_002913642.1] [location=complement(4214399..4215451)] [gbkey=CDS]

MKKRRSANLHHLCCEALPEDTRLTPQVEIDNIHQRHTTDVYEHALTITAWQQIYDQLHPGQFRGEFTEIL

LDEIQVFREYTGLALRQSCLVWPNSFWFGIPATRGEQGFIGSQCLGRAEIATRPGGTEFELSTPDDYTIL

GVVISQEVIARHASFLHHPERVLHMLRNQSALAVREPHKAALWGFVQQALATFSEHPDTLHQPAVRKVLR

DNLLLAMGTMLEEAQPMVSAESVSHQSYRRLLAQAREYVLENSAEPLTVLDLCQQLYVSRRTLQNAFHAI

LGIGPNAWLKRIRLNAVRRELISPWSERETVKEAAMQWGFWHLGQFATDYQQLFAEKPSMTLHHRLRQWV

>lcl|NZ\_FO834906.1\_prot\_WP\_004151997.1\_4061 [gene=eutK] [locus\_tag=BN49\_RS22020] [protein=ethanolamine utilization microcompartment protein EutK] [protein\_id=WP\_004151997.1] [location=complement(4215497..4215982)] [gbkey=CDS]

MINALGLLEVEGMVAAVDAADAMLKAANVRLLSHEVLDPGRLTLVVEGDLAACRAALDAGAAAARRTGCV

ISRREIGRPEEDTQRLIGGFQPPPPAPMPPADPASSEALLTLLASVRQGMTAGEVAAHFAWPLDKARQAL

EQLFSAGTLRKRSSRYRLKNP

>lcl|NZ\_FO834906.1\_prot\_WP\_004174905.1\_4062 [gene=eutL] [locus\_tag=BN49\_RS22025] [protein=ethanolamine utilization microcompartment protein EutL] [protein\_id=WP\_004174905.1] [location=complement(4215994..4216653)] [gbkey=CDS]

MPALDLIRPSVTAMRVIASVNDGFARELKLPSHIRSLGLITADSDDVTYIAADEATKQAMVEVVYGRSLY

AGAAHGPSPTAGEVLIMLGGPNPAEVRAGLDAMMAHIEGGAAFQWANDAQDTAFLAHVVSRTGSYLSSAA

GIALGDPIAYLVAPPLEATFGIDAAMKSADVQLVTYVPPPSETNYSAAFLTGSQAACKAACNAFTDAVLD

IARHPVQRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004213213.1\_4063 [gene=eutC] [locus\_tag=BN49\_RS22030] [protein=ethanolamine ammonia-lyase subunit EutC] [protein\_id=WP\_004213213.1] [location=complement(4216663..4217562)] [gbkey=CDS]

MDQKQIEDIVRSVMASMGQPQSQPQAPAASTPACHAACASEAVVESCTLDLGSAEAKAWIGVQHPHRAEV

LTELKRSTAARVCTGRAGPRPRTQALLRFLADHSRSKDTVLKEVPEAWVKAQGLLEVRSEISDKNLYLTR

PDMGRRLSPEAIDALKAQCVMDPDVQVVVSDGLSTDAITANYEEILPPLLAGLKQAGLKVGTPFFVRYGR

VKIEDQIGEILGAKVVILLVGERPGLGQSESLSCYAVYSPRVATTVEADRTCISNIHQGGTPPVEAAAVI

VDLAKRMLEQKASGINMSR

>lcl|NZ\_FO834906.1\_prot\_WP\_004152001.1\_4064 [gene=eutB] [locus\_tag=BN49\_RS22035] [protein=ethanolamine ammonia-lyase subunit alpha] [protein\_id=WP\_004152001.1] [location=complement(4217583..4218944)] [gbkey=CDS]

MKLKTTLFGNVYQFKDVKEVLAKANELRSGDVLAGVAAESSQQRVAAKQVLSDMTVADIRNNPVIPYEED

CVTRLIQDDVNETAYQRIKHWTISDLREYVLNDEVTSDDIAFVRKGLTSEVVAAVAKICSNADLIYGGKK

MPVIKKANTTIGLPGTFSCRLQPNDTRDDVQSIAAQIYEGLSFGAGDAVIGVNPVTDDVENLSRVLDTVY

GVIDKFNIPTQGCVLAHVTTQIEAIRRGAPGGLIFQSICGSEKGLKEFGVELAMLDEARAVGAEFNRIAG

ENCLYFETGQGSALSAGANFGADQVTMEARNYGLARHYDPFLVNTVVGFIGPEYLYNDRQIIRAGLEDHF

MGKLSGISMGCDCCYTNHADADQNLNENLMILLATAGCNYIMGMPLGDDIMLNYQTTAFHDTATVRQLLG

LRPSPEFERWLETMGIMANGRLTKRAGDPSLFF

>lcl|NZ\_FO834906.1\_prot\_WP\_021312790.1\_4065 [gene=eutA] [locus\_tag=BN49\_RS22040] [protein=ethanolamine ammonia-lyase reactivating factor EutA] [protein\_id=WP\_021312790.1] [location=complement(4218956..4220359)] [gbkey=CDS]

MNTRQLLSVGIDIGTTTTQVIFSRLELVNRAAVSQVPRYEFIKRDISWQSPVFFTPVDKQGELKEAELEA

LILAQYRAAGIAPQAVDSGAIIITGESAKTRNARPAVMALSQSLGDFVVASAGPHLESVIAGHGAGAQTL

SRQRMCRVLNIDIGGGTSNYALFDAGNVSATACLNVGGRLLETDAQGRVVHAHPPGQRIVDALFGAGTNA

LALTAGQLAQVASRMAALIVEVIDGTLSPLAQGLMQTEVLPAGVQPEVITLSGGVGECYRHQPADPFCFS

DIGPLLATALHEHPRLREMNVQFPAQTVRATVIGAGAHTLSLSGSTIWLEGVPLPLRNLPVAIPQDAADL

PNAWLQALTQLDLAPEADAYVLALPASLPVRYATLLTVIDALLAFVARFPNPRPLLLVAEQDFGKALGML

LRPQLPHLPLAVIDEVSIRAGDYIDIGTPLFGGSVVPVTVKSLAFPS

>lcl|NZ\_FO834906.1\_prot\_WP\_004149260.1\_4066 [gene=eutH] [locus\_tag=BN49\_RS22045] [protein=ethanolamine utilization protein EutH] [protein\_id=WP\_004149260.1] [location=complement(4220356..4221588)] [gbkey=CDS]

MGINEIIMYIMMFFMLIAAVDRILSQFGGSARFLGKLGKSIEGSGGQFEEGFMAMGALGLAMVGMTALAP

VLAHLLGPVIIPLYEMLGANPSMFAGTLLACDMGGFFLAKELAGGDVAAWMYSGLILGSMMGPTIVFSIP

VALGIIEPTDRRWLALGVLAGIVTIPIGCIAGGLVAMYSGVEINGQPVEFTFALILMNMIPVIIVAVLVA

LGLKFIPEKMINGFQIFAKFLVALITIGLAAAVIKFLLGWELIPGLDPIFMAPGDQPGEVMRAIEVIGSI

SCVLLGAYPMVLLLTRWFEKPLMRVGNLLKINNMAAGGMVATLANNIPMFGMMKQMDTRGKVINCAFSVS

AAFALGDHLGFAAANMNAMIFPMIVGKLVGGVTAIGVAMLLVPKDENVPAPANNEAEAHS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530602.1\_4067 [gene=eutG] [locus\_tag=BN49\_RS22050] [protein=ethanolamine utilization ethanol dehydrogenase EutG] [protein\_id=WP\_016530602.1] [location=complement(4221788..4222975)] [gbkey=CDS]

MQAELQTALFHAFDTLNLQQMKSFNVPPVTLHGVGTLAACGPQAQSRGLRHLFVMVDSFLHQAGMTAGLE

RSLAMKGIAMTLWPCPAGEPCVTDVCAAVAQLRDARCDGVVAFGGGSVLDAAKAVALLVANPEQTLGKMT

EHSELRPRLPLIAVPTTAGTGSETTNVTVIIDAVSGRKQVLAHASLMPDVAILDAALTEGVPPHITAMTG

IDALTHAVEAYSARHATPFTDSLAMGAIVMIGEALPKAVGCGQDLAARENMLLASCMAGMAFSSAGLGLC

HAMAHQPGAALHIPHGLANAMLLPTVMEFNRMVRRARFSQIGRALTGKKTDDREAIAAVRELIAEVGLTM

RLTEAGATSAHYAAWAQAAQEDICLRTNPRTASREQIIELYAAAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530603.1\_4068 [gene=eutJ] [locus\_tag=BN49\_RS22055] [protein=ethanolamine utilization protein EutJ] [protein\_id=WP\_016530603.1] [location=complement(4222965..4223804)] [gbkey=CDS]

MAHDEQRWLSPRLQKAAALCNQAPAASESPLWLGIDLGTCDVVSMVVDRDGQPVAVCLDWADVVRDGIVW

DFFGAVTLVRRHLATLEQQLGCRFTHAATSFPPGTDPRISINVLESAGLEISHVLDEPTAVADLLQLDNA

GVVDIGGGTTGIAIVKQGRVTYSADEATGGHHISLTLAGNRGIGLEEAEQYKRSHAGEIWPVVKPVYEKM

AEIVARHIAGQGIVDLWLAGGACMQPGVHELFRQRFPAIPVHLPQYSLFMTPLAIANSGREKAEGMYAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004152003.1\_4069 [locus\_tag=BN49\_RS22060] [protein=aldehyde dehydrogenase EutE] [protein\_id=WP\_004152003.1] [location=complement(4223814..4225217)] [gbkey=CDS]

MNQQDIEQVVKAVLLKMKDSSQPAGTVHDMGVFASLDDAVAAATVAQQGLKRVAMRQQVIQAIREAGEKY

ARELAELAVTETGMGRVEDKFAKNVAQARGTPGVECLTPQVLTGDNGLTLIENAPWGVVASVTPSTNPAA

TVINNAISLIAAGNSVVFAPHPAAKKVSQRAITLLNQAVVAAGGPANLLVTVANPDIDTAQRLFKYPGIG

LLVVTGGEAVVEAARKHTNKRLIAAGAGNPPVVVDETADLPRAAQAIVKGASFDNNIICADEKVLIVVDS

VADELMRLMEGQQAVKLTAAQAEQLQPLLLKNIDERGKGTVSRDWVGRDAGKIAAAIGLQVPAQTRLLFV

ETPASHPFAVTELMMPVLPVVRVANVEEAIALAVQLEGGCHHTAAMHSRNIDNMNQMANAIDTSIFVKNG

PCIAGLGLGGEGWTTMTITTPTGEGVTSARTFVRLRRCVLVDAFRIV

>lcl|NZ\_FO834906.1\_prot\_WP\_002913719.1\_4070 [gene=eutN] [locus\_tag=BN49\_RS22065] [protein=ethanolamine utilization microcompartment protein EutN] [protein\_id=WP\_002913719.1] [location=complement(4225229..4225516)] [gbkey=CDS]

MKLAVVTGYVVCTVRHEGLAHDKLLMVEMLNARGEPDGQCAVAIDSIGAGCGEWVLLVSGSSARQAHAHG

ASPVDLCVIGIVDEAAADGQVLFHK

>lcl|NZ\_FO834906.1\_prot\_WP\_000387720.1\_4071 [gene=eutM] [locus\_tag=BN49\_RS22070] [protein=ethanolamine utilization microcompartment protein EutM] [protein\_id=WP\_000387720.1] [location=complement(4225645..4225935)] [gbkey=CDS]

MEALGMIETRGLVALIEASDAMVKAARVKLVGVKQIGGGLVTAMVRGDVAACKAATDAGAAAAQRIGELV

SVHVIPRPHGDLEEVFPISFKGDSNI

>lcl|NZ\_FO834906.1\_prot\_WP\_004213203.1\_4072 [gene=pta] [locus\_tag=BN49\_RS22075] [protein=phosphate acetyltransferase] [protein\_id=WP\_004213203.1] [location=complement(4225974..4226990)] [gbkey=CDS]

MIIDQCRKLALRAPARVVFPDALDVRVLKAAHYLQQQGLAHPILVASPFALRQFALGERLPLTGVQVIDP

HSNLAMREAFAAAWQARAGDKAPADAVDKLADPLMFAAAMVSAGQAEVCIAGNLSSTASVLRAGLRLIGL

QPGCKTLSSLFLMLPQYTGQPLGFADCSVVPQPTAAQLADIAIASAETWQAIAGEAPRVAMLSFSTHGSA

RHPCVANVQQATEIVRQRAPQLMVDGELQFDAAFVPDVAAHKAPGSPLQGRANVLVFPSLEAGNIGYKIA

QRLGGYRAIGPLIQGLAAPLHDLSRGCSVEEIIELALVASVPRQTDASRIPDSSTLVE

>lcl|NZ\_FO834906.1\_prot\_WP\_004180847.1\_4073 [gene=eutT] [locus\_tag=BN49\_RS22080] [protein=ethanolamine utilization cob(I)yrinic acid a,c-diamide adenosyltransferase EutT] [protein\_id=WP\_004180847.1] [location=complement(4226980..4227786)] [gbkey=CDS]

MNDFITEAWLRANHTLSEGGEIHLPADARLTPSARELLESRHLRVKFLDRQGRLFVEDDEQTPQPVHVLT

SSDHPPQACCELCHQPVGKKPDTLTHLTADTLVAKNDPRLAFRAVLDSTIALTVWLQIELAEPWQPWLTD

IRSRLGNIMRADALEEPLAAQSIAGFSEAQLHRLSHQPLRYLGHDHLVPEARHGRDVALLNLLRGKVREA

EVTAAQVFITPQFAVRRADIMQALNRLSSAVYVMMILGVTDAPPALSQLQQLGGEDDH

>lcl|NZ\_FO834906.1\_prot\_WP\_004185056.1\_4074 [gene=eutQ] [locus\_tag=BN49\_RS22085] [protein=ethanolamine utilization acetate kinase EutQ] [protein\_id=WP\_004185056.1] [location=complement(4227783..4228472)] [gbkey=CDS]

MKKLITANDIRAAHARGEQAMSVVLRASIITPEAREVAELLGFTITEDDGAAPAATAADSDKTESQRIRE

TILAQLPEGQFTESLVAQLMEKVMKEKQSLEQEAMQPGFEAVTGKGGIKVIDGSSVKFGRFDGAQPHCVG

LTDLVTDQDGSSMAAGFMQWENAFFPWTLNYDEIDMVLEGELHVRHQGETLVAKAGDVMFIPKGSSIEFG

TPSTVRFLYVAWPANWQSL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913727.1\_4075 [gene=eutP] [locus\_tag=BN49\_RS22090] [protein=ethanolamine utilization acetate kinase EutP] [protein\_id=WP\_002913727.1] [location=complement(4228450..4228929)] [gbkey=CDS]

MKRIAIVGAVGAGKTTLFNALQGNYSLARKTQALEFNDRGDIDTPGEYFSHPRWYHALITTLQDVDTLIY

VHAANDTESRLPPGLLDIGSRKHLIVAISKTDLPDANVAAVRQLLDGMGFQAPVFALNGCDPQSVAPLEN

YLSELSQKEEGPGEETHYR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043711.1\_4076 [gene=eutS] [locus\_tag=BN49\_RS22095] [protein=ethanolamine utilization microcompartment protein EutS] [protein\_id=WP\_046043711.1] [location=complement(4228942..4229277)] [gbkey=CDS]

MDKERIIQEFVPGKQVTLAHLIAHPGAELAKKIGVPESGAISIMTLTPGETAMIAGDLAMKAADVHIGFL

DRFSGALVIYGSVGAVEEALLQTIGGLGRLLNYTLCELTKS

>lcl|NZ\_FO834906.1\_prot\_WP\_004185057.1\_4077 [gene=maeB] [locus\_tag=BN49\_RS22100] [protein=NADP-dependent oxaloacetate-decarboxylating malate dehydrogenase] [protein\_id=WP\_004185057.1] [location=complement(4229497..4231776)] [gbkey=CDS]

MDEQLKQSALDFHEFPVPGKIQVSPTKPLATQRDLALAYSPGVAAPCLEIEKDPLAAYKYTARGNLVAVV

SNGTAVLGLGNIGALAGKPVMEGKGVLFKKFAGIDVFDIEVDELDPDKFINVVAALEPTFGGINLEDIKA

PECFYIEQQLRERMNIPVFHDDQHGTAIISTAAILNGLRVVEKNLSDVRMVVSGAGAAAIACMNLLVALG

MQKHNIVVCDSKGVIYKDREPNMAETKAAYAVEDDGKRTLDDVIDGADIFLGCSGPKVLTQEMVKKMARA

PLILALANPEPEILPPLAKQVRDDAIICTGRSDYPNQVNNVLCFPFIFRGALDVGATAINEEMKLAAVHA

IAELAHAEQSEVVASAYGDQDLSFGPDYIIPKPFDPRLIVKIAPAVAKAAMDSGVATRPIADFDAYIEKL

SEFVYKTNLFMKPIFSQARKEPKRVVLAEGEETRVLHATQELVSLGLAKPILVGRPSVIEMRIQKLGLQI

KAGVDFEIVNNESDPRFKEYWSEYYQLMKRRGITQEQAQRAVISNTTVIGAIMVHRGEADAMICGTIGEY

HDHYRVVQPLFGYRDGVSTAGAMNALLLPSGNTFIADTYVNHDPSPEELAEITLMAAESVRRFGIEPRVA

LLSHSNFGSADCPSASKMRKTLELVKARAPELMIDGEMHGDAALVESIRNDRMPDSPLKGAANILVMPNM

EAARISYNLLRVSSSEGVTVGPVLMGVAKPVHILTPIASVRRIVNMVALAVVEAQTEPL

>lcl|NZ\_FO834906.1\_prot\_WP\_004174884.1\_4078 [gene=tal] [locus\_tag=BN49\_RS22105] [protein=transaldolase] [protein\_id=WP\_004174884.1] [location=4232071..4233027] [gbkey=CDS]

MNQLDSIKQFTTVVADSGDIESIRHYHPEDATTNPSLLLKAAGLASYSGLIDDAIAWAKKQGGGREAQVA

HACDKLAVNFGAEILKSIPGRVSTEVDARLSFNREKSIEKARHLVALYQEMGIDKSRILIKLASTWEGIR

AAEVLEKEGIHCNLTLLFSFAQARACAEAGVYLISPFVGRIYDWYQARKPLEPYVVEEDPGVKSVRNIYD

YFKQHKYNTIVMGASFRRTEQILALVGCDRLTIAPPLLKELQASDTPVVRKLIPASQILPRPVPLSEAEF

RWEHNQDPMAVEKLAEGIRLFAVDQRKLEDLLAAKLSL

>lcl|NZ\_FO834906.1\_prot\_WP\_016532125.1\_4079 [gene=tkt] [locus\_tag=BN49\_RS22110] [protein=transketolase] [protein\_id=WP\_016532125.1] [location=4233044..4235038] [gbkey=CDS]

MSRRELANAIRALSMDAVQKANSGHPGAPMGMADIAEVLWNDFLKHNPQNPDWVDRDRFILSNGHASMLL

YSLLHLTGYDLPLSELKQFRQLHSKTPGHPEHGYTPGVETTTGPLGQGLANAVGMAIAERTLAAQFNRPG

HEIIDHHTWVFMGDGCLMEGISHEACSLAGTLGLGKLIGFYDHNGISIDGKTEGWFSDDTAKRFRAYHWH

VIGDIDGHDPQAIKQAITEAQAVKDKPSLIICRTIIGFGSPNKAGSEESHGAALGEKEVALARQQLGWKY

PPFEIPKEIYAGWDARPRGEKAEHAWNEKFAAYQQQFPELAAELTRRMNGALPEDFAATARDYVAKLQAE

PAKIASRKASQNALNAYGPHLPELLGGSADLAPSNLTIWSGSTSIKEDPAGNYIHYGVREFGMTAVANGI

ALHGGFIPYTSTFLMFVEYARNAARMAALVKARQIMVYTHDSIGLGEDGPTHQAVEQLASLRLTPNFSTW

RPCDQVETAVAWQAAIARQGGPTALILSRQNLAQMPRTPEQVQDIARGGYVLKDAGGKPDLILIATGSEV

EITVLAAEKLLAKGVNVRVVSLPSTDVFDAQDEAWRESVLPSDVSARVAVEAGIADYWYKYVGLKGKIVG

MTGYGESAPAEQLFPFFGFTVDHIVATAEQVLNG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532124.1\_4080 [locus\_tag=BN49\_RS22115] [protein=DUF1176 domain-containing protein] [protein\_id=WP\_016532124.1] [location=complement(4235028..4236074)] [gbkey=CDS]

MLFRVIFFLFLAVLPCSQAWSAPTQQRFNDWLVTCNNQNFCVTRNVGLHHGLVMTLSRSAGAVTDASLRI

ELGGTGNPVATLAPIAPRLLLDGKPLPLTDKRWHIEDKLIKTADSVTIDAFLQQVQEGKALSLANGLQTI

SLQGLKAALFFIDDRQKRVGSETAWVGKGEEPPLSVPPAPALRAVASAETAQSPLGREELNDLMDYGNER

MTNSHCSLDPFRREIRVTALTDDKVLLMTSCESGAYNTVWLAWLISRQRPYVARQVRLTLPFQPPGEAPR

EIELINASYDDHRHELVTLDKGRGAGDCGIQTRWRFDGQRFSLSRYAQQPTCDNWQGPDAWPTLWITR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913754.1\_4081 [gene=nudK] [locus\_tag=BN49\_RS22120] [protein=GDP-mannose pyrophosphatase NudK] [protein\_id=WP\_002913754.1] [location=complement(4236138..4236734)] [gbkey=CDS]

MSLNIHVIKDKILSENWFVLRNMTYELTRADGSVVRHKREVYDRGNGATVLLYNRHKQTVVLVRQFRVAT

WVNGNHDGMLIETCAGLLDNDEPEACIRKEAVEETGYEVGEVRKLFELFMSPGGVTEVVHFFIAEYSDAQ

RTTSGGGVDDEAIEVLELPFSQALQMVADGEIRDGKAVILLQYLQTSGLMSGNSDKSD

>lcl|NZ\_FO834906.1\_prot\_WP\_046043714.1\_4082 [gene=aegA] [locus\_tag=BN49\_RS22125] [protein=formate-dependent uric acid utilization protein AegA] [protein\_id=WP\_046043714.1] [location=complement(4236793..4238775)] [gbkey=CDS]

MNHFILSDSRKCIGCQACEVACVMAHNEEQHVLTPQRFLPRITVIKAEGQRNAITCRHCEDAPCVRSCPN

DAIAQSGDSVQVRQEKCIGCKSCMVACPFGVMQVVVTPQAAGLVKASAHKCDLCQGREAGPACVENCPAQ

ALTLADDETLITLAKQRRLRSACQEVQPWQRATSLCSQPNAGAKVRQMAMTPPRGEPDKLAAEVRKSHFE

EIYQPFTPQQAQQQAARCLTCGEHSICEWTCPLHNHIPQWIELVKAGNIAAAVALSHQTNCLPEITGRVC

PQDRLCEGACTLRDESGAVTIGNIERYISDQALASGWRPDLSQVKPSGKRVAIIGAGPAGLACADMLVRH

GVQPVVFDRHPEIGGLLTFGIPAFKLDKSLLARRRAIFSEMGIRFELNCEVGKDISMATLLADYDAVFVG

AGTYRSMKAGLPNEEAPGVYDALPFLIANTKQVMGLAASAQEPYVNTAGLNVVVLGGGDTAMDCVRTALR

HGARQVTCAYRRDEANMPGSKKEVKNAREEGALFEFNVQPVTLELDENGRVNGVRFLRTELGAPDAGGRR

RTTPIPGSEFVMPADAVIMAFGFHPHRMPWLEAAGVALDSQGRIKAGVESRYRYQTSQEKIFAGGDAVRG

ADLVVTAMAEGRHAAQGILDYLARKTTPLH

>lcl|NZ\_FO834906.1\_prot\_WP\_004185072.1\_4083 [gene=acrD] [locus\_tag=BN49\_RS22130] [protein=multidrug efflux RND transporter permease AcrD] [protein\_id=WP\_004185072.1] [location=4239148..4242261] [gbkey=CDS]

MANFFIDRPIFAWVLAILLCLTGTLAILSLPVEQYPDLAPPNVRITANYPGASAQTLENTVTQVIEQNMT

GLDNLMYMSSQSSATGQATITLSFTAGTDPDEAVQQVQNQLQSAMRKLPQAVQNQGVTVRKTGDTNILTL

AFVSTDGSMDKQDIADYVASNIQDPLSRVNGVGDIDAYGSQYSMRIWLDPAKLNSYQMTTKDVTDAISSQ

NAQIAVGQLGGTPSVDKQALNATINSQSLLQTPEQFRNITLRVNQDGSEVTLGDVATVEMGAEKYDYLSR

YNRQPASGLGIKLASGANEMATAERVINRLNELAQFFPHGLEYKVAYETTSFVKASITDVVKTLLEAILL

VFLVMYLFLQNFRATLIPTIAVPVVLMGTFAVLYACGYSINTLTMFAMVLAIGLLVDDAIVVVENVERIM

SEEGLSPREATRKSMGQIQGALVGIAMVLSAVFVPMAFFGGTTGAIYRQFSITIVAAMVLSVLVAMILTP

ALCATLLKPVKPGESHERKGFFGWFNRTFNRSASRYETFVGKILHRSLRWMLIYVVLLGGMVFLFLHLPT

SFLPLEDRGMFTTSVQLPSGSTQQQTLKVVQKAEDYFLNNEKQNVESVFATVGSGPGGNGQNVARMFVRL

KDWDQRDPQTGTSFAIIERATKAFNQINEARVIASSPPAISGLGSSAGFDMELEDHAGKGHDALMAARDT

LLELAGKNPLLTRVRHNGLDDSPQLQVDIDQRKAQALGVSIDDINDTLQTAWGSSYVNDFMDRGRVKKVY

VQAAAKYRMLPDDINLWYVRNSSGTMVPFSAFATSRWETGSPRLERYNGYSAVEIVGEAAPGISTGTAMD

MMEKLAAQLPTGFGLEWTAMSYQERLSGAQAPALYAISLLVVFLCLAALYESWSVPFSVMLVVPLGVIGA

LLATWMRGLENDVYFQVGLLTVIGLSAKNAILIVEFANELNEKGQDLLSATLSACRQRLRPILMTSLAFI

FGVLPMATSTGAGSGSQHAVGTGVMGGMISATVLAIFFVPLFFVLVRRRFPLKERPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_100181659.1\_4084 [gene=ypfM] [locus\_tag=BN49\_RS30580] [protein=protein YpfM] [protein\_id=WP\_100181659.1] [location=complement(4242389..4242448)] [gbkey=CDS]

MIEHELGNWKDFIEGMLRK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532119.1\_4085 [locus\_tag=BN49\_RS22135] [protein=ArsC family reductase] [protein\_id=WP\_016532119.1] [location=4242814..4243167] [gbkey=CDS]

MLTMYGIKNCDTIKKARRWLEAHQIEYRFHDYRADGLERAQLDTFIADLGWQALLNTRGTTWRKLDESLR

NSIDNADAAAALMLEMPAIIKRPLLCAPGRPMLLGFSEASYQQFNEV

>lcl|NZ\_FO834906.1\_prot\_WP\_002913766.1\_4086 [gene=dapE] [locus\_tag=BN49\_RS22140] [protein=succinyl-diaminopimelate desuccinylase] [protein\_id=WP\_002913766.1] [location=4243171..4244298] [gbkey=CDS]

MSCPVIELAQQLIRRPSLSPDDAGCQALMIERLRAIGFTVEPMDFGDTQNFWAWRGHGETLAFAGHTDVV

PAGDADRWINPPFEPTIRDGMLFGRGAADMKGSLAAMVVAAERFVAQYPNHRGRLAFLITSDEEASAKNG

TVKVVETLMARNERLDYCLVGEPSSTEVVGDVVKNGRRGSLTCNLTIHGVQGHVAYPHLADNPVHRAAPM

LAELVNIEWDKGNEFFPPTSMQIANVQSGTGSNNVIPGDMFVQFNFRFSTELTDEMIKSRVIALLEKYQL

RYSVEWWLSGQPFLTGRGKLVDAVVNAIEHYNEIKPQLLTNGGTSDGRFIARMGAQVVELGPVNATIHKI

NECVNAADLQLLARMYQRVMEQLVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913768.1\_4087 [locus\_tag=BN49\_RS22145] [protein=YpfN family protein] [protein\_id=WP\_002913768.1] [location=4244325..4244528] [gbkey=CDS]

MEWLIKHWWILVLVFLVGVIINVIKDLNRVDHKKFLNNKPDLPPHRDFNDKWDDDDDWPKHDQSKKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002913770.1\_4088 [gene=ypfH] [locus\_tag=BN49\_RS22150] [protein=esterase] [protein\_id=WP\_002913770.1] [location=complement(4244577..4245272)] [gbkey=CDS]

MKHDHFIVQSPATPAQQLLLLFHGVGDNPVSMGQIGSWFAPQFPDALIVSIGGVEPCGPNGRQWFSLQGV

TEENRQQRIDAIMPTFIEIVRYWQEKSGVSPLATALIGFSQGAIMSLESIKAAPDLASRVIAFNGRYATL

PETATTATTIHLIHGGEDRVIDLAWAVSAEEALQQAGGDVTLDIVDDLGHAIDDRSMQLAIERLRYTVPK

HYFDEALSGSTPKGDDIIEML

>lcl|NZ\_FO834906.1\_prot\_WP\_032411596.1\_4089 [locus\_tag=BN49\_RS22155] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_032411596.1] [location=complement(4245349..4247352)] [gbkey=CDS]

MMDALLNLTAQMAREGIRRLLVLSGDESWTLQQAQALRERLGGDGLWVGPEPVSAPCVAPGALKTLLGRE

VMHAFFDARRGFDVAAMAALSGTLRAGSWLVLLTPPFADWPTRADEDSLRWSDTPDPIVTPNFVHRCCRQ

FIADPEVLLWRQSDRPRFPLAAPCPDWHPADGRPQAEQAAILEQLIRLPPGIAAVTAERGRGKSALAGML

LRQLGGEAIVTAPTRSAVEVLASFAGETLRFMAPDALLASKEKAAWLIVDEAAAIPAPLLRQLVSRFPRT

LLTTTVQGYEGTGRGFLLKFCASLPHLQSFTLSAPIRWAAGCPLESAISQLLIFNDEAFRDAPMGEIALE

AVNQSCWQTQPALPEAMYQLLSGAHYRTSPLDLRRMMDAPGQAFRCARAGGAVAGALWLVAEGGLSPELS

RAVWAGFRRPRGNLVAQSLAAHGGSPLAATLRGLRVSRIAVHPTRQREGLGRKMIADIAADAAGYDYLSV

SFGYTAELWRFWQRCGFTLVRLGTHREASSGCYTAMALYPLTAAGRQLAQREAQRLQRDEYWLRPWREES

APLPAVADAMLSDEDWLEAASFAFAHRPLAAALGCLNRLLMQADMLLPALRGRLQGKEEAALCAVLQLTG

RKALQARWRREAADALRSLDAARADALRQQVAHLQFF

>lcl|NZ\_FO834906.1\_prot\_WP\_016531424.1\_4090 [locus\_tag=BN49\_RS22160] [protein=neutral zinc metallopeptidase] [protein\_id=WP\_016531424.1] [location=complement(4247362..4248237)] [gbkey=CDS]

MRWQGRRESDNVEDRRGQSGSPFGGGGGGGFRLPSGKGGIVLLIIVLVAGYYGVDLTGMLTGEPMPQQQT

STQRSISPKDDEAGKFTSVILATTEDTWGPIFEKMGRQYPQPKLVIYRGATRTGCGTGQSVMGPFYCPAD

STVYIDLSFYDEMKNKLGADGDFAQGYVIAHEVGHHVQKLLGIEPKVRQQQQHATQAEANRLSVKMELQA

DCFAGVWGHNMQQQDILETGDLQEALNAAEAIGDDRLQQQSQGRVVPDSFTHGTSKQRYTWFKRGFDSGD

PAQCNTFGSAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913801.1\_4091 [locus\_tag=BN49\_RS22165] [protein=phosphoribosylaminoimidazolesuccinocarboxamide synthase] [protein\_id=WP\_002913801.1] [location=complement(4248357..4249070)] [gbkey=CDS]

MKKQAELYRGKAKTVYSTDNPDLLVLEFRNDTSAGDGARIEQFDRKGMVNNKFNHFIMSKLAEAGIPTQM

EALLSDTECLVKKLDMVPVECVVRNRAAGSLVKRLGIEEGIELNPPLFDLFLKNDAMHDPMVNDSYCETF

GWVSKENLARMRELTYKANDVLKKLFDDAGLILVDFKLEFGLFKGEVVLGDEFSPDGSRLWDKNTLDKMD

KDRFRQSLGGLIEAYEEVAHRLGVKLD

>lcl|NZ\_FO834906.1\_prot\_WP\_004149279.1\_4092 [gene=bamC] [locus\_tag=BN49\_RS22170] [protein=outer membrane protein assembly factor BamC] [protein\_id=WP\_004149279.1] [location=complement(4249287..4250321)] [gbkey=CDS]

MAYSVQKSRLAKVAGVSLVLLLAACSSDSRYKRQVSGDEAYLQASPLSELHAPAGMILPIQVGDYNIPVA

NSTGAVGKALDIRPPAQPLALVSGARTQFNGDTATLMVENGRSGSLWAQVTSILQAKNYVIAKRDDASQT

LNTDWVEWNRLDEDQQYRGRYQISVKPQGYQQAVVVKLVNLEQAGKPVADPASLQRYSTAMLNVISEGLD

MNATSAQNAAQRSAGATFDVQSAADDTGLPMLVVRAPFNLVWQRLPGALEKVGMKVTDSTRSQGSMALTY

KPLSDSSWQELGARDPQLVSGDYKLQVGDLDNRSSLQFIDPKGHTLTQSQNDALVAVFQAAFNK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913803.1\_4093 [gene=dapA] [locus\_tag=BN49\_RS22175] [protein=4-hydroxy-tetrahydrodipicolinate synthase] [protein\_id=WP\_002913803.1] [location=complement(4250338..4251216)] [gbkey=CDS]

MFTGSIVALVTPMDENGNVCRTSLKKLIDYHVANGTSAIVSVGTTGESATLSHEEHGDVVMMTLELADGR

IPVIAGTGANATAEAISLTKRFNDSGVVGCLTVTPYYNRPTQEGLFQHFKAIAEHTDLPQILYNVPSRTG

CDMLPETVGRLAEIKNIVGIKEATGNLSRVHQIKELVSDDFILLSGDDATGMDFMQLGGVGVISVTANVA

AREMADMCRLALAGQFAEARAINQRLMPLHTKLFVEPNPIPVKWGCKALGLVATDTLRLPMTPITDHGRE

AVTAALKHAGLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913804.1\_4094 [locus\_tag=BN49\_RS22180] [protein=glycine cleavage system transcriptional repressor] [protein\_id=WP\_002913804.1] [location=4251370..4251936] [gbkey=CDS]

MTASLQHYLVITALGADRPGIVNTITRHVSSCGCNIEDSRLAMLGDEFTFIMLLSGSWNAINLIESTLPL

KGAELELLIVMKRTTARPPQAMPNTVWVQVEVPDSPHIIERFTALCDTWNMNIAELVSRTQPGDGDSAQL

FIQITAHSPATQNAANIEQAFKALCTELNAQGSINIVNYSQHDEQDGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002913805.1\_4095 [gene=bcp] [locus\_tag=BN49\_RS22185] [protein=thioredoxin-dependent thiol peroxidase] [protein\_id=WP\_002913805.1] [location=4251940..4252410] [gbkey=CDS]

MTPLKAGDIAPKFSLPDQDGEEVNLTDFQGQRVLVYFYPKAMTPGCTVQACGLRDNMDDLKKAGVEVLGI

STDKPEKLSRFAEKELLNFTLLSDENHQVCEQFGVWGEKSFMGKTYDGIHRISFLIDADGKIEHVFDDFK

TSNHHDVVLNWLKENA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913806.1\_4096 [locus\_tag=BN49\_RS22190] [protein=AI-2E family transporter] [protein\_id=WP\_002913806.1] [location=complement(4252472..4253533)] [gbkey=CDS]

MLEMLMQWYRRRFSDPEAIALLVILLAGFGIMFFFSGLLAPLLVAIVLAYLLEWPTVRLERIGLSRTWAT

SLVLILFVGILLLLAFVVLPVAWQQGIYLIRDMPGMLNKLSDFAATLPRRYPALMDAGIIDAMAENMRTR

MLTVGDSVVKYSLASLVGLLTLAVYLVLVPLMVFFLLKDKEQMLNAVRRVLPRNRGLAGQVWKEMNQQIT

NYIRGKVLEMIVVSVATWIGFILFGLNYSLLLAVLVGFSVLIPYIGAFVVTIPVVGVALFQFGAGTEFWS

LFAVYLIIQGLDGNLLVPVLFSEAVNLHPLVIILSVVIFGGLWGFWGVFFAIPLATLIKAVVHAWPDGLA

VDD

>lcl|NZ\_FO834906.1\_prot\_WP\_004221267.1\_4097 [locus\_tag=BN49\_RS31190] [protein=hypothetical protein] [protein\_id=WP\_004221267.1] [location=complement(4253588..4253704)] [gbkey=CDS]

MFPGRIPASLAGVGRLENMFFMAENGLTAAHQKAKSFL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913807.1\_4098 [gene=bepA] [locus\_tag=BN49\_RS22200] [protein=beta-barrel assembly-enhancing protease] [protein\_id=WP\_002913807.1] [location=4253756..4255219] [gbkey=CDS]

MFRQLKKTLVATAIASLTLGSIGPAFADSADTLPDMGTSAGSTLSIGQEMQMGDYYVRQLRGSAPLINDP

LLVQYINGLGMRLVAHANSVRTPFHFYLINNDQINAFAFFGGNVVLHSALFRYSDNESELASVMAHEISH

VTQRHLARAMEDQKRNAPLTWVGALGSILLAMASPQAGMAALTGTLAGTQQGMISFTRQNEEEADRIGIQ

VLQRSGFDPQAMPMFMGKLLDESRYSTRPPEMLLTHPLPESRLADARNRANQMRPVVVQSSADFYLAKAR

TLGMYTNGDNKLGTDLLNAWDKGNIRQQHAAQYGRALLAMESNNFDQARKTLQPLLNADPQNAWYLDLAT

DIDLGQKKTSDAINRLKNARELRTNPVLQLNLANALLQGGQPGEAATILNRYTFTYKEDGNGWDLLAQAE

GALGNRDQELAARAESMALVGQLEQAISLLSSASSQVKLGSLQQARYDARIDQLRDLQARFRPYQKM

>lcl|NZ\_FO834906.1\_prot\_WP\_002913810.1\_4099 [gene=arsC] [locus\_tag=BN49\_RS22205] [protein=arsenate reductase (glutaredoxin)] [protein\_id=WP\_002913810.1] [location=4255229..4255588] [gbkey=CDS]

MTDAVKIYHNPRCSKSRETLSLLQSRGIDPEVVLYLETPPDAGTLRQLLQLLGMESPRELMRQKEDLYKS

LNLADPALSNAALIQAMVDNPKLIERPIVVSRGQARIGRPPEQVLEIVS

>lcl|NZ\_FO834906.1\_prot\_WP\_002913812.1\_4100 [locus\_tag=BN49\_RS22210] [protein=Rpn family recombination-promoting nuclease/putative transposase] [protein\_id=WP\_002913812.1] [location=4255716..4256627] [gbkey=CDS]

MKKPTSTPHDAVFKTYLSHPDTARDFLQLYLPETLLKVCDLRTLHLESGHFVEDDLRPFYADILYSLKTT

AGDGYIYALIEHQSTPDRHMAFRLMRYAIAAMQRHLDAGHDRLPLVIPVLFYHGLVSPYPFSLRWLDEFV

APELAGHLYHGAFPLADITVIPDDEIATHQRMATLELLQKHIRQRDLAQLLDKLSELLLTGLATESQVQA

LMHYLVQAGNTREPIKFIRELALRTPQHKETLMTIAEYLEQQGLERGLAQGRQEGRKEEAQRIAVAMLHS

GLPRDLVARLTGLTEQELTPLAD

>lcl|NZ\_FO834906.1\_prot\_WP\_020947395.1\_4101 [locus\_tag=BN49\_RS22215] [protein=DnaA inactivator Hda] [protein\_id=WP\_020947395.1] [location=complement(4256624..4257325)] [gbkey=CDS]

MNAPAQLSLPLYLPDDETFASFWPGDNPSLLAALQNVLRQEHSGYIYIWSREGAGRSHLLHAACAELSQR

GDAVGYVPLDKRTWFVPEVLEGMEQLALVCIDNIECVAGDEPWEMAIFNLYNRILESGKTRLLITGDRPP

RQLNLGLPDLASRLDWGQIYKLQPLSDEDKLQALQLRARLRGFEMPEDVCRFLLKRLDREMRSLFMTLDQ

LDHASITAQRKLTIPFVKEILKL

>lcl|NZ\_FO834906.1\_prot\_WP\_002913824.1\_4102 [gene=uraA] [locus\_tag=BN49\_RS22220] [protein=uracil permease] [protein\_id=WP\_002913824.1] [location=complement(4257424..4258710)] [gbkey=CDS]

MTRRAIGVSERPPLLQTIPLSLQHLFAMFGATVLVPILFHINPATVLLFNGIGTLLYLFICKGKIPAYLG

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ANMAGLLPADGQSPDSKTIIISMVTLAVTVFGSVLFRGFLAIIPILIGVLVGYALSFVMGVVDTTPIAEA

HWFALPTFYTPRFEWFAIFTILPAALVVIAEHVGHLVVTANIVKRDLIRDPGLHRSMFANGLSTIVSGFF

GSTPNTTYGENIGVMAITRVYSTWVIGGAAIIAILLSCVGKLAAAIQIIPVPVMGGVSLLLYGVIGASGI

RVLIESKVDYSKAQNLILTSVILIIGVSGAKVHIGAAELKGMALATIVGIALSLIFKLISVLRPEEVVLD

AADSEEFK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913827.1\_4103 [gene=upp] [locus\_tag=BN49\_RS22225] [protein=uracil phosphoribosyltransferase] [protein\_id=WP\_002913827.1] [location=complement(4258806..4259432)] [gbkey=CDS]

MKIVEVKHPLVKHKLGLMREHDISTKRFRELASEVGSLLTYEATADLETEKVTIEGWNGPVEVEQIKGKK

ITVVPILRAGLGMMEGVLEHVPSARISVVGIYRNEETLEPVPYFQKLVSNIDERMALVVDPMLATGGSMI

ATIDLLKNAGCTSIKVLVLVAAPEGIAALEKAHPDVELYTASVDKGLNEHGYIIPGLGDAGDKIFGTK

>lcl|NZ\_FO834906.1\_prot\_WP\_004174870.1\_4104 [locus\_tag=BN49\_RS22230] [protein=6-phospho-beta-glucosidase] [protein\_id=WP\_004174870.1] [location=complement(4259650..4261083)] [gbkey=CDS]

MSGFKAGFLWGGAVAAHQLEGGWQEGGKGISVADVMTAGAHGVPREITDGVVAGKNYPNHEAIDFYHRYP

QDLALFAEMGFKCFRTSIAWTRIFPQGDELEPNEAGLQFYDDLFDECLKHGIEPVITLSHFEMPYHLVTE

YGGWRNRKLIDFFVRFARVVFTRYQHKVKYWMTFNEINNQANFHEDFAPFTNSGLKYLPDEDREPVMYQA

AHYELVASALAVKAAREINPALQIGCMIAMCPIYPLTCAPDDMMMAMNAMHRRYWFTDVHVRGRYPQHLL

NYFARRGFTLDITEADRQALTEGCVDYIGFSYYMSFATKATEDNPLLDYDETTSLVSNPYVKKSDWGWQI

DPVGLRYSLNWFWDHYQLPLFIVENGFGAIDVREADGSVNDQYRIDYLSAHIAEMKKAVVEDGVDLMGYT

PWGCIDLVSAGTGEMKKRYGFIYVDKDNEGNGTLARSRKKSFAWYQQVIASNGENLS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529174.1\_4105 [locus\_tag=BN49\_RS22235] [protein=ROK family protein] [protein\_id=WP\_016529174.1] [location=complement(4261093..4261986)] [gbkey=CDS]

MKIAAFDIGGTALKMGVMARDGRLLETARQSINDSDGDRILQAMLSWLAAHPSCEGIAISAPGYIDPHSG

LITMGGAIRRFDNFAMKSWLETRTGLPVSVENDANCVLLAERWQGKAAEMANFLVLTIGTGIGGAIFCQH

QLINGARFRAGEFGYMLTDRPGGRDPRRYSMNENCTLRVLRHRYAQHIGAPLDSVTGELIFDRYDAGDQV

CQRLVAEFFNGLGHGLYNLVHIFDPQTIFIGGGVVERPGFLTLLRQHLAWFGIADYLDTVSHGNDAGLIG

AVYHFNQLYRSPDDDRH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913836.1\_4106 [gene=purM] [locus\_tag=BN49\_RS22240] [protein=phosphoribosylformylglycinamidine cyclo-ligase] [protein\_id=WP\_002913836.1] [location=4262250..4263287] [gbkey=CDS]

MTDKTSLSYKDAGVDIDAGNALVDRIKGVVKKTRRPEVMGGLGGFGALCALPQKYREPVLVSGTDGVGTK

LRLAMDLKRHDTIGIDLVAMCVNDLVVQGAEPLFFLDYYATGKLDVDTAASVINGIAEGCLQSGCALVGG

ETAEMPGMYHGEDYDVAGFCVGVVEKSEIIDGSKVTDGDVLVALASSGPHSNGYSLVRKIIEVSGVDPQT

TDLDGKPLADHLLAPTRIYVKSVLDLIASVDVHAIAHLTGGGFWENIPRVLPDNTQAIIDESSWQWPSVF

NWLQTAGNVSQHEMYRTFNCGVGMIIALPAAEADKAIALLNDKGENAWKIGYIKASDSEQRVVIA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530015.1\_4107 [gene=purN] [locus\_tag=BN49\_RS22245] [protein=phosphoribosylglycinamide formyltransferase] [protein\_id=WP\_016530015.1] [location=4263284..4263925] [gbkey=CDS]

MKNIVVLISGSGSNLQAIIDACGRKQINGTLRAVFSNKADAFGLERARLAGIPAHALAQSQFADREAFDR

QLMHEIDAYAPDLVVLAGYMRILSPAFVSHYQGRLLNIHPSLLPKYPGLHTHRQVLENGDEEHGTSVHFV

TDELDGGPVILQAKVPVFAGDSEEEITARVQAQEHAIYPLVISWFVDGRLRMAGNHAWLDERQLPQQGYA

ADE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913838.1\_4108 [gene=ppk1] [locus\_tag=BN49\_RS22250] [protein=polyphosphate kinase 1] [protein\_id=WP\_002913838.1] [location=4264106..4266166] [gbkey=CDS]

MGQEKLYIEKELSWLSFNERVLQEAADKSNPLIERMRFLGIYSNNLDEFYKVRFAELKRRIIISEEQGST

AHSRHLLGKIQARVLKADQEFDSLYNELLLEMARNQIFLINERQLSVNQQAWLRNYFKQYLRQHISPILI

NRETDLVQFLKDDYTYLAVEIIRGENINYALLEIPSDKVPRFVNLPPEAPRRRKPMILLDNILRYCLDDI

FKGFFDYDALNAYSMKMTRDAEYDLVHEMESSLMELMSSSLKQRLTAEPVRFVYQRDMPDAMVEMLRDKL

SISNYDSMLPGGRYHNFKDFIGFPNVGKANLVNKPMPRLRHLWFDKFRNGFDAIRERDVLLYYPYHTFEH

VLELLRQASFDPSVLAIKINIYRVAKDSRIIDAMIHAAHNGKKVTVVVELQARFDEEANIHWAKRLTEAG

VHVIFSAPGLKIHAKLFLISRKEGDEVVRYAHIGTGNFNEKTARIYTDYSLLTADARITNEVRRVFNFIE

NPYRPVSFDYLLVSPQNSRRLLYEMIDREIANAQNGQPSGITLKLNNLVDKGLVDRLYAASSSGVPVNLL

IRGMCSLIPGLEGISENIRVISIVDRFLEHDRVYCFENGGDKQVWLSSADWMTRNIDYRIEVAAPLLDPR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002913839.1\_4109 [gene=ppx] [locus\_tag=BN49\_RS22255] [protein=exopolyphosphatase] [protein\_id=WP\_002913839.1] [location=4266170..4267702] [gbkey=CDS]

MPINDNTPRPQEFAAVDLGSNSFHMVIARVVDGAMQIIGRLKQRVHLADGLDENSVLSEEAMTRGLNCLS

LFAERLQGFSPSSVCIVGTHTLRQATNAAEFLKRAEKVIPYPIEIISGNEEARLIFMGVEHTQPERGRKL

VIDIGGGSTELVIGEDFEPRLVESRRMGCVSFSQAYFPGGVINKENFQRARLAAVQKLETLAWQFRIQGW

TVALGASGTIKAAQEVLVAMGEKDGFITPERLEMLVNELLKHKNFDALSLPGLSEDRKAVFAPGLAILCG

VFDALAIKELRLSDGALREGVLYEMEGRFRHQDIRSRTAQSLANQYNIDREQARRVLETTTQMLEQWQEQ

NPKLANPHLAALLKWAVMLHEVGLNINHSGMHRHSAYILQNSDLPGFNQEQQMLMATLVRYHRKAIKLDD

LPRFTLFRKKQFLPLIQLLRLGVLLNNQRQATTTPPTLRLQTEAHHWTLTFPHNWFSQNALVLLDLEKEQ

QYWEGVPEWMLKIAEEEPDA

>lcl|NZ\_FO834906.1\_prot\_WP\_016530313.1\_4110 [locus\_tag=BN49\_RS22260] [protein=sensor domain-containing phosphodiesterase] [protein\_id=WP\_016530313.1] [location=complement(4267756..4269984)] [gbkey=CDS]

MNLLKYYQQYRDKWWALPLVLPALLLPVARWANTYTMLNGHMVFLYYLPLALVLSLMMFFGWAAIPGIII

GLLLTLAHGMMLEQSIGVLFHFLIPCVLCWGGYRIFVPQRQQVSHGNVRLMPHRLFWQMLLPSVIFLILS

QIAEYLGLHPRTTEMTGVTPFSLRSLITFQALMVGCLTGMPLCYFVLRVIRNPFHLRGFISQVRLQIDPK

IKKIEIICWATVLILLLWLLLMPLNDSSTIFSTNYTLSLLMPVMLWGAMRFGYRFISLIWTPVLIAVIHF

HYRYLPIYPSYNTQLAITSSSYLVFSFIVAYTAMLATQQRLIYARVRQMAFLDPVVHMPNLRALSRALNG

TSWSTLCFLRIPELELLGRHYGVLLRIQYKQMLANHLRTLLQPNEAVYHLAGHDLVFRLNSEGHQARIHL

IDRSLRQFRFHWDGVPLQPRIGMSYCSVRSPVKHLYLLLGELNTIADMSLASGHPENLQRRGAGHVQQDL

KDKVVMMNRILKALEHDHFVLMAQPIQGIRGDRYHEVLVRMEGESGELTGPNEFLPVAHEFGLSTRVDQW

VIEHTLAFMDANRRALPGLRLAINLSPVSLSRSQFPQEVEALLQAYNIEPWQIIFELTENYALSNPELVC

QTLEHLRALGCRVAIDDFGTGYASYARLKTMNVDILKIDGSFIRNLLASSLDYQVVDSICRLARMKNMQV

VAEYVESPEIRQAVITLGIDYMQGYDIGVPVPLTQLAEEMTG

>lcl|NZ\_FO834906.1\_prot\_WP\_004174861.1\_4111 [locus\_tag=BN49\_RS22265] [protein=DUF2633 family protein] [protein\_id=WP\_004174861.1] [location=4270355..4270528] [gbkey=CDS]

MRKRHRFNRRMTRIVLLISFLFFFGRFVYSSIGAWYHHQDKKASQESSLTVEPSPRE

>lcl|NZ\_FO834906.1\_prot\_WP\_004221278.1\_4112 [locus\_tag=BN49\_RS22270] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004221278.1] [location=complement(4270625..4271536)] [gbkey=CDS]

MRGIRETFMTTLNLGNLATFRLVVQRGSFSAAADALGISQPAVSLQVRQLEQFLQTRLLERTGRGIKATA

AGMALLAHSEQIDRAVNSAVQSVSAFSQEVNGSLTLGTGATACIHLLPPLLQHLRQQHPLLTVGVTTGNT

LDIVRAVEENRLDLGLVTLPVQGRSLAVTAMLDEEFVTIYASRETEMPAVYTPAELQAQPLIAFEAGSGT

RDLIDRWFRSAGLAVTPVMQLGSIEAIKRMVRAGLGYSIVPRMAVERVEDRDGLRVHSLAPRLYRQLAVV

MRQDKIVTKGIAEMLRLLHTVRL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043718.1\_4113 [locus\_tag=BN49\_RS22275] [protein=MFS transporter] [protein\_id=WP\_046043718.1] [location=4271610..4272842] [gbkey=CDS]

MEINAIPRRLAFTAGGQQLINWGISFYMPGTFAGAIAADKGWSLPQIYLGLTLAMLMMAAVSPFVARLLA

RFGGRLVVTSGTLLIAASCAMMAWRPSLAGWYGAWLLTGIGMRLSLYDALFAAVVNLYGQQARKTISHIT

LAGGLASALFWPLGEALLTIMPWQNALRIYALFGLLSAWLSYQLPRQRLSSAAKSPASPATAEGDRRNGA

RYAIFIALITFISNGTSTHLPEFISHFGLPVAVGVLWGFGQTGARLGEVLAGPRATSLTLTRFTALAMPF

CFLLGLSSTTFAGCAAGFVLGYGAINGLVTIVKATLPLALFSAESYASRTGLLLIPGQLMAAVSPFAYAW

LNHRLGIIGGMWVSTGLTLIVAGLALAMVREAGKAQDERNVEYPAAAVDQPIAKNNLAEE

>lcl|NZ\_FO834906.1\_prot\_WP\_042941338.1\_4114 [locus\_tag=BN49\_RS22280] [protein=anaerobic sulfatase maturase] [protein\_id=WP\_042941338.1] [location=4273136..4274314] [gbkey=CDS]

MSANFNTVAKPGGNRCNLACRYCFYLENEVPRPGYATMDDLTLEAYIHNTISSTPSQNVEFCWQGGEPTL

RGLDFFAKVVELQQRYRGNKIIANSLQTNGILLNDKWARFLRRHGFLVGLSIDGPASLHDSWRTTGCGKP

TWEKVEQAIHCLQQHDVPVNAMVVVSRQSASQGKSLYRCLSRELNLHHLQFIPLVDSPAPWSVTPEGWGK

FLCSVFDDWLENDVGRVFIQYFDNLLGVWAGQPATLCTMQPVCGQSLLVEQNGDVYSCDHFVSAEYKLGN

LKQDAMAAMASSPFQQQFGKQKGQLSARCQSCHWRFACHGGCPKHRFTIHDDEAQNYLCSGYLTFFGHIT

PYMNVMRRLLLNCQPPALIMSLIPEIRQNILQLTESEDERTK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530460.1\_4115 [locus\_tag=BN49\_RS22285] [protein=sulfatase-like hydrolase/transferase] [protein\_id=WP\_016530460.1] [location=4274298..4276166] [gbkey=CDS]

MKEPNKIDGNRRDLLKGLGIAAVVSLLPETGNAAQNNAAPKAAWDIPFTGEIPDTLPEGYNILLITCDQE

RYFERYPFPVPGRERLMKTGITFTNHQNTANVCTPSRSVMYTGLHMPHTRMFDNLGFPWMNYDLDPELRT

VGHMMRELGYYTAYKGKWHLTREIDQPVAGKSVEEMDLGEIPTPRLHEIMEKYGFSDYHGIGDVIGKSKG

GYFFDSVTTGQTISWLRNTGRPLNDENKPWFAAVNLVNPHDVMFIDTDEHGEQVQWKGPMDKENHTLLPT

HPPHNQIYQQSWPDYPLPANRHQPLDEPGRSAAHKEYQNARAVMEGQFPDEDRRWRKLLDYYFNCIRDND

QHLEAILNELDNLQLTQNTIIVFTADHGELGGSHQMHGKGSSVYKEQIHVPMIIRHPAYPGNICCNSLTN

HLDLVPTLIGLTGRDRSLREKVLKGRKGRDMSPLLAHPEQAGLNALRPGSLYCYGMILYMDAQYTAKFRK

LAGEKLPHDQFKKAIASLHPDFSHRSGIRMINDGHYKFARYFSLKQHHIPASLAELLENNDVELFDLVND

PEENHNLAREPEKYRDLLMTMNDKLNQLTAAEIGEDDGSYMPPFEGSQWDLTAAQMHQYMRD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151979.1\_4116 [gene=guaA] [locus\_tag=BN49\_RS22290] [protein=glutamine-hydrolyzing GMP synthase] [protein\_id=WP\_004151979.1] [location=complement(4276261..4277838)] [gbkey=CDS]

MTENIHKHRILILDFGSQYTQLVARRVRELGVYCELWAWDVTEAQIREFNPSGIILSGGPESTTEENSPR

APQYVFEAGVPVFGVCYGMQTMAMQLGGHVEGSNEREFGYAQVEVVNDSALVRGIEDSLTADGKPLLDVW

MSHGDKVTAIPADFVTVASTDNCPFAIMANEEKRFYGVQFHPEVTHTRQGMRMLERFVRDICQCEALWTP

AKIIDDAVERIRQQVGDDKVILGLSGGVDSSVTAMLLHRAIGKNLTCVFVDNGLLRLNEAQQVMEMFGDH

FGLNIVHVEGEQRFLDALAGESDPEAKRKIIGRVFVEVFDEEALKLDDVKWLAQGTIYPDVIESAASATG

KAHVIKSHHNVGGLPKEMKMGLVEPLRELFKDEVRKIGLELGLPYDMLYRHPFPGPGLGVRVLGEVKKEY

CDLLRRADAIFIEELHKADLYNKVSQAFTVFLPVRSVGVMGDGRKYDWVVSLRAVETIDFMTAHWAHLPY

DFLGRVSNRIINEVNGISRVVYDISGKPPATIEWE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151980.1\_4117 [gene=guaB] [locus\_tag=BN49\_RS22295] [protein=IMP dehydrogenase] [protein\_id=WP\_004151980.1] [location=complement(4277906..4279372)] [gbkey=CDS]

MLRIAKEALTFDDVLLVPAHSTVLPNTADLSTQLTKTIRLNIPMLSAAMDTVTEARLAIALAQEGGIGFI

HKNMSIERQAEEVRRVKKHESGVVTDPQTVLPTTTLREVKELTERNGFAGYPVVTEENELVGIITGRDVR

FVTDLNQPVSVYMTPKERLVTVREGESREVVFAKMHEKRVEKALVVDESFHLRGMITVKDFQKAERKPNA

CKDEQGRLRVGAAVGAGAGNEERVDALVAAGVDVLLIDSSHGHSEGVLQRIRETRAKYPDLQIIGGNVAT

GAGARALAEAGCSAVKVGIGPGSICTTRIVTGVGVPQITAVSDAVEALEGTGIPVIADGGIRFSGDIAKA

IAAGAAAVMVGSMLAGTEESPGEIELYQGRSYKSYRGMGSLGAMSKGSSDRYFQSDNAADKLVPEGIEGR

VAYKGRLKEIIHQQMGGLRSCMGLTGCGTIDLLRTKAEFVRISGAGIQESHVHDVTITKESPNYRLGS

>lcl|NZ\_FO834906.1\_prot\_WP\_004174856.1\_4118 [gene=xseA] [locus\_tag=BN49\_RS22300] [protein=exodeoxyribonuclease VII large subunit] [protein\_id=WP\_004174856.1] [location=4279531..4280922] [gbkey=CDS]

MLPSQSPAIFTVSRLNQTVRLLLEREMGQVWISGEISNFSQPSSGHWYFTLKDDNAQVRCAMFRNSNRRV

TFRPQHGQQVLVRANITLYEPRGDYQIIVESMQPAGEGLLQQKYEQLKAQLTAEGLFEQKHKQALPSPAH

CVGVITSKTGAALHDILHVLRRRDPGLPVIIYPTAVQGDDAPGQIVRAIALANARQECDVLIVGRGGGSL

EDLWSFNDERVARAIFASQIPIVSAVGHETDVTIADFVADLRAPTPSAAAEIVSRNQQELLRQLQSGQQR

LEMAMDYFLASRQRRFTQLFHRLQQQHPQLRLARQQTALERLRQRMRIAVESQLKRAEQRQKRTVQRLNH

YNPQPRIHRAQSRIQQLEYRLAEIMRGRLSERRERFGNAVTHLEAVSPLATLARGYSVTSVSDGTVLKQT

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>lcl|NZ\_FO834906.1\_prot\_WP\_004144303.1\_4119 [locus\_tag=BN49\_RS22305] [protein=zinc ribbon domain-containing protein] [protein\_id=WP\_004144303.1] [location=complement(4280906..4281124)] [gbkey=CDS]

MELDCPLCHAPLDVKGSSAHCAQCERVFTLEARCPECHQPLEVLKACGAVDYFCQHGHGLISKKRVEFIP

LV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043722.1\_4120 [locus\_tag=BN49\_RS22310] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_046043722.1] [location=complement(4281174..4282253)] [gbkey=CDS]

MQIGFIGLGAVVETAYLPALRRLGDVIDRCQGYDLDCSRALPGIQRCSSLSALLAEPLDTLFITTSSLQH

LPVLERALASGISRIVVEKPIVANLEQAARLRALLAPPEQAARVLALDHWMARGVALNAPGPLWRAEGEA

SGLPPPHLSAQDIVWLEGSLQEPSGFNSAGEPVALNFATGELDTRQLRHPDGVILDIGTHVLAMLRETLH

ASGSDTALSLSLRVAKDRLGHDIAPGDTSTAEGVAHLQGTLGTIPLNIWLNKYAGPAGGQKGMRIGLRDG

RIITFDRAPEGEVVTLQDGERVQRWTRPGAIYTHCLDEQILGADNLFIRAPDSVAGLTQRRLEEVEWLLR

LQQQLRGPH

>lcl|NZ\_FO834906.1\_prot\_WP\_004144309.1\_4121 [gene=der] [locus\_tag=BN49\_RS22315] [protein=ribosome biogenesis GTPase Der] [protein\_id=WP\_004144309.1] [location=complement(4282371..4283849)] [gbkey=CDS]

MIPVVALVGRPNVGKSTLFNRLTRTRDALVADFPGLTRDRKYGRAEVEGREFICIDTGGIDGTEEGVETR

MAEQSLLAIEEADVVLFMVDARAGLMPADIAIAKHLRSREKPTFLVANKTDGIDVDQAMADFWSLGLGDI

YPIAASHGRGVTSLLEQALLPWVDEVNPQEEVDEDAEYWAKFEAEQNGEAEEEPEDDFNPQDLPIKLAIV

GRPNVGKSTLTNRILGEDRVVVYDMPGTTRDSIYIPMQRDEREYVLIDTAGVRKRGKITDVVEKFSVIKT

LQAIEDANVVLLVIDAREGISDQDLSLLGFILNSGRSLVIVVNKWDGLSQEVKEQVKETLDYRLGFIDFA

RVHFISALHGSGVGNLFESVREAYDSATRRVSTAMLTRIMNMAAEDHQPPLVRGRRVKLKYAHAGGYNPP

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SK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531536.1\_4122 [gene=bamB] [locus\_tag=BN49\_RS22320] [protein=outer membrane protein assembly factor BamB] [protein\_id=WP\_016531536.1] [location=complement(4283963..4285141)] [gbkey=CDS]

MQLRKLLLPGLLSVTLLSGCSLFNSEEDVVKMSPLPTVENQFTPSTSWSTSVGDGIGEFYSNLHPAFADG

VVYAADRKGTVKALNADDGKEVWSVNLAEKDGWFSRTPALLSGGVTVSGGHVYIGSEKAQLYALNTSDGT

VAWQTRVAGEALSRPVVSDGMVLVHTSNGQLQALNETDGAVKWTVNLDMPALSLRGESAPATAYGAAIVG

GDNGRVSAVLMLQGQMIWQQRISTATGPTEIDRLNDVDTTPIIVNGVVYALAYNGNLTALDLRSGQIMWK

RELGSVNDFIVDGNRIYLVDQNDRLLALTTDGGVTLWTQSDLLHRLLTAPVLYNGNLVVGDSEGYMHWVN

PEDGHFVAQQKVDSSGFLTDPVVADGRLLIQAKDGTLYAITR

>lcl|NZ\_FO834906.1\_prot\_WP\_002913890.1\_4123 [locus\_tag=BN49\_RS22325] [protein=YfgM family protein] [protein\_id=WP\_002913890.1] [location=complement(4285152..4285772)] [gbkey=CDS]

METFNNENDQVDALKRFFAENGKALAVGVILGIGALVGWRYWTSHQQDTARDASLAYEKATSALKSNTPE

VLSGAEKFAADNKNTYGAFASLELAQHFVEQNDLPNAEKQLQQGLAAASDDNLKSVISMRLARVQLQMKQ

ADAALKTLDSIKGEGWTAIVADLRGEILLSKGDKQGARAAWEAGVKSDASPALSEMMRMKMNNLSI

>lcl|NZ\_FO834906.1\_prot\_WP\_004149335.1\_4124 [gene=hisS] [locus\_tag=BN49\_RS22330] [protein=histidine--tRNA ligase] [protein\_id=WP\_004149335.1] [location=complement(4285807..4287081)] [gbkey=CDS]

MAKNIQAIRGMNDYLPGETALWQRIEGSLKQVLGSYGYSEIRLPIVEQTPLFKRAIGEVTDVVEKEMYTF

EDRNGDSLTLRPEGTAGCVRAGIEHGLLYNQEQRLWYVGPMFRHERPQKGRYRQFHQIGAEVFGLQGPDI

DAELIMLTARWWRELGISEHVSLELNSIGSLEARANYRDALVAYLEQFTDKLDEDSKRRMYTNPLRVLDS

KNPDVQALLNDAPALGDYLDEESKAHFAGLCALLDDAGIRYTVNQRLVRGLDYYNRTVFEWVTTSLGSQG

TVCAGGRYDGLVEQLGGRATPGVGFAMGLERLVLLVQAVNPEFKADPVVDIYLVASGTDTQSAAMRLAEQ

VRDALPGVKLMTNHGGGNFKKQFARADKWGARVALVVGESEIADGNVVVKDLRSGEQTTVTQESVAAHLR

TLLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002913892.1\_4125 [gene=ispG] [locus\_tag=BN49\_RS22335] [protein=flavodoxin-dependent (E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase] [protein\_id=WP\_002913892.1] [location=complement(4287173..4288294)] [gbkey=CDS]

MHNQAPIQRRKSKRIYVGNVPIGDGAPIAVQSMTNTRTTDVAATVNQIKALERVGADIVRVSVPTMDAAE

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LEKDLQEKYGEPTPQALLESAMRHVDHLDRLNFDQFKVSVKASDVFLAVESYRLLAKQIDQPLHLGITEA

GGARSGAVKSAIGLGLLLSEGIGDTLRVSLAADPVEEIKVGFDILKSLRIRSRGINFIACPTCSRQEFDV

IGTVNALEQRLEDIITPMDVSIIGCVVNGPGEALVSTLGVTGGNKKSGLYEDGVRKDRLDNNDMIDQLEA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004149336.1\_4126 [gene=rodZ] [locus\_tag=BN49\_RS22340] [protein=cytoskeleton protein RodZ] [protein\_id=WP\_004149336.1] [location=complement(4288321..4289316)] [gbkey=CDS]

MNTEATQDHQEANTTGARLRHAREQLGLSQQAVAERLCLKVSTVRDIEDDKAPADLASTFLRGYIRSYAR

LVHIPEDELLPMMAKQAPIRAAKVAPMQSFSLGKRRKKRDGWLMSFTWLVLFVVIGLSGAWWWQDHKAQQ

EEISTMADQSSAELNGGDANSQNVPLDTSAPAAPTADSAANSAPTDTASAPTTSAPAQTPADNNAVVAPS

QANVDTAGTTPAAPATTPASPLPTDQANVTTPAASAQDLVMNFSADCWLEVSDATGKKLFSGLQRKGGNL

NLSGQAPYKLKIGAPAAVQIQYLGKPVDLSRFIRTNQVARLTLNAESSPAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002913894.1\_4127 [locus\_tag=BN49\_RS22345] [protein=bifunctional tRNA (adenosine(37)-C2)-methyltransferase TrmG/ribosomal RNA large subunit methyltransferase RlmN] [protein\_id=WP\_002913894.1] [location=complement(4289593..4290759)] [gbkey=CDS]

MSEQIVTPDTAALTVPNKDAKINLLDLNRQQMREFFKNMGEKPFRADQVMKWMYHYCCDDFDEMTDINKV

LRSKLKEVAEIRAPEVVEEQRSTDGTIKWAIAVGDQRVETVYIPEEDRATLCVSSQVGCALECKFCSTAQ

QGFNRNLRVSEIIGQVWRAAKIVGAVKTTGVRPITNVVMMGMGEPLLNLNNVVPAMEIMLDDFGFGLSKR

RVTLSTSGVVPALDKLGDMIDVALAISLHAPNDTIRDEIVPINKKYNIETFLNSVRGYISKSNANQGRVT

IEYVMLDHVNDGTEHAHELAALLKDTPCKINLIPWNPFPGAPYGRSSNSRIDRFSKVLMEYGFTTIVRKT

RGDDIDAACGQLAGDVIDRTKRTLRKRMQGEAIDVKAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004144312.1\_4128 [gene=ndk] [locus\_tag=BN49\_RS22350] [protein=nucleoside-diphosphate kinase] [protein\_id=WP\_004144312.1] [location=complement(4291243..4291674)] [gbkey=CDS]

MAIERTFSIIKPNAVAKNVIGSIFSRFEAAGFKIVGTKMLHLTVEQARGFYAEHEGRPFFDGLVEFMTSG

PIVVSVLEGENAVQRHRDLLGATNPANALAGTLRADYADSFTENGTHGSDSVESAAREIAFFFAEGEVCP

RTR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043725.1\_4129 [gene=pbpC] [locus\_tag=BN49\_RS22355] [protein=peptidoglycan glycosyltransferase PbpC] [protein\_id=WP\_046043725.1] [location=complement(4291835..4294159)] [gbkey=CDS]

MRVLPRVKRRWRWLAAFIFLLWLAVLAADRLWPLPLHDVTPARVVVAEDGTPLWRFADAQGVWRYPVTLA

DVSPRYLQALIQYEDRWFWRHPGVNPFAVLRAAWQDLTSGRVISGGSTLTMQVARLLDPHPRTFGGKLRQ

LWRALQLEWHLSKSDILTLYLNRAPFGGTLQGIGAASWAYLGKPPARLSYGEAALLAVLPQAPSRLRPDR

WPQRAQAARDKVLTRMVSQGVWPEQAVKEAMEEPVWLFPRQMPQLAPLFSRRALATSRDEKVVTTLDAGL

QRQLEDLALNWKSRLPPRSSLAMVVVDHTDMKVRGWVGSADITDDSRFGHIDMVSAVRSPGSVLKPFIYA

MAMDEGLIHPASLLQDVPRRFSDYRPGNFDSGFHGPVSASEALVRSLNLPAVQVLEAYGPKRFAANLRNA

GLPLTLPAGTEPNLSLILGGAGARLEDIVAAYSAFARHGKAARLRLKPSEPLTERALMSPGAAWIVRHIL

AGEAQPVPDASLPQAVPLAWKTGTSYGYRDAWAVGLNARYLIGIWTGRPDGTPVVGQFGFASAVPLLNQV

NNLLLARPAMSRGGLPSDPRPATVSQGTICWPGGQDLPAGDSNCRRRLASWLLDASQPPTLLLPGQESVR

GIRFPVWRNEHGERVAADCPGARESQVEVWPLPLDPWLPASERRRARLGPASESCPPLQTQDTAPLVLSG

IRDGAVIKRLPGEARVMLPLQTSGGEGRRWWFINGEPLEAAGARTTLMLDKPGEWQLVVMDEAGQTAAAS

FTLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043727.1\_4130 [locus\_tag=BN49\_RS22360] [protein=alpha-2-macroglobulin family protein] [protein\_id=WP\_046043727.1] [location=complement(4294160..4299109)] [gbkey=CDS]

MKPFRLAALSLALLTAFSLTGCDDSGTPQASAPAPAADSNPGATAKPDRAQLAALAEKSQGKALTLLDAS

EVQLDGAATLVLTFSVPLQPDQDFSRSVHLVDKKSGKVDGAWELAPNLKELRLRHLEPKRELIVSVDPTL

TALNKATLDKPFEKTLTTRDIAPSVGFASRGSLLPGNVVAGLPVMALNVDNVDVNFFRIKPESLSAFVSQ

WEYRNSLSNWESDELLKMADLVYTGRFDLNPARNTREKLLLPLSDIKPLQQPGVYVAVMNPAGRYSYSNA

ATLFTLSDIGVSAHRYHNRLDVFTQSLENGAAQSGIEVQLLNAKGQTLAEAKSDSQGHVTLQTDKEAALL

LARKEGQTTLLDLKLPALDLAEFSIAGAPGFSKQFFMFGPRDLYRPGETVILNALLRDSDGKPLAEQPVK

LEVVQPDGQVIRSVMSKPVNGLYQFTYPLDSGAATGMWHIRASAGDNQPREWDFHVEDFMPERMALNLTP

QAAPVAPDADVTFGVSGAYLYGAPASGNQLQGKLFLRPLRDAVAALPGFQFGDIAEENLSRSLDEVQLTL

DEKGHGEVTTSSQWQDSHSPLQVVLQASLLESGGRPVTRTVKQPIWPAEALPGIRPQFTLKDVYDYRTDT

TVKQPVVDENSNAAFDIVYADVKGEKKAISGLQVRLIRERRDYYWNWSDSEGWQSQFDQKDLQEGEESLD

LQAGQIGKVSFPVEWGSYRLEVKGPDDVVSSVRFWAGYSWQDNSEGAGAARPDRVTMKLDKPSYKPGDTI

RLHIAAPAAGKGYAMVESSEGPLWWQEIDVPAEGMDLSIPVDKTWNRHDLYLSTLVVRPGDKSRSATPKR

AVGLLHLPLGDENRRLTLALEAPDKMRPNQPLTVKVKASVKEGEAPKQVNVLLSAVDSGVLNITDYATPD

PWNAFFGQKRYGADIYDIYGQVIEGQGRVASLCFGGDGDELKRGGKPPVNHVTIVAQQAQPVVLNDQGEG

TVTLPIGDFNGELRVMAQAWTADDFGSSEDKVVVAAPVIAELNTPRFLASGDTTRLALDLSNLTDKPQTL

QVHLTASGLVTLTDGQLPPVQLAPGARSTLFIPVSALAGFGDGQVNATISGLSLPGETFAPLQKQWKIGV

RPAYPAQTVNSGAVLQPGESWQPPAAQSQGFAPQTLQGQLLLSGKPPLNLARYIRELKAYPYGCLEQTAS

GLFPSLYTSAAQLKALGISGDSDEKRRAAIDVGISRLLQMQLENGGFALWDREGPEEYWLTAYAMDFLVR

ASEQGYSVPVNAINKGNERLLRYLQEPGLMTVRYSDDAQASRFAAQAYAALVLARQQKAPLGALREIWSR

HDQARSGLPLLQLGIALKTMGDAPRGDAALKLAVATPRQDENRWLGDYGSPLRDNALKLALLEENKLLPE

VQNQLLSTLSEEAYGQSWLSTQETNALFLAGRTLADLPGSWQAQTSLQAEPLAGDKAQTRNLDGDRLAAL

QVSNTGSQPLWLRLDSSGYPQSAPQPGGNVLGIERTIFDTQGQQKSLPSLRSGELVLVKLEVTAKRNVPD

ALVVDLLPAGLELENQNLANSSASLQENGDAVQNLLNQMQQADIQHIEFRDDRFVAAVAVNEGQPVTLVY

LARAVTPGTYQVPQPQVESMYAPQWRATGAASGPLTVTP

>lcl|NZ\_FO834906.1\_prot\_WP\_016532527.1\_4131 [gene=sseA] [locus\_tag=BN49\_RS22365] [protein=3-mercaptopyruvate sulfurtransferase] [protein\_id=WP\_016532527.1] [location=4299315..4300172] [gbkey=CDS]

MSTSFFVAADWLAEHIDDPEIQIIDARMAPAGQEALRDMAAEYRAGHVPNALFFDIEALSDHTSPLPHMM

PRAEAFAVAMRELGVCSDKHLVVYDEGNLFSAPRAWWMLRTFGVEKVSILAGGLEGWRRDELPLEQGMPE

VAEGEFDVRFDPQQIKRLTDVLLVSHEGSAQIVDARPAARFNGQADEPRPGLRRGHIPGALNVPWTDLVI

NGELKTVDELNDIFLRQGIDFERPIIASCGSGVTAAVVVLALTTLGVNGVCLYDGSWSEWGARSDLPIEP

APAAP

>lcl|NZ\_FO834906.1\_prot\_WP\_042942911.1\_4132 [locus\_tag=BN49\_RS22370] [protein=hypothetical protein] [protein\_id=WP\_042942911.1] [location=4300399..4301241] [gbkey=CDS]

MALVSNPHSAYSPRLPWLGGIAGLLAGGAILYFWPQWNRTWLSLVPAPVSVYTRFLGVTLEDVPLVTYCH

QALLGFLMVLLAPGYGKSTLAAWMMHNPASSRRWSGEVFRAWVTKFGLLVMVFCNLFFLSRVPSGTLALY

IFILQHISVAAAVASGVLLLRDARRLARTFDAQLADLRLLMILTLGFQTILPAQIALMSARGVNTPLGWY

IVIAQMAGVLLAFMLVGGLVAALRSLLGEERCRAWRGDMALFNGIVTLCVTGFLLYHMVSAYPRIFAALH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913952.1\_4133 [gene=sseB] [locus\_tag=BN49\_RS22375] [protein=enhanced serine sensitivity protein SseB] [protein\_id=WP\_002913952.1] [location=complement(4301312..4302088)] [gbkey=CDS]

MSDTKNELETLLEKAATEPAHRPAFFSALLEATVWVPGRAADGEQIVEDSALDLQHWEKDDGTSVIPFFT

SLEALQQAVADEQAFVMMPARTLMAMTLGESLFLNPKLPSGKEFTPREISHLLGEEGSPLSTQTVLEGGE

ALLLSEVAEPPAQMVDSLTTLFKTLKTVKRAFLCSIKERADAPANLLIGIEAEGDIEAIIQTTGSVATDT

LPGDEPIDICQVVEGEKGISHFMIAHITPFYEKRWGSFLRDFKQNRII

>lcl|NZ\_FO834906.1\_prot\_WP\_016532529.1\_4134 [gene=pepB] [locus\_tag=BN49\_RS22380] [protein=aminopeptidase PepB] [protein\_id=WP\_016532529.1] [location=complement(4302187..4303473)] [gbkey=CDS]

MTEAMKITLSTQPADGRWGEKATWSINNDGIALHLNGKDDLGLIQRAARKIDGMGIKHVALSGEGWNTDR

AWAFWAGYKGPKGQRQVEWPSLDDAQRSELDNRLTIIDWVRDTINAPAEELGPEQLAQRAVDLLCGVAGE

KISYRITKGEDLREQGYLGLHTVGRGSERPPVLLALDYNPTSDKEAPVYACLVGKGITFDSGGYSIKQSA

FMDSMKSDMGGAATITGALAFAITRGLNKRVKLFLCCADNLISGNAFKLGDIIHYRNGKTVEVMNTDAEG

RLVLADGLIDASAQKPELLIDAATLTGAAKTALGNDYHALFSFDDALANRLLASAQAENEAFWRLPLAEF

HRNQLPSNFADLNNTGSAAYPAGASTAAGFLSHFVENYHQGWLHIDCSATYRKSAVEQWSAGATGLGVRT

IANLLTAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913954.1\_4135 [gene=iscX] [locus\_tag=BN49\_RS22385] [protein=Fe-S cluster assembly protein IscX] [protein\_id=WP\_002913954.1] [location=complement(4303544..4303744)] [gbkey=CDS]

MALKWTDSREIGEALYDAYPDLDPKTVRFTDMHQWICDLEEFDDDPNASNEKILEAILLVWLDEAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002913956.1\_4136 [gene=fdx] [locus\_tag=BN49\_RS22390] [protein=ISC system 2Fe-2S type ferredoxin] [protein\_id=WP\_002913956.1] [location=complement(4303746..4304081)] [gbkey=CDS]

MPKIVFLPHQDLCPDGIVVEAETGETILDAALRSGIEIEHACEKSCACTTCHCIVREGFDSLAESSEDED

DMLDKAWGLEPDSRLSCQARVTDEDLVVEIPRYTINHAREH

>lcl|NZ\_FO834906.1\_prot\_WP\_004149343.1\_4137 [gene=hscA] [locus\_tag=BN49\_RS22395] [protein=Fe-S protein assembly chaperone HscA] [protein\_id=WP\_004149343.1] [location=complement(4304083..4305933)] [gbkey=CDS]

MALLQISEPGLSAAPHQRRLAAGIDLGTTNSLVATVRSGQAETLPDHQGRYLLPSVVNYHASGLTVGYDA

RLNAAQDPANTISSVKRMMGRSLADIQNRYPHLPYQLQASENGLPMIQTAGGLLNPIRVSADILKALAAR

ATEALAGELDGVVITVPAYFDDAQRQGTKDAARLAGLHVLRLLNEPTAAAIAYGLDSGQEGVIAVYDLGG

GTFDISILRLSRGVFEVLATGGDSALGGDDFDHLLADYLREQAGFSDRSDNRLQRELLDAAIAAKIALSD

AEAAHVEVGGWQGDITRSQFNDLIAPLVKRTLMACRRALKDAGVEAQEVLEVVMVGGSTRVPLVRERVGE

FFGRTPLTSIDPDKVVAIGAAIQADILVGNKPDSELLLLDVIPLSLGLETMGGLVEKVIPRNTTIPVARA

QEFTTFKDGQTAMSIHVMQGERELVQDCRSLARFALRGIPALPAGGAHIRVTFQVDADGLLSVTAMEKST

GVEASIQVKPSYGLTDGEIATMIKDSMSYAEQDIQARMLAEQKVEAARVLESLTSALAADAALLSAAERQ

AIDAAAEQVRAAAAGDDADAIKEAIKNIDTQTQEFAARRMDQSVRIALKGQSVDEV

>lcl|NZ\_FO834906.1\_prot\_WP\_004174835.1\_4138 [gene=hscB] [locus\_tag=BN49\_RS22400] [protein=co-chaperone HscB] [protein\_id=WP\_004174835.1] [location=complement(4305949..4306464)] [gbkey=CDS]

MDYFTLFGLPASYTLSLEQLAVRYQDLQRQYHPDKFASAPAAEQLAAVQHSATINQAWQTLRHPLTRAEY

LLSLHGFDLASEQHTVRDTAFLMEQLELREELDEIGQAKDDARLEGFIKRVKALFDTRQQLMVDQLHNES

WEAAADTVRKLRFLDKLRSSAEELEEKLLDF

>lcl|NZ\_FO834906.1\_prot\_WP\_002913979.1\_4139 [gene=iscA] [locus\_tag=BN49\_RS22405] [protein=iron-sulfur cluster assembly protein IscA] [protein\_id=WP\_002913979.1] [location=complement(4306539..4306862)] [gbkey=CDS]

MSITLSDSAAARVNAFLANRGKGFGLRLGVRTSGCSGMAYVLEFVDEPAAEDTVFEDKGVKVVIDGKSLQ

FLDGTQLDFVKEGLNEGFKFTNPNVKDECGCGESFNV

>lcl|NZ\_FO834906.1\_prot\_WP\_002913991.1\_4140 [gene=iscU] [locus\_tag=BN49\_RS22410] [protein=Fe-S cluster assembly scaffold IscU] [protein\_id=WP\_002913991.1] [location=complement(4306880..4307266)] [gbkey=CDS]

MAYSEKVIDHYENPRNVGSFDNSDENVGSGMVGAPACGDVMKLQIKVNNEGIIEDARFKTYGCGSAIASS

SLVTEWVKGKSLDEAQAIKNTDIADELELPPVKIHCSILAEDAIKAAIADYKSKREAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002913992.1\_4141 [gene=iscS] [locus\_tag=BN49\_RS22415] [protein=cysteine desulfurase] [protein\_id=WP\_002913992.1] [location=complement(4307293..4308507)] [gbkey=CDS]

MKLPIYLDYSATTPVDPRVAEKMMQFLTMDGTFGNPASRSHRFGWQAEEAVDIARNQIAELVGADPREIV

FTSGATESDNLAIKGAANFYQKKGKHIITSKTEHKAVLDTCRQLEREGFEVTYLAPQSNGIIDLKELEAA

MRDDTILVSIMHVNNEIGVVQDIATIGEMCRARGIIYHVDATQSVGKLPIDLSQLKVDLMSFSGHKIYGP

KGIGALYVRRKPRIRIEAQIHGGGHERGMRSGTLPVHQIVGMGEAYRIAKEEMESEMARLRTLRNRLWNG

VKDMEEVYLNGDLEQGAPNILNVSFNYVEGESLIMALKDLAVSSGSACTSASLEPSYVLRALGMTDELAH

SSIRFSLGRFTTEEEIDYAIDLIRKSIGRLRELSPLWEMFKQGVDLNSIEWSHH

>lcl|NZ\_FO834906.1\_prot\_WP\_002913993.1\_4142 [gene=iscR] [locus\_tag=BN49\_RS22420] [protein=Fe-S cluster assembly transcriptional regulator IscR] [protein\_id=WP\_002913993.1] [location=complement(4308686..4309177)] [gbkey=CDS]

MRLTSKGRYAVTAMLDVALNSETGPVPLADISERQGISLSYLEQLFSRLRKNGLVSSVRGPGGGYLLGKD

AGSIAVGEVISAVDESVDATRCQGKGGCQGGDKCLTHALWRDLSERLTGFLNNITLGELVNNQEILDVSG

RQHQHETQRNARTQDAIDVKLRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002913994.1\_4143 [gene=trmJ] [locus\_tag=BN49\_RS22425] [protein=tRNA (cytosine(32)/uridine(32)-2'-O)-methyltransferase TrmJ] [protein\_id=WP\_002913994.1] [location=complement(4309412..4310146)] [gbkey=CDS]

MLQNIRIVLVETSHTGNMGSVARAMKTMGLTNLWLVNPLVKPDSQAIALAAGASDVIGNAQIVDTLDEAL

AGCSLVVGTSARSRTLPWPMLDPRECGLKSVAEGQHAPVALVFGRERVGLTNDELQKCHYHVAIAANPEY

SSLNLAMAVQVIAYEVRMAWLAAQEQAQPAVEHEEAPYPLVDDLERFYDHLEQTLLATGFIRPNHPGQVM

NKLRRLFTRARPESQELNILRGMLASIEQQNKGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016532534.1\_4144 [gene=suhB] [locus\_tag=BN49\_RS22430] [protein=inositol-1-monophosphatase] [protein\_id=WP\_016532534.1] [location=4310267..4311070] [gbkey=CDS]

MHPMLNIAVRAARKAGNLIAKHYETPDTVETSQKGSNDFVTNVDKTAEAIIIETIRKSYPQHTIITEESG

EHAGEEQDVQWVIDPLDGTTNFVKRLPHFSVSIAVRIKGRTEVAVVYDPMRNELFTATRGQGAQLNGYRL

RGSNARDLDGTIIATGFPFKAKQHATTYMNILGNMFTECADFRRTGSAALDLAYVAAGRVDGYFEIALKP

WDFAAGELIAREAGAIVCDFTGGHNYMLTGNIVAGNPRVVKAMLANMREQLSDALKR

>lcl|NZ\_FO834906.1\_prot\_WP\_016532535.1\_4145 [locus\_tag=BN49\_RS22435] [protein=hypothetical protein] [protein\_id=WP\_016532535.1] [location=complement(4311117..4311953)] [gbkey=CDS]

MAANIVSPAQSGRFYYGCAGAAGLLAGLAIVFWFPALASWWPSDLVRVYHAMPYVMRFGVASVADIPLVA

YATLTLSGFVLAFCHPGHSKLPIVAWAVHNQPSPREMVDWILRSWVLQFGFLVIIFWRFAFMGKLSSDRL

MQIVGIFNDVCYLATLVLAGILLRDGWRDFQGVAAPAGNIRIPLIFALSFYLPFQLVWILLSAQQYELPL

WGWLLLVPAMVGVLLARLTVVGIALCFRGWLGPQGCLRWRGPLALFSGLTVLCIGGNAVIRQILNMIK

>lcl|NZ\_FO834906.1\_prot\_WP\_004185122.1\_4146 [locus\_tag=BN49\_RS22440] [protein=nickel/cobalt transporter] [protein\_id=WP\_004185122.1] [location=complement(4312053..4313033)] [gbkey=CDS]

MSVIFTPRARSSRWKALWPLALLLAVSIIGGIWLWRAWPQVLMQSAVWQRSLNLELSRLLQAVAENPAAA

GLSLLGFSFVYGVLHALGPGHGKIVITTWLATHPAKLKSSIGLTLAASLLQGLVAIALVVVVLALLQLPA

RQLHLSSFWLEKGSYLLVGALGLLLCWRALKKLRLLLRRPTFTAFTPHHVHNEHCGCGHQHLPAPEQLQA

GDDWRARAAIVLSMGMRPCSGAIMVLLFSKVIGVFGWGMAAALAMAAGTSLTITALALLVHGFRQLAIRL

SRHQAPALWKQVSWATLALAGGVILLAAAGVMWLSAVPAGGGIRPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151988.1\_4147 [locus\_tag=BN49\_RS22445] [protein=DUF1007 family protein] [protein\_id=WP\_004151988.1] [location=complement(4313024..4313662)] [gbkey=CDS]

MNRVKQCTSAAFFMVLSWSAAAHPHSFISLQSEPVVKDGLLSAFKMRWTMDEITSSDLLYDAGNAKPGSE

VWKKLAAEVMANVLGQHYFSELWHNGQRVKFDNRPDGYGLERDGLQAVLTFTLPLATPQPIAGQTFTFST

FDPTYYVDMFYDKDSDFSLPAGLRAACKATVMTPKPNDKMLSYAQSLDKADAPPEDMALGSYFAQKVTLT

CQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002914002.1\_4148 [gene=csiE] [locus\_tag=BN49\_RS22450] [protein=stationary phase inducible protein CsiE] [protein\_id=WP\_002914002.1] [location=4313787..4315064] [gbkey=CDS]

MMTVIEPPSALSSPQRRSQVLLMFYLPGQSVTTERLGRINLVDETTARQDIEETGREIQRYHRLTLQSQV

DGSYRIEGAALDQRLCLLHALRRGLRLCPQFVNHHFTPALKTQLKQEGIARTLYDDTNLQALVNRCARAL

NRQFDCRDVQFLRLYLQYCLLEHHRGYSPDFNEEQQRWAQTAAEFTLAQEIVRHWQRRVGAPPHVGEPFF

LSLLFMLLKTPDPVRDGHPHDRRLRLAISGLIHRFQILAGRAFSDEQGLSDQLYIHLSQALIRSVFAIGI

DSTLTEEVTRLYPRLLRTTQAALSEFEEAWHIRFNEEETGLIAVIFGAWLMQKSDLHEKQVLLLTDDNPA

IEEALEQQLRELTLLPLNIKYQSVERFQKEGAPKGVTLIVTPYATALPLFSPPLIHAENYFTERQQQHIC

AMLED

>lcl|NZ\_FO834906.1\_prot\_WP\_004149349.1\_4149 [locus\_tag=BN49\_RS22455] [protein=3-phenylpropionate MFS transporter] [protein\_id=WP\_004149349.1] [location=complement(4315061..4316197)] [gbkey=CDS]

MVLHSTRWLALSYFTYFFSYGIFLPFWSVWLAGNGLTPETIGILLGAGLVARFLGSLLIAPRVSDPSRLI

AALRVLALLTLLFALAFWAGSHVAWLLAIIIGFNLFFSPLVPLTDALANTWQKQITMDYGRVRLWGSIAF

VIGSALTGKLVSLFDYRAILLMLSLGVASMLLGMLLKPSVMPQGESRQQQGAGMAAWLTLVRQSWRFLAC

VCLLQGAHAAYYGFSAIYWQQAGYSASAVGYLWSLGVVAEVVIFALSKKVFRRFSARDLLLLSAVCGLIR

WGLMGWTTALPGLILAQILHCGTFTVCHLAAMRYIAARQGSEVIRLQAVYSAVAMGGSIAIMTVFAGFLY

QHLHQGVFWVMALLTLPAMAIRPKAVAA

>lcl|NZ\_FO834906.1\_prot\_4150 [locus\_tag=BN49\_RS22460] [protein=aldose 1-epimerase] [pseudo=true] [location=complement(4316280..4317109)] [gbkey=CDS]

MAEEWILENAHLRMCVSSLGGKVQSLFSRQYQAPVLYENPAGGMFPMLPLANRVAGNRFIFHGQEIVLPR

HHADEYFFLHGDGWLQRWDIIECGAEYCVLQLRRQRACGFDYLAQLRYQLLRNQLIAELTLTHYGEVPAL

YGCGFHPFFPFDERSKVQFQVSGYWPEGENHLPLNWQGNLPDYANFSVAQFGEDRWLNVGYSGWGGRG\*A

MT\*\*ISQFYRKLRG\*CCSECKVNHSFASSRKAIR\*TPTTWTGSRGCEF\*AREISSIFR\*KSSSRGH

>lcl|NZ\_FO834906.1\_prot\_WP\_002914018.1\_4151 [locus\_tag=BN49\_RS22465] [protein=sugar porter family MFS transporter] [protein\_id=WP\_002914018.1] [location=complement(4317109..4318545)] [gbkey=CDS]

MNNAQTHLKMGYVWTICLVAACGGLLFGYDWVVIGGAKPFYEAWFSITDPAQSGWAMSSALLGCIFGALI

SGWCADKLGRKLPLILSAVLFSASAWGTAVASHFDMFVVYRIVGGVGIGLASALSPLYIAEVSPAEKRGR

FVAVNQLTIVIGVLAAQLINLMIAEPVEPGATQQMIVDSWNGQMGWRWMFGAELVPALAFLVLMFFVPES

PRWLMKAGKPERARAALERIGSADYADRILREIAHTLEKDNNKVSYGALLAPQVKPIVIIGMVLAIFQQW

CGINVIFNYAQEIFASAGFDINSTLKSIVATGVVNLVFTIAALPLVDKIGRRKLMLLGASGLTLIYVLIA

GAYAMGIMGWPVLLLVLAAIAIYALTLAPVTWVLLAEIFPNRVRGLAMSLGTLALWIACFLLTYTFPLLN

AGLGAAGSFLLYGVICAAGYLYILRNVPETKGITLEALEEQLAQRHTGVNAAKQEQMR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043731.1\_4152 [locus\_tag=BN49\_RS22470] [protein=DUF5107 domain-containing protein] [protein\_id=WP\_046043731.1] [location=complement(4318615..4321890)] [gbkey=CDS]

MYGSVKVWQEIISLPTWTTGAEDPNPMFLEKRVYQGSSGSVYPYGVIDTLTGEREMRDYQAVWMENDFLR

VMLLPELGGRIHRAYDKVKQRDFVYYNEVVKPALVGLLGPWISGGIEFNWPQHHRPTTFKPVDFSIQQGE

NGAQTVWMGEAEPMRGLQVMAGFTLYPDRALIEITGKIFNGNATPRHFLWWANPAVKGGDAHQSVFPPDV

TAVFDHGKRDVSAFPIATGTYYKVDYSAGVDISRYKNVPVPTSYMAEKSDYDFVGAYHHDERGGLLHVAD

HHVSPGKKQWSWGYGDFGQAWDRNLTDENGPYIELMTGVFTDNQPDFTWLAPYEEKVFVQNFLPYSELGM

VQNANTQLALKLVRESGQLQLGVYAIAPLNHIVVELSADHQPLYETQLTLKPGESWQQTLPENGVGRLTL

KVKTAENQPLLDYQEHITQQTPLPEPAIAPALPEAIHNGDELYFIGQHLEQYNHASRYAGDYYRRAVELD

PQDYRNNVALGTLAFNSADWALAEQCARAALQRAHRLNKNPRDGEASMLLASVLERMGDDAGAWDHYYKA

SWSGNCRDAAWWSLARLAMKRGDVADALEKVNTSLRFNASNPLAMGLKALALANSGQKKAALEFIFASLE

QYPLSYPLHCARWMIERSDDAREALLRITGRRGVNASLLAGWLLSIGQTSAVKEVLAVLDSQEALPMLWR

ASLSDDANERQQFIAAAEHCHAHNVRFPNSLDEVQMLQSLGDSAFARYLLGCFWYSKRRYDEAVSCWRET

LEKSPDYAPAHRLLGVYSWNKQQDATQALAYLQRAVALEPDNARFLFELDFLQKLLARPVHERLTTLVER

KAVVLKRDDLTAELLSLWNASGHYADAAAILDTRVFHPWEGGEGKITGQYLLNQLHRALQFIERGAFKQA

TDCLKAALRYPDNLGEGRLPGQTDNDIWYLLGYCAEQAGDAQQAAEYYQLARQGGSTLDAGRYYNDQPAD

YLFWQGIALRKSGNPAQAEQHFRHFIDWAAQHRDDVPQVDFFAVSLPDLVVLDVSAQQRHQQHCLFIEAL

GHLRLGNVSACQQRMQQLLQINPAHDKAHLIRHALQSGIFS

>lcl|NZ\_FO834906.1\_prot\_WP\_004214134.1\_4153 [locus\_tag=BN49\_RS22475] [protein=ROK family transcriptional regulator] [protein\_id=WP\_004214134.1] [location=4322003..4323199] [gbkey=CDS]

MQRTGFNNARVRQANKSIFLSHLWREKQLSKSQLSQLTGLSIPAVSNILAELLSEGLIGHSTEHLSKRGV

NSGSYQIPEHGAWTLCMNITPTSIEYQLADARLLAVDGHQHLPVNAPTPQALLEAIVECWRHIHRRYPQH

SINLALGVHGQVDPITGVSQTMPQARWKTPIEIKYLLEERLGVQVRVDNDCVMLALAEKWQHQGTQQDFC

VINVDYGIGSSFVINDHIYRGSLYGSGQIGHTIVNPDGKACDCGRYGCLETVASLSALKKQARMWLKTQP

EATLSPEQLTTASLIEAWKEGDVQIRAWVDNAANAIGLSLYNFLNILNINQIWLYGRSCAFGEQWLESIV

KQTGFNPFDHRDTPRAHATQIGFGQLTRAQQLMGIGYLYVEEQLQTLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002914024.1\_4154 [locus\_tag=BN49\_RS22480] [protein=DoxX family protein] [protein\_id=WP\_002914024.1] [location=4323273..4323695] [gbkey=CDS]

MNTLRYFDFGASRSLLLLIARIAVVILFILFGYPKLLGFDGTVQYMAASGAPMPTLAAIIAVIMEVPAAI

LIVLGFFTRPLAVIFIFYTLGTAVIGHHYWDMTGDAVLPNMINFWKNVSIAGAFLLLAVTGPGAISLDRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914027.1\_4155 [locus\_tag=BN49\_RS22485] [protein=serine hydroxymethyltransferase] [protein\_id=WP\_002914027.1] [location=complement(4323751..4325004)] [gbkey=CDS]

MLKREMNIADYDAELWQAMEQEKVRQEEHIELIASENYTSPRVMQAQGSQLTNKYAEGYPGKRYYGGCEY

VDVVEQLAIDRAKELFGADYANVQPHSGSQANFAVYTALLQPGDTVLGMNLAQGGHLTHGSPVNFSGKLY

NIIPYGIDESGKIDYDDMAKQAQEHKPKMIIGGFSAYSGIVDWAKMREIADSIGAYLFVDMAHVAGLIAA

GVYPNPVPHAHVVTTTTHKTLAGPRGGLILAKGGSEELYKKLNSAVFPSAQGGPLMHVIAAKAVALKEAM

EPEFKVYQQQVAKNAKAMVEVFLNRGYKVVSGGTENHLFLLDLVDKNLTGKEADAALGRANITVNKNSVP

NDPKSPFVTSGIRIGSPAVTRRGFKEAEVKELAGWMCDVLDNINDDAVIERVKGKVLDICARFPVYA

>lcl|NZ\_FO834906.1\_prot\_WP\_004185137.1\_4156 [gene=hmpA] [locus\_tag=BN49\_RS22490] [protein=NO-inducible flavohemoprotein] [protein\_id=WP\_004185137.1] [location=4325330..4326520] [gbkey=CDS]

MLDAQTIATVKATIPLLVETGPKLTAHFYDRMFAHNPELKEIFNMSNQRNGDQREALFNAIAAYASNIDN

LPALLPAVEKIAQKHTSFQIKPEQYNIVGSHLLATLDEMFSPGQEVLDAWGKAYGVLANVFIGREAEIYQ

QNASKTGGWEGTRAFRIVKKTPRSQLITSFELEPVDGQPVADYQPGQYLAIWLKPEGFEYQEIRQYSLTR

KADGKGYRIAVKREEGGQVSSWLHNHASEGDVVYLAAPAGDFFLNVKPQTPVTLLSGGVGQTPMLAMLDA

LAKSGHQGQVNWFHAAENGDVHAFADEVKALGAALPAFTSHVWYRTPTEADRQAGRFDSEGLMDLAAVAD

NIRDPQMQYYLCGPVAFMQFAAKQLVELGVNKDNIHYECFGPHKVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002914032.1\_4157 [gene=glnB] [locus\_tag=BN49\_RS22495] [protein=nitrogen regulatory protein P-II] [protein\_id=WP\_002914032.1] [location=complement(4326595..4326933)] [gbkey=CDS]

MKKIDAIIKPFKLDDVREALAEVGITGMTVTEVKGFGRQKGHTELYRGAEYMVDFLPKVKIEIVVTDDIV

DTCVDTIIRTAQTGKIGDGKIFVFDVARVIRIRTGEEDDAAI

>lcl|NZ\_FO834906.1\_prot\_WP\_004149357.1\_4158 [gene=glrR] [locus\_tag=BN49\_RS22500] [protein=two-component system response regulator GlrR] [protein\_id=WP\_004149357.1] [location=complement(4326999..4328336)] [gbkey=CDS]

MTIRKPARLLLVDDDPGLLKLLGMRLVSEGYSVVTAESGPEALRVLGREKVDLVISDLRMDEMDGLQLFS

EIQKGHPGMPVIILTAHGSIPDAVAATQQGVFSFLTKPVDKDALYKAIDEALEQRSPATDEAWRQAIVTR

SPLMLRLLEQAGMVAQSDVSVLINGQSGTGKEIVAQAIHNASPRHDKPFVAINCGALPEQLLESELFGHA

RGAFTGAVSNREGLFQAAEGGTLFLDEIGDMPVALQVKLLRVLQERKVRPLGSNRDIEINVRIISATHRD

LPKAMARGEFREDLFYRLNVVNLKIPPLSERTEDIPLLANHLLRQSADRHKPFVRAFSSDAMKRLMAAKW

PGNVRQLVNVIEQCVALTSSPVIGDALVEQALEGENTALPTFVEARNQFELNYLRKLLQITKGNVTHAAR

MAGRNRTEFYKLLSRHELDANDFKE

>lcl|NZ\_FO834906.1\_prot\_WP\_002914033.1\_4159 [gene=qseG] [locus\_tag=BN49\_RS22505] [protein=two-component system QseEF-associated lipoprotein QseG] [protein\_id=WP\_002914033.1] [location=complement(4328323..4329009)] [gbkey=CDS]

MSQFLAWRRSLSGWLLSGIACLTLAGCSAGFSPHTAEGTAAPGQAQHQVADFVAVDCADIWAHSSDASDK

NPLYWLRGIDCADRLAPAQARAEAKRHTDDSWQDAFRRGILLADAKITPEERRDLVARLDTFSPQIAVQV

RPLYQLWRDGQTRQLQLVEERARYAKLQQSSDSELETLRQQELALREQLELTTRKLENLTDIERQLSSRK

PGGNFGSEKVPEVIHDDP

>lcl|NZ\_FO834906.1\_prot\_WP\_002914044.1\_4160 [locus\_tag=BN49\_RS22510] [protein=HAMP domain-containing histidine kinase] [protein\_id=WP\_002914044.1] [location=complement(4329039..4330460)] [gbkey=CDS]

MKRLSLFPRSLRQLVTLSFVLILLPLLVLAWQAWQSLNALSAQAAHINRTTLVDARRSEAMINAALEMER

SYRQYCVLDDPTLARVYQNQRQRYSQMLDAHAGVLPDEKLWQALRQDVSDLAQLQCKNSGPDAQAAARLE

VFASNNSDMVQATRAVVYSRGQQLQQEIAERGQFFGWQALVLFLLSLALVLLFTRMIIGPVKGIERMINQ

LGAGKSLDDAALFTGPRELRSVGKRIIWLSERLAWLESQRHQFLRHLSHELKTPLASMREGTELLADRVA

GPLTPEQQEIVEILDSSSRNLQKLIEQLLDYNRKQADGPVAREAVDLVDLVENVVAAHSLPARAKLMHTE

LTLQARRCLAEPALLISVMDNLYSNAVHYGAESGNIRIHSYRHGEQVRIDVANSGEPIPAAEKNMIFEPF

YQGSHQRKGAVKGSGLGLSIARDCVRQMQGELSLVDAPAGQVCFRITLPSAPE

>lcl|NZ\_FO834906.1\_prot\_WP\_023301576.1\_4161 [gene=purL] [locus\_tag=BN49\_RS22515] [protein=phosphoribosylformylglycinamidine synthase] [protein\_id=WP\_023301576.1] [location=complement(4331051..4334938)] [gbkey=CDS]

MMEILRGSPALSAFRINKLLARFQAANLPVSAIYAEYIHFADLNAPLSADDRERLARLLQYGPSLSSHTP

TGKLLLVTPRPGTISPWSSKATDIAHNCGLAQVVRLERGVAYYVEASTLTEAQWAAVAAELHDRMMESVF

DALEAGEKLFAHHQPTPVTSVDLLGEGRQALIDANLRLGLALADDEIDYLQDAFTRLGRNPNDIELYMFA

QANSEHCRHKIFNADWIIDGEQQPKSLFKMIKNTFEKTPDYVLSAYKDNAAVMEGSEVGRYFADHQTGRY

DFHQEPAHILMKVETHNHPTAISPWPGAATGSGGEIRDEGATGRGAKPKAGLVGFSVSNLRIPGFEQPWE

EDFGKPDRIVTALDIMTEGPLGGAAFNNEFGRPALNGYFRTYEEKVTSHNGEELRGYHKPIMLAGGIGNI

RGEHVQKGEITVGAKLIVLGGPAMNIGLGGGAASSMASGQSDADLDFASVQRDNPEMERRCQEVIDRCWQ

LGDANPILFIHDVGAGGLSNAMPELVSDGGRGGKFQLRDILSDEPGMSPLEIWCNESQERYVLAVAPEQL

PLFDELCRRERAPYAVIGEATAEQHLSLSDSHFNDQPIDLPLDVLLGKTPKMTRDVQTLKAQGSALDRQP

IILADAVNRVLHLPTVAEKTFLVTIGDRTVTGMVARDQMVGPWQIPVANCAVTTASLDSYYGEAMAMGER

APVALLDFAASGRLAVGEALTNIAATQIGELNRVKLSANWMAAAGHPGEDAGLYEAVKAVGEELCPALGL

TIPVGKDSMSMKTRWQEGSEQREMTSPLSLVISAFARVEDVRHTVTPQLSTEDNALLLIDLGKGHNALGA

TALAQVYRQLGDKPADVRDVAQLKGFWNAMQALVAQRKLLAYHDRSDGGLLVTLAEMAFTGHCGVEADIA

ALGDDHLAALFNEELGAVIQVRAADREAVEAILAVNGLADCVHYLGKAVEGDRFVLTAGGQTVFSESRTT

LRMWWAETTWQMQRLRDNPACADQEHEAKANDADPGLNVKLSFDINDDVAAPYIATGARPKVAVLREQGV

NSHVEMAAAFHRAGFDAIDVHMSDLLAGRTGLGDFHALVACGGFSYGDVLGAGEGWAKSILFNERVRDEF

ATFFHRPQTLALGVCNGCQMMSNLRELIPGSDLWPRFVRNQSDRFEARFSLVEVTQSPSLLLEGMVGSRM

PIAVSHGEGQVEVRDSAHLAQLESKGLVALRFVDNFGKVTETYPANPNGSPNGITAVTSESGRATIMMPH

PERVFRTVSNSWHPENWGEDSPWMRIFRNARKQLG

>lcl|NZ\_FO834906.1\_prot\_WP\_004144346.1\_4162 [gene=mltF] [locus\_tag=BN49\_RS22520] [protein=membrane-bound lytic murein transglycosylase MltF] [protein\_id=WP\_004144346.1] [location=4335114..4336730] [gbkey=CDS]

MPHIRRQPCVFSGHRLLRNLKLQKINSLKKLKINYLLIGIVTLLLAAALWPSIPWSGKPENRVAGIIARG

ELRISTINSPMTFATMNNKAFGLDYELAKQFADYLGVTLKITVRQNISQLFDDLDDGQADMLAAGLVYNQ

ERVKNYQAGPTYYSVSQQLVYRVGNTRPRTLAALTAEQLTIAPGHVAINDLQTLKAEKYPDLAWRVDEKR

GTTALMQAVIDGKLDYTIADSVAVSLFQRVHPELAVALDITDEQPVTWFSARDDDNSLSAAMLDFFNNIN

EDGTLARLEEKYLGHGNDFDYVDTRTFLRAVENILPEVQPLFEKYAREIDWRLLAAIAWQESHWDPQATS

PTGVRGMMMLTRNTAQSLGLTDRTDAAQSIDGGMRYLQDMMDKVPDSIPKDERIWFALAAYNMGYAHMLD

AMALTRKQKGNPNSWADVKLRLPLLSQKPYYSKLKYGYARGHEAYAYVENIRKYQISLVGYLSEKERQQQ

QTLALAEDYPAVLPNELEQPQETTLPFFKFRADKQMDNARMKLPGHLY

>lcl|NZ\_FO834906.1\_prot\_WP\_023342648.1\_4163 [gene=tadA] [locus\_tag=BN49\_RS22525] [protein=tRNA adenosine(34) deaminase TadA] [protein\_id=WP\_023342648.1] [location=complement(4336727..4337236)] [gbkey=CDS]

MSDLELNDEYWMRHALTLAKRAWEEGEVPVGAVLVHNNQVIGEGWNRPIGRHDPTAHAEIMALRQGGLVL

QNYRLIDATLYVTLEPCVMCAGAMVHSRIARLVFGARDAKTGAAGSLMDVLHHPGMNHRVEISEGVLAES

CSAMLSDFFRWRREEKKAQKKAREQTGES

>lcl|NZ\_FO834906.1\_prot\_WP\_004144348.1\_4164 [gene=yfhb] [locus\_tag=BN49\_RS22530] [protein=phosphatidylglycerophosphatase C] [protein\_id=WP\_004144348.1] [location=complement(4337299..4337910)] [gbkey=CDS]

MFFDLDGTLHQQDMFGSFLRYLLRHLPLNLLLVVPMGPVILAGLAVSGRAARWPMSLLLWATTFGRREAV

LKRLEAEFVGWFRHHVTAFPVVHARLTAYLTSTDADVWLITGSPQSLVEQVYRDTLWLPRVNLIASRTAR

RWGGWVLTLRCLGHEKVVQLEKKIGAPLRLYSGYSDSEQDNPLLGFCQHRWRVTPQGELQQLE

>lcl|NZ\_FO834906.1\_prot\_WP\_032105315.1\_4165 [locus\_tag=BN49\_RS22535] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_032105315.1] [location=4338147..4338995] [gbkey=CDS]

MNCLTRIRQRYPTLAASDKKLADYILSQPDETRHLSSQQLAAEAGVSQSSVVKFAQKLGFKGFPALKLAL

SEALASSPDPHSVPVHNHIRGDDPLRLVGEKLIKDNVAAMHASLDVNTEETLREAVTLLRNARRVIVTGI

GASGLVARNFSWKLMKIGINAVSEQDMHALLATVQAMSSDDLLLAISYSGERREINMAAGEALRVGCKIL

AITGFSPNALQQQATHCLYTIAEEQAMRSAAISSTSAQMMLTDLLFMGLVQQDLERAPERIRHSEALVKK

LV

>lcl|NZ\_FO834906.1\_prot\_WP\_004144350.1\_4166 [locus\_tag=BN49\_RS22540] [protein=YfhL family 4Fe-4S dicluster ferredoxin] [protein\_id=WP\_004144350.1] [location=4339052..4339312] [gbkey=CDS]

MALLITKKCINCDMCEPECPNEAISMGDSIYEINSDRCTECVGHYDTPTCQKVCPIPNTILKDPAHVESE

EQLWDKFVLMHHADKI

>lcl|NZ\_FO834906.1\_prot\_WP\_004144351.1\_4167 [gene=acpS] [locus\_tag=BN49\_RS22545] [protein=holo-ACP synthase] [protein\_id=WP\_004144351.1] [location=complement(4339325..4339705)] [gbkey=CDS]

MAILGLGTDIVEIARIEAVIARSGDRLARRVLSDHEWSIWEQHQQPVRFLAKRFAVKEAAAKALGTGIRN

GLAFNQFEVYNDELGKPKLRLWGEANLLAERMGVSAIHVTLADERHYACATVIVES

>lcl|NZ\_FO834906.1\_prot\_WP\_016532635.1\_4168 [gene=pdxJ] [locus\_tag=BN49\_RS22550] [protein=pyridoxine 5'-phosphate synthase] [protein\_id=WP\_016532635.1] [location=complement(4339705..4340436)] [gbkey=CDS]

MAELLLGVNIDHIATLRNARGTAYPDPVQAAFIAEQAGADGITVHLREDRRHITDRDVRILRQTLHTRMN

LEMAVTEEMLTIACETKPHFCCLVPEKRQEVTTEGGLDVAGQRDKMRDACQRLADAGILVSLFIDADEAQ

IKAATDVGAPYIEIHTGCYADAKTDAEQARELERIAKAATYAASLGLKVNAGHGLTYHNVKAIAALPEMH

ELNIGHAIIGRAVMSGLKEAVAEMKRLMLEARG

>lcl|NZ\_FO834906.1\_prot\_WP\_002914062.1\_4169 [gene=recO] [locus\_tag=BN49\_RS22555] [protein=DNA repair protein RecO] [protein\_id=WP\_002914062.1] [location=complement(4340448..4341185)] [gbkey=CDS]

MDGWQRAFVLHSRPWSETSLMLDVFTEESGRVRLVAKGARSKRSNLKGALQPFTPLLVRFGGRGEVKTLR

SAEAVSLALPLSGITLYSGLYVNELISRVLEHETRFSELFFDYLHCIQALAGASGSPEPALRRFELALLG

HLGYGVDFLHCAGSGEPVDDTMTYRYREEKGFIASLVIDNNTFTGHHLKALASREFPDVDTLRAAKRFTR

IALKPYLGGKPLKSRELFRQFMPARKARADNTNND

>lcl|NZ\_FO834906.1\_prot\_WP\_002914063.1\_4170 [gene=era] [locus\_tag=BN49\_RS22560] [protein=GTPase Era] [protein\_id=WP\_002914063.1] [location=complement(4341197..4342102)] [gbkey=CDS]

MSEEKSYCGFVAIVGRPNVGKSTLLNKLLGQKISITSRKAQTTRHRIVGIHTEGPYQAIYVDTPGLHMEE

KRAINRLMNKAASSSIGDVELVIFVVEGTRWTQDDEMVLNKLRDAKAPVILAVNKVDNVQEKADLLPHLQ

FLASQMNFLDIVPISAETGTNVDTIAAIVRKHLPEAIHHFPEDYITDRSQRFMASEIIREKLMRFLGAEL

PYSVTVEIERFVSNERGGYDINGLILVEREGQKKMVIGNKGAKIKTIGIEARKDMQEMFEAPVHLELWVK

VKSGWADDERALRSLGYVDDL

>lcl|NZ\_FO834906.1\_prot\_WP\_002914065.1\_4171 [gene=rnc] [locus\_tag=BN49\_RS22565] [protein=ribonuclease III] [protein\_id=WP\_002914065.1] [location=complement(4342099..4342779)] [gbkey=CDS]

MNPIVINRLQRKLGYTFHHQELLQQALTHRSASSKHNERLEFLGDSILSFVIANALYHRFPRVDEGDMSR

MRATLVRGNTLAEIAREFELGECLRLGPGELKSGGFRRESILADTVEALIGGVFLDSDIQNVERLILSWY

QTRLDEISPGDKQKDPKTRLQEYLQGRHLPLPSYLVVQVRGEAHDQEFTIHCQVSGLSEPVVGTGSSRRK

AEQAAAEQALKKLELE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532638.1\_4172 [gene=lepB] [locus\_tag=BN49\_RS22575] [protein=signal peptidase I] [protein\_id=WP\_016532638.1] [location=complement(4343029..4344003)] [gbkey=CDS]

MANMFALILVIATLVTGVLWCLDKFIFAPKRRERQAAAQAATGEQLDKKTLKKVGPKPGWLETGASVFPV

LAIVLVVRSFIYEPFQIPSGSMMPTLLIGDFILVEKFAYGIKDPIYQKTLIETGHPKRGDIVVFKYPEDP

RLDYIKRAVGLPGDKVTYDPVAKQVSIQPGCSSGQACGNALPVTYSNVEPSDFVQTFSRSNGGEASSGFW

QLPKGETKADGIRLTERQETLGDVTHRILMVPIAQDQVGMYYHQSGLPLATWIVPPGQYFMMGDNRDNSA

DSRYWGFVPEANLVGKATAIWMSFEKQEGEWPTGVRLSRIGGIH

>lcl|NZ\_FO834906.1\_prot\_WP\_002914069.1\_4173 [gene=lepA] [locus\_tag=BN49\_RS22580] [protein=translation elongation factor 4] [protein\_id=WP\_002914069.1] [location=complement(4344019..4345818)] [gbkey=CDS]

MKNIRNFSIIAHIDHGKSTLSDRIIQICGGLSDREMEAQVLDSMDLERERGITIKAQSVTLDYKASDGET

YQLNFIDTPGHVDFSYEVSRSLAACEGALLVVDAGQGVEAQTLANCYTAMEMDLEVVPVLNKIDLPAADP

ERVADEIEDIVGIDAHDAVRCSAKTGVGVTDVLERLVRDIPPPEGDPDAPLQALIIDSWFDNYLGVVSLV

RIKNGTMRKGDKIKVMSTGQVYNADRLGIFTPKQVDRTELKCGEVGWLVCAIKDILGAPVGDTLTAARNP

ADKALPGFKKVKPQVYAGLFPVSSDDYEAFRDALGKLSLNDASLFYEPESSTALGFGFRCGFLGLLHMEI

IQERLEREYDLDLITTAPTVVYEVETTSKEVIYVDSPSKLPPLNNIQELREPIAECHMLLPQEFLGNVIT

LCVEKRGVQTNMVYHGKQVALTYEIPMAEVVLDFFDRLKSTSRGYASLDYNFKRFQASNMVRVDVLINGE

RVDALALITHNDNAPYRGRELVEKMKDLIPRQQFDIAIQAAIGNHIIARSTVKQLRKNVLAKCYGGDVSR

KKKLLQKQKEGKKRMKQVGNVELPQEAFLAILHVGKDGK

>lcl|NZ\_FO834906.1\_prot\_WP\_004144354.1\_4174 [gene=rseC] [locus\_tag=BN49\_RS22585] [protein=SoxR-reducing system protein RseC] [protein\_id=WP\_004144354.1] [location=complement(4346004..4346483)] [gbkey=CDS]

MIKEWATVVSWHNGVAQVHCDVKASCSSCASRAGCGSRVLNKLGPQTSHTISVPCEQPLAAGQKVELGIA

ESSLLGSAMLVYMAPLAGLFVMASIFQVLFASDIASLCGALLGGVGGFLVARGLSPRLAARQSWQPVILN

VALPPDLLRVDTPSSDMGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002914070.1\_4175 [gene=rseB] [locus\_tag=BN49\_RS22590] [protein=sigma-E factor regulatory protein RseB] [protein\_id=WP\_002914070.1] [location=complement(4346480..4347436)] [gbkey=CDS]

MKQLWCAMSLMAGSLLFSVNASADTSSGALLQQMNLASQSLNYELSFVSISKQGVESLRYRHARLNNQPL

AQLLQLDGPRREVVLRGTEISYFEPGLDPFTLNGDYIVDSLPSLVYSDFKRLSAAYDFISVGRTRIADRL

CDVIRVVARDGTRYSFIAWLDAETKLPLRVDLLDRDGETLEQFRVVSFNVGDNVSASMETLAKANLPPQL

SVPEGGDKANFNWAPTWLPQGVTEVSSSQRRLPTFDGPVESRLYSDGLFSFSININRATAASSDQLLRTG

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>lcl|NZ\_FO834906.1\_prot\_WP\_002914072.1\_4176 [gene=rseA] [locus\_tag=BN49\_RS22595] [protein=anti-sigma-E factor RseA] [protein\_id=WP\_002914072.1] [location=complement(4347436..4348086)] [gbkey=CDS]

MQKEKLSALMDGETLDNELLNELSRSSEMQKTWESYHLIRDTLRGDTAEVLQFDISARVMAAIENEPVRQ

TAPLIPESQPAPHQWRQMPFWNKVRPWASSLTQMGVAACVSLAVIVGVQHYNGQSDSAQQPEAPVFNTLP

MMGKASPVSLGVPADASAGSGQQAQVQEQRRRINAMLQDYELQRRLHAEQLQFGQAQTQQAAVQVPGYQT

LGTQSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002914074.1\_4177 [gene=rpoE] [locus\_tag=BN49\_RS22600] [protein=RNA polymerase sigma factor RpoE] [protein\_id=WP\_002914074.1] [location=complement(4348119..4348694)] [gbkey=CDS]

MSEQLTDQVLVERVQKGDQKAFNLLVVRYQHKVASLVSRYVPPGDIADVVQESFVKAWRALDSFRGDSAF

YTWLYRIAVNTAKNYLVAQGRRPPSSDVDANEAENFESGGALKEISNPENLMLSEELRQIVFRTIESLPE

DLRMAITLRELDGLSYEEIAAIMDCPVGTVRSRIFRAREAIDNKVQPLIRR

>lcl|NZ\_FO834906.1\_prot\_WP\_121980491.1\_4178 [gene=rseD] [locus\_tag=BN49\_RS30595] [protein=rpoE leader peptide RseD] [protein\_id=WP\_121980491.1] [location=complement(4348691..4348786)] [gbkey=CDS]

MHSNSQLAHNADFGWCFEDAWELGLGRHYLG

>lcl|NZ\_FO834906.1\_prot\_WP\_002914076.1\_4179 [gene=nadB] [locus\_tag=BN49\_RS22605] [protein=L-aspartate oxidase] [protein\_id=WP\_002914076.1] [location=4349115..4350734] [gbkey=CDS]

MNTTPDFSCDVLIIGSGAAGLSLALRLAEHSSVTVLSKGPISEGSTFYAQGGIAAVFDETDSIESHVEDT

LIAGAGLCDRHAVTFVASNARSCVQWLIDQGVLFDTQVQANGEESYHLTREGGHSHRRILHAADATGKAV

ETTLVDKALAHPNIRILERSNAVDLIVSDKIGLPGTRRVVGAWIWNRNKERVETCSAKAVVLATGGAAKV

YQYTTNPDVSSGDGIAMAWRAGCRVANLEFNQFHPTALYHPQARNFLLTEALRGEGAHLKRPDGTRFMPD

FDERGELAPRDIVARAIDHEMKRLGVDCMFLDISHKPEAFVRQHFPMIYEKLLGLGIDLTKEPVPVVPAA

HYTCGGVMVDDNGRTDVDGLYAIGEVSYTGLHGANRMASNSLLECLVYGWSAAEDITRRLPLAQKVATLP

AWDESQVEIPDELVVIQHNWHELRLLMWDYVGIVRTTRRLERALRRITMLQQELDEYYARFRVSNNLLEL

RNLVQVAELIVRCAMLRKESRGLHYTLDYPQPLPDSGPSILSPLAHIKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002914079.1\_4180 [locus\_tag=BN49\_RS22610] [protein=tRNA1(Val) (adenine(37)-N6)-methyltransferase] [protein\_id=WP\_002914079.1] [location=complement(4350719..4351456)] [gbkey=CDS]

MSQSKFALPRNGFTFKRFFVAHDRCAMKVGTDGILLGAWAPIAGVKHVLDIGAGSGLLALMLAQRTGDDV

HVEAVELDEEAAAQARENALASPWASRIEVWQADIHQWQPSQTRRYELIISNPPFFAEGVPCATSQREQA

RYTTTLDHASLLTCAAEHITEEGFFCVVLPVDIGNAFIERARAMGWHLRLRTDVAETELRPPHRVLLAFS

PTAGECFSDRLAIRGPEQQYSEGFTALTEDFYLFM

>lcl|NZ\_FO834906.1\_prot\_WP\_002914082.1\_4181 [gene=srmB] [locus\_tag=BN49\_RS22615] [protein=ATP-dependent RNA helicase SrmB] [protein\_id=WP\_002914082.1] [location=4351588..4352919] [gbkey=CDS]

MTVTTFSELELDENLLEALQDKGFTRPTAIQAAAIPPALDGRDILGSAPTGTGKTAAYLLPALQHLLDFP

RKKSGPPRILILTPTRELAMQVADHARELAKHTHLDIATITGGVAYMNHAEVFSENQDIVVATTGRLLQY

IKEENFDCRAVETLILDEADRMLDMGFAQDIETIAGETRWRKQTMLFSATLEGDAIKDFAERLLEEPVEV

SANPSTRERKKIHQWYYRADDIEHKTKLLVNLLQQPEATRAIVFVRKRERVHELANWLREAGINTCWLEG

EMVQAKRNEAIKRLTDGRVNVLIATDVAARGIDIPDVSHVFNFDMPRTADTYLHRIGRTGRAGKKGTAIS

LVEAHDHLLLGKIGRYIEEPLKARVIDELRPTTRAPSEKLTGKPSKKVLAKRAQKKKDEKEKPRVKKRHR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002914084.1\_4182 [gene=grcA] [locus\_tag=BN49\_RS22620] [protein=autonomous glycyl radical cofactor GrcA] [protein\_id=WP\_002914084.1] [location=complement(4352965..4353348)] [gbkey=CDS]

MITGIQITKAANDDLLNSFWLLDSEKGEARCLCAKGGFAEDDVVAVSKLGEIEYREIPVDVKPEVRVEGG

QHLNVNVLRRETLLDAVEHPEKYPQLTIRVSGYAVRFNSLTPEQQRDVIARTFTESL

>lcl|NZ\_FO834906.1\_prot\_WP\_002914088.1\_4183 [gene=ung] [locus\_tag=BN49\_RS22625] [protein=uracil-DNA glycosylase] [protein\_id=WP\_002914088.1] [location=4353661..4354350] [gbkey=CDS]

MTTPLTWHDVLADEKQQPYFLNTLKTVAEERQSGITIYPPQKDVFNAFRFTELGDVKVVILGQDPYHGPG

QAHGLAFSVRPGVAIPPSLLNMYKELEATIPGFTRPTHGYLESWARQGVLLLNTVLTVRAGQAHSHASLG

WETFTDKVIALINEHCEGVVFLLWGSHAQKKGAIIDRQRHCVLKAPHPSPLSAHRGFFGCNHFVQTNQWL

VDRGETPIDWMPVLPAESE

>lcl|NZ\_FO834906.1\_prot\_WP\_002914089.1\_4184 [locus\_tag=BN49\_RS22630] [protein=tRNA/rRNA methyltransferase] [protein\_id=WP\_002914089.1] [location=complement(4354409..4355494)] [gbkey=CDS]

MSDELKNKSGKVKVMYVRSDDDSDKRTHNPRTGKGGGRPGKSRVDGRSRPARDERNSRGDDRKRDDRKRD

DRKRDDFHRDDASPWRTVSRAPGDETPVKEDHGGISGKSFIDPEVLRRQRAEETRVYGENACQALFQSRP

EAIVRAWFIQSVTPRFKEALRWMAANRKAYHVVDEAELAKASGTEHHGGVCFLIKKRHGTSVAQWVAKAG

EEDCVLALEDVGNPHNLGAIMRSCAHFGVKGVVVQDAGVLESGAAIRTAEGGAEHVEPITGDSFIDTLDQ

FRKAGYAIVSTSSHNGTPLFKAELPKKMVLALGQERDGLSDAAISSADLSVAIDGTGNVESLNVSVATGV

LLAEWWRQNKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529941.1\_4185 [gene=trxC] [locus\_tag=BN49\_RS22635] [protein=thioredoxin TrxC] [protein\_id=WP\_016529941.1] [location=4355698..4356123] [gbkey=CDS]

MNTVCASCQALNRLPDDRSADGAKCGRCGHDLFDGDVINATGATLDKLLKDDLPVVVDFWAPWCGPCRSF

APILEDVAEERSGKMRFVKVNTEAERELSARFRIRSIPTIMMFKNGEVIDMLNGAVPKAPFDSWLNEAGQ

Q

>lcl|NZ\_FO834906.1\_prot\_WP\_002914092.1\_4186 [gene=tapT] [locus\_tag=BN49\_RS22640] [protein=tRNA-uridine aminocarboxypropyltransferase] [protein\_id=WP\_002914092.1] [location=4356193..4356891] [gbkey=CDS]

MTDNAVLRLRAERLARATRPFLARGNRIRRCQRCLLPLKQCLCATLTSAQAASRFCLVMFDTEPMKPSNT

GRLIADILPDTEAFQWSRTEPPQALLDLVAHPDYQPMVVFPASYAGPDRQVLSAPPSGKPPLFIMLDGTW

TEARKMFRKSPYLDALPIISVDLSRISAYHLREAHADGQYCTAEVAIALLDLAGDAPAAAALGEHFTRFR

TRYLAGKTQHKGSITAGQVENV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529940.1\_4187 [gene=pat] [locus\_tag=BN49\_RS22645] [protein=protein lysine acetyltransferase] [protein\_id=WP\_016529940.1] [location=4356926..4359583] [gbkey=CDS]

MSQRGLEALLRPKSIAVIGASMKPQRAGYLMMRNLLAGGFNGPVMPVTPAWKAVLGVLAWPTIESLPFTP

DLAVLCTNARRNLELLEALGQKGCKTCIILSSQPEQYPALLECAARYQMRLLGPNSLGLLAPWQGLNASF

SPVPIHRGKLAFISQSAAVSNTILDWAQQREMGFSYFIALGDSLDIDVDDLLDFLARDSKTSAILLYLEH

LSDARRFVSAARSASRNKPILVIKSGRSPAAQKLLHVNSGMDPAWDAAIQRAGLLRVQDTHELFSAVETL

SHMRPLRGEKLMIVSNGAAPAALALALDELWLRNGKLATLSEETRDALRQALPVGVEIANPLDLRDDASS

EHYQRAVNVLLNSQDYDALLVIHSPSAAAPGTESALALIDALKHHPRGKYVTVLTNWCGEFSSQEARRLF

SDAGLPTYRTPEGTITAFMHMVEYRRNQKQLRETPVLPDSLTANTSEAHALLQQAIDDGATTLDTHEVSP

VLRAYGIHTLPTWIAADSAEAVHIAEQIGYPVALKLRSPDIPHKSEVQGVMLYLRTAAEVQQAADAMIDR

VKLAWPQARIHGLLVQSMANRAGAQELRVVVEHDPVFGPLIMLGEGGVEWRAEDQAAVALPPLNMNLARY

LVIQAIKNKKIRGRSALRPLDIAGLSQLLVQVSNLIVDCPEIQRLDIHPLLASGNEFTALDVTLGLAPFS

GDSESRLAIRPYPHQLEEWVVMKNGDRCLFRPILPEDEPQLLAFIAQVTKEDLYYRYFSEINEFTHDDLA

NMTQIDYDREMAFVAVRTSAEKSEILGVTRAISDPDNIDAEFAVLVRSDLKGLGLGRRLLEKLIAYTQSH

GLQRLNGITMPNNRGMIGLARKLGFTVDIQLEDGIVSLSLPLNQG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529939.1\_4188 [gene=pssA] [locus\_tag=BN49\_RS22650] [protein=CDP-diacylglycerol--serine O-phosphatidyltransferase] [protein\_id=WP\_016529939.1] [location=4359704..4361059] [gbkey=CDS]

MLSKFKRNKHQQHLAQLPKLSQSVDDLEFFYAPAEFREALLTRIAHATQRICIIALYLEQDDGGKGILQA

LYDAKRQRPELDVRVLVDWHRAQRGRIGAAASNTNADWYCRMANENPGVDIPVYGVPINTREALGVLHFK

GFIIDDCVLYSGASLNDVYLHQHDKYRYDRYQCIRNGKMADIMFDWVDNNLVQGRGVNRLDRPDRPKSPE

IKNDIRQYRQELRDRSYHFVGTAGDEELSVTPLVGLGKSSLLNKTIFHLMPCAEHKLTICTPYFNLPAVL

VRNIIQLLRDGKQVEIIVGDKTANDFYIPEDQPFKIIGALPYLYEINLRRFLSRLQYYVNTDQLIVRLWK

DDDNSYHLKGMWVDDEWMLLTGNNLNPRAWRLDLENAILIHDPKRQLGAMREKELKLIRTHTTVVKHYRD

LQSIADYPVKVRKLIRRLRRIRIDRLISRIL

>lcl|NZ\_FO834906.1\_prot\_WP\_004899914.1\_4189 [locus\_tag=BN49\_RS22655] [protein=YfiM family lipoprotein] [protein\_id=WP\_004899914.1] [location=4361101..4361424] [gbkey=CDS]

MRTILVIASLLLTGCSHMANDAWSGQDKAQHFLASAMLSAAGNEYAQYQGYSRDRSAAIGLMFSVSLGAS

KELWDSRPAGSGWSWKDFAWDVAGATTGYAVWQLAHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043736.1\_4190 [locus\_tag=BN49\_RS22660] [protein=MFS transporter] [protein\_id=WP\_046043736.1] [location=complement(4361428..4362726)] [gbkey=CDS]

MTESSITERGAPELADTRRRIWAIVGASSGNLVEWFDFYVYSFCSLYFAHIFFPSGNTTTQLLQTAGVFA

AGFLMRPIGGWLFGRIADRRGRKTSMLISVCMMCFGSLVIACLPGYAVIGTWAPALLLLARLFQGLSVGG

EYGTSATYMSEVAVEGKKGFYASFQYVTLIGGQLLAVLVVVALQQVLSDEDLHAWGWRIPFALGAVLAIV

ALWLRRQLDETSKQETRALKEAGSFKGLWRNRRAFAMVLGFTAAGSLTFYTFTTYMQKYLVNTAGMTAST

SSVIMTAALFVYMLVQPLFGAFSDKVGRRTSMLCFGVLATLFTVPILSALQKVSSPYAAFGLVICALLIV

SFYTSISGILKAEMFPAQVRALGVGLSYAVANALFGGSAEYVALSLKSAGIEHAFYWYVTVMAAIAFLVS

LMLHRKGKGLRL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043738.1\_4191 [gene=gmhB] [locus\_tag=BN49\_RS22695] [protein=D-glycero-beta-D-manno-heptose 1,7-bisphosphate 7-phosphatase] [protein\_id=WP\_046043738.1] [location=complement(4368702..4369268)] [gbkey=CDS]

MAKSVPAIFLDRDGTINVDHGYVHEIDNFEFIDGVIDAMRELKEMGYALVLVTNQSGIARGKFTEAQFET

LTEWMDWSLADRGVDLDGIYYCPHHPQGAVEEYRQSCDCRKPHPGMLISARDYLHIDMAASYMVGDKLED

MQAAAAADVGTKVLVRTGKPLTEEAEKAADWVLNSLAELPAAIKKQQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002889450.1\_4192 [gene=metN] [locus\_tag=BN49\_RS22700] [protein=methionine ABC transporter ATP-binding protein MetN] [protein\_id=WP\_002889450.1] [location=4369457..4370488] [gbkey=CDS]

MIKLSNITKVFQQGNRSIQALNNVSLHVPAGQIYGVIGASGAGKSTLIRCVNLLERPTEGSVQVDGQELT

ALSEKELTRARRQIGMIFQHFNLLASRTVFGNVALPLELDNTPQAEIKRRVTELLDLVGLGDKHDSYPAN

LSGGQKQRVAIARALASNPKVLLCDEATSALDPATTRSILELLKDINRRLGLTILLITHEMDVVKRICDC

VAVISNGQLIEQDTVSEVFSHPKTPLAQQFIQSTLHLDIPDDYQARLKPTATADSVPMLRMEFTGHSVDA

PLLSETARRFNVNNNIISAQMDYAGGVKFGIMLTEMHGTQEDTQAAIAWLQEHHVKVEVLGYV

>lcl|NZ\_FO834906.1\_prot\_WP\_002889448.1\_4193 [locus\_tag=BN49\_RS22705] [protein=methionine ABC transporter permease MetI] [protein\_id=WP\_002889448.1] [location=4370481..4371134] [gbkey=CDS]

MSEAMMWLLLRGVWETLAMTFVSGFFGFVLGLPVGVLLYVTRPGQIVANAKLYRTLSALVNIFRSIPFII

LLVWMIPFTRVIVGTSIGLQAAIVPLTVGAAPFIARMVENALLEIPTGLIEASRAMGATPLQIVRKVLLP

EALPGLVNAATITLITLVGYSAMGGAVGAGGLGQIGYQYGYIGYNATVMNTVLVLLVVLVYLIQFSGDRI

VRAVTHK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531975.1\_4194 [gene=metQ] [locus\_tag=BN49\_RS22710] [protein=methionine ABC transporter substrate-binding lipoprotein MetQ] [protein\_id=WP\_016531975.1] [location=4371178..4371993] [gbkey=CDS]

MAFNFKTFAAVGALIGSLALVGCGQDEKDPNHIKVGVIVGAEQQVAEVAQKVAKEKYGLDVELVTFNDYV

LPNEALSKGDIDVNAFQHKPYLDQQIKDRGYKLVAVGNTFVYPIAGYSKKIKSLDELQSGSQIAVPNDPT

NLGRSLLLLQQVGLIKLKDGVGLLPTSLDIVENPKNLKIVELEAPQLPRSLDDAQIALAVINTTYASQIG

LTPAKDGIFVEGKESPYVNLIVAREDNKDAENVKKFVQAYQSDEVYEAANKIFNGGAVKGW

>lcl|NZ\_FO834906.1\_prot\_WP\_002889443.1\_4195 [gene=rcsF] [locus\_tag=BN49\_RS22715] [protein=Rcs stress response system protein RcsF] [protein\_id=WP\_002889443.1] [location=4372101..4372508] [gbkey=CDS]

MRALPICLLALMLSGCSMLSRSPVEPAQSTATPPVKSEPSKPRATRPAPVRIYTDASELVGKPFRDLGEV

SGESCQASNQDSPPNIPTARKRLQINAARMKANAVLLHRCEVTSGTPGCYRQAVCLGSALNVSAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002889441.1\_4196 [gene=tsaA] [locus\_tag=BN49\_RS22720] [protein=tRNA (N6-threonylcarbamoyladenosine(37)-N6)-methyltransferase TrmO] [protein\_id=WP\_002889441.1] [location=4372505..4373212] [gbkey=CDS]

MSAFQFAQIGVIRSPYKEKFAVPRQPGLVKHGGGELHLVAPYNQADAVRGLESFSHLWILFVFHQTMEGG

WRPTVRPPRLGGNARMGVFATRSTFRPNPIGMSLVELKGIRCQKDQVILELGSLDLVDGTPVVDIKPYLP

FAEALPDASASYAQQAPLAGMNVSFTPEIDAQLLTLEKRYPHIKAFIREVLAQDPRPAYRKEEQAGKTYA

VWLLDFNVRWRVTASGFEVFALEAR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530170.1\_4197 [gene=proS] [locus\_tag=BN49\_RS22725] [protein=proline--tRNA ligase] [protein\_id=WP\_016530170.1] [location=4373324..4375042] [gbkey=CDS]

MRTSQYLLSTLKETPADAEVISHQLMLRAGMIRKLASGLYTWLPTGVRVLKKVENIVREEMNNAGAIEVL

MPVVQPSELWQESGRWEQYGPELLRIADRGDRPFVLGPTHEEVITDLIRNELNSYKQLPLNFYQIQTKFR

DEVRPRFGVMRSREFLMKDAYSFHTSQESLQETYDAMYAAYSKIFSRMGLDFRAVQADTGSIGGSASHEF

QVLAQSGEDDVIFSDSSDYAANIEFAEAVAPKEPRAAATQEMTLVDTPNAKTIAELVEQFNLPIEKTVKT

LLVKAVEDSASPLVALLVRGDHELNEVKAEKLPQVASPLTFATEEEIRALVNAGPGSLGPVNMPVPVIID

RTVAVMSDFAAGANIDGKHYFGINWDRDVATPEVADIRNVVAGDPSPDGKGTLLIKRGIEVGHIFQLGTK

YSEAMKAAVQGEDGRNQILTMGCYGIGVTRVVAAAIEQNFDDRGIVWPDAIAPFQVAILPMNMHKSYRVQ

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DIVEFLVKAIKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004212714.1\_4198 [locus\_tag=BN49\_RS22730] [protein=YaeF family permuted papain-like enzyme] [protein\_id=WP\_004212714.1] [location=4375101..4375943] [gbkey=CDS]

MTAHLLRSGLLTFALLLLTACTLDVGRSSPSTSAADDHSSSWAVTLQRQSSIAGSGLREIAESDLRSGDL

LFSSSLGVTSLGIRAFSASSVSHVALYVGEGQVAEATGAGVQVITLQQALAHSDKLFALRVPDLTPDQAT

AMKSFAWQVKDSGYNYRGIIQFIPYMVTKPLCSLNPFSRDFRQQCVSGLAKAQLGDAASGDKKAWFCSEF

VSEAFVRAGHPLTLAQAAWISPSDLLHMREGDVATFKPETQLQYVGHLKLGVYLQAGKLVGLNKPKDGAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002889435.1\_4199 [gene=nlpE] [locus\_tag=BN49\_RS22735] [protein=envelope stress response activation lipoprotein NlpE] [protein\_id=WP\_002889435.1] [location=complement(4376075..4376773)] [gbkey=CDS]

MKKIVFSVIAACSLFALFGCNHRAETDTVQPAAMEELKPMQQSWRGVLPCADCEGIDTSLFLEKDGTWVM

NEHYQGARREPSSFASYGTWARTADKLVLTNSKGEKSYFRAKGDKLEMLDRNGSPIQSPLNYTLEPVKAS

LPTTPMAMRGMYFYMADAATFTDCATGKRVAVANNAQLERDYAAARGTDTRPVLLVVEGHFTLEANPDTG

EMMKTLMTDQAGKFIPGKDCSH

>lcl|NZ\_FO834906.1\_prot\_WP\_002889433.1\_4200 [gene=arfB] [locus\_tag=BN49\_RS22740] [protein=aminoacyl-tRNA hydrolase] [protein\_id=WP\_002889433.1] [location=complement(4376816..4377229)] [gbkey=CDS]

MITISRSVALADDEIVLSGIRAQGAGGQHVNKASTAIHLRFDIKASSLPEFYKERLLAASHHLISADGVV

IIKAQEYRSQEMNREAAIARLVALIKELTAVQKSRRETRPTRASKERRLASKAQKSSVKALRGKVRQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002889431.1\_4201 [locus\_tag=BN49\_RS22745] [protein=YaeQ family protein] [protein\_id=WP\_002889431.1] [location=complement(4377226..4377771)] [gbkey=CDS]

MALKATIYKAAVNVADLDRNQFLDANLTLAQHPSETQERMMLRLLAWIKYADERLQFTRGLSSDDEPELW

LLNDHLGVDLWIELGLPDERRIKKACSRAQAVALFAYNSRAAEIWWQQNQSKLAAYPKLTIWYLDDAQLA

LLSAFADRTMTLQATLQEGSIWLSDARNNLEIQLTAWQASA

>lcl|NZ\_FO834906.1\_prot\_WP\_002889429.1\_4202 [locus\_tag=BN49\_RS22750] [protein=YaeP family protein] [protein\_id=WP\_002889429.1] [location=4377968..4378168] [gbkey=CDS]

MDHYCELIRKRYAEIASGDLGYIPDALGCVLKVLNEIAADEALSESVREKAAYAAANLLVSDYVNE

>lcl|NZ\_FO834906.1\_prot\_WP\_002889424.1\_4203 [gene=rof] [locus\_tag=BN49\_RS22755] [protein=Rho-binding antiterminator] [protein\_id=WP\_002889424.1] [location=4378155..4378415] [gbkey=CDS]

MSMNDTYQPINCDDYDNLELACQHHLVLTLALKDGEQLQAKASDLISRKNIEYLVVELAGNVRELRLDKI

ASFSHPEIGTVVVSES

>lcl|NZ\_FO834906.1\_prot\_WP\_046043741.1\_4204 [gene=tilS] [locus\_tag=BN49\_RS22760] [protein=tRNA lysidine(34) synthetase TilS] [protein\_id=WP\_046043741.1] [location=complement(4378429..4379742)] [gbkey=CDS]

MFVDMTADIAHTLHPHRQLLVAFSGGLDSTVLLHQLVLLREQDPSLTLRAVHVNHGLSAHADDWVAHCRQ

ICQQWQVPLVVHHVTLARGGLGVEAHARAARYQAFQDTLNAGEVLVTAQHQDDQCETLLLALKRGSGPTG

LSAMAPSSVFAGSRLLRPLLNETRESLRQWALAHQLSWIEDESNQDDTYDRNFLRLRVIPVLRERWPHFS

EAVARSASLCAEQEQLLDEMLAAELASLVAEDGSLAIAPLASMSPPRRAALLRRWLAGQQAPMPAREVPE

RLWHEVALAREDASPCLRLGEFTVRRFQQRLYWVKYLPGQTDSVQRWPDWRQPLRLADGLGELTLQPGGR

LRPPSADEPVTVRFRASGHLHIVGRHGGRKLKKLWQELGVAPWRRDTTPLLFYGETPIAAADDLFVTTEG

EVKDGEGVRLMWRKTGD

>lcl|NZ\_FO834906.1\_prot\_WP\_002889387.1\_4205 [locus\_tag=BN49\_RS22765] [protein=VOC family protein] [protein\_id=WP\_002889387.1] [location=complement(4379796..4380185)] [gbkey=CDS]

MLGLKRVHHIAIIATDYARSKAFYCDILGFTLQSEFYRAERDSWKGDLALNGEYVIELFSFPFPPARPSR

PEACGLRHLAFSVDDIDAAVAHLTAHGVECEAIRVDPFTGKRFTFFSDPDDLPLEIYQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002889384.1\_4206 [locus\_tag=BN49\_RS22770] [protein=lysine decarboxylase LdcC] [protein\_id=WP\_002889384.1] [location=complement(4380232..4382385)] [gbkey=CDS]

MNIIAIMGPHGVYHKDEPIKELEAALQRQGFQTIWPQNSADLLQFIEHNPRICGVIFDWDEYSVDLCSDI

NQLNEYLPLYAFINAHSTMDVSSQDLRMTLWFFEYALGLSEEIATRIGQYTREYLENITPPFTRALFNYV

QEGKYTFCTPGHMGGSAYQKSPVGCLFYDFFGGNTLKADVSISVTELGSLLDHTGPHLEAEEYIARAFGA

EQSYMVTNGTSTSNKIVGMYSAPAGSTLLIDRNCHKSLAHLLMMSDVVPLWLKPTRNALGILGGIPRREF

TRDSIQQKVRDTGGAQWPVHAVITNSTYDGLLYNTTWLKETLDVPSIHFDSAWVPYTHFHPIYQGKSGMS

GERIPGKVIFETQSTHKMLAALSQASLIHIKGNYDEETFNEAFMMHTSTSPSYPIVASIETAAAMLRGNS

GKRLIQRSIERALDFRKEVQRLREESDGWFFDIWQPEAVDKAECWPVAPGEDWHGFKDADADHMYLDPVK

VTILTPGMDEQGNMDEEGIPAALVAKFLDERGVVVEKTGPYNLLFLFSIGIDKTRAMGLLRGLTEFKRAY

DLNLRVKNMLPDLYAEDPDFYRNMRIQDLAQGIHRLIRQHQLPQLMLSAFDVLPEMKMTPHHAWQRQIKG

EVETIELENLVGRISANMILPYPPGVPLLMPGEMITEESRAVLDFLLMLCSIGRHYPGFETDIHGAKRDE

DGVYRVRVLKNDERLAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145855.1\_4207 [gene=accA] [locus\_tag=BN49\_RS22775] [protein=acetyl-CoA carboxylase carboxyl transferase subunit alpha] [protein\_id=WP\_004145855.1] [location=complement(4382499..4383458)] [gbkey=CDS]

MSLNFLDFEQPIAELEAKIDSLTAVSRQDEKLDINIDEEVHRLREKSVELTRKIFADLGAWQVAQLARHP

RRPYTLDYVRLAFDEFDELAGDRAFADDKAIVGGIARLDGRPVMIIGHQKGRETKEKIRRNFGMPAPEGY

RKALRLMEMAERFKMPIITFIDTPGAYPGVGAEERGQSEAIARNLREMSRLSVPVICTVIGEGGSGGALA

IGVGDKVNMLQYSTYSVISPEGCASILWKSADKAPLAAEAMGIIAPRLKELKLIDSIVPEPLGGAHRNPE

AMAASLKAQLLADLADLDLLSEEELLNRRYQRLMSYGYA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529375.1\_4208 [gene=dnaE] [locus\_tag=BN49\_RS22780] [protein=DNA polymerase III subunit alpha] [protein\_id=WP\_016529375.1] [location=complement(4383471..4386953)] [gbkey=CDS]

MAEPRFVHLRVHSDYSMIDGLAKTGPLVKKAASLGMPALAITDFTNLCGLVKFYGTGHGAGIKPIVGADF

HVQCDLLGDEFTELTVLAANNTGYQNLTLLISRAYQRGYGALGPWIDRDWLVEHQEGLILLSGGRKGDVG

VSLIRGNMPLVEQCVAFYEEHFPDRYFLELIRTGRQDEEAYLHAAVALAEARGLPVVATNDVRFLDTSDF

DAHEIRVAIHDGFTLDDPKRPRNYSPQQYMRSEEEMCELFADIPEALANSVEIAKRCNVTVRLGEYFLPQ

FPTGDMTTEDFLVMKSKEGLEERLAFLFPDPEERAKRRPEYDERLDIELQVINQMGFPGYFLIVMEFIQW

SKDNGVPVGPGRGSGAGSLVAYALKITDLDPLEFDLLFERFLNPERVSMPDFDVDFCMEKRDQVIEHVAD

MYGRDAVSQIITFGTMAAKAVIRDVGRVLGHPYGFVDRISKLVPPDPGMTLAKAFEAEPQLPEIYEADEE

VKALIDMARKLEGVTRNAGKHAGGVVIAPTKITDFAPLYCDEQGLHPVTQFDKNDVEYAGLVKFDFLGLR

TLTIINWALEMINKRREKNGEGPLDIAAIPLDDKKSFDMLQRSETTAVFQLESRGMKDLIKRLQPDCFED

MIALVALFRPGPLQSGMVDNFIDRKHGREEISYPDVQWQHESLKPVLEPTYGIILYQEQVMQIAQVLSGY

TLGGADMLRRAMGKKKPEEMAKQRSIFEDGAKKNGIDGELAMKIFDLVEKFAGYGFNKSHSAAYALVSYQ

TLWLKVHYPAEFMAAVMTADMDNTEKVVGLVDECWRMGLKILPPDINSGLYHFHVNDDGEIVYGIGAIKG

VGEGPIEAIIEARNNGGYFRELFDLCARTDIKKLNRRVLEKLIMSGAFDRLGPHRAALMNSLGDALKAAD

QHAKAEAIGQADMFGVLAEEPEQIEQSYASCQPWPEQVVLDGERETLGLYLTGHPINQYLKEIERYVGGV

RLKDMHPTERGKVTTAAGLVIAARVMVTKRGNRIGICTLDDRSGRLEVMLFTDALDKYQQLLEKDRILIV

SGQVSFDDFSGGLKMTAREVMDIDEAREKYARGLAISLTDRQIDDQLLNRLRQSLEPHRSGTIPVHLYYQ

RADARARLRFGATWRVSPSDRLLNDLRGLIGSEQVELEFD

>lcl|NZ\_FO834906.1\_prot\_WP\_002889376.1\_4209 [gene=rnhB] [locus\_tag=BN49\_RS22785] [protein=ribonuclease HII] [protein\_id=WP\_002889376.1] [location=complement(4386971..4387570)] [gbkey=CDS]

MMEFVYPHTHLVAGVDEVGRGPLVGAVVTAAVILDPAKPIVGLNDSKKLSEKRRLALFDEIKEKALCWSL

GRAEPHEIDELNILHATMLAMQRAVAGLSIVPEFVLIDGNRCPSLPMPSQAVVKGDSRVAEISAASILAK

VTRDAEMATLDLAFPHYGFAQHKGYPTAVHLQKLQEHGATEHHRRSFGPVKRALGLASN

>lcl|NZ\_FO834906.1\_prot\_WP\_002889374.1\_4210 [gene=lpxB] [locus\_tag=BN49\_RS22790] [protein=lipid-A-disaccharide synthase] [protein\_id=WP\_002889374.1] [location=complement(4387567..4388718)] [gbkey=CDS]

MAEQRPLTIALVAGETSGDILGAGLIRALKARIPNARFVGVAGPLMQAEGCEAWYEMEELAVMGIVEVLG

RLRRLLHIRADLTRRFGELRPDVFVGIDAPDFNITLEGNLKKQGIKTIHYVSPSVWAWRQKRVFKIGRST

DLVLAFLPFEKAFYDKFNVPCRFIGHTMADAMPLDPDKGAARDRLGIPHSVRCLALLPGSRGAEVEMLSA

DFLKTAQLLRATYPDLQVVVPLVNAKRREQFERIKAETAPDMIVHMLDGQARDAMIASDAALLASGTAAL

ECMLAKCPMVVGYRMKPFTFWLAKRLVKTDYVSLPNLLAGRELVKELLQDECEPQALAAALQPLLADGKT

SHEMHETFRALHQQIRCNADEQAADAVLELAKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004178647.1\_4211 [gene=lpxA] [locus\_tag=BN49\_RS22795] [protein=acyl-ACP--UDP-N-acetylglucosamine O-acyltransferase] [protein\_id=WP\_004178647.1] [location=complement(4388718..4389506)] [gbkey=CDS]

MIDKTAFVHPTAIVEEGAVIGANVHIGPFCIVGANVEIGEGTVLKSHVVVNGHTKIGRDNEIYQFASIGE

VNQDLKYAGEPTRVEIGDRNRIRESVTIHRGTVQGGGLTKVGNDNLLMINAHVAHDCTLGDRCILANNAT

LAGHVSLDDYVIIGGMTAVHQFCVIGSHVMVGGCSGVAQDVPPFVIAQGNHATPFGVNIEGLKRRGFSRE

AITAIRNAYKLLYRSGKTLEEAKPEIAELAAQHPEVQPFVDFFARSTRGLIR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145858.1\_4212 [gene=fabZ] [locus\_tag=BN49\_RS22800] [protein=3-hydroxyacyl-ACP dehydratase FabZ] [protein\_id=WP\_004145858.1] [location=complement(4389510..4389965)] [gbkey=CDS]

MTTDTHTLHIEEILELLPHRYPFLLVDRVLDFEEGRFLRAVKNVSVNEPFFQGHFPGKPILPGVLILEAM

AQATGILAFKSVGKLEPGELYYFAGIDEARFKRPVVPGDQMIMEVTFEKTRRGLTRFKGVALVDGKVVCE

ATMMCARSREA

>lcl|NZ\_FO834906.1\_prot\_WP\_004204453.1\_4213 [gene=lpxD] [locus\_tag=BN49\_RS22805] [protein=UDP-3-O-(3-hydroxymyristoyl)glucosamine N-acyltransferase] [protein\_id=WP\_004204453.1] [location=complement(4390071..4391096)] [gbkey=CDS]

MPSIRLADLAQQLDAELHGDGDIVITGVASMQSAKTGQITFMVNPKYREHLAACQASAVVMTQDDLPFAH

SAALVVRNPYLTYARMAQILDTTPQPAQDIAPSAVIDPTAKLGSNVAIGANAVIESGVVLGDNVVIGAGC

FVGKNTKIGAGSRLWANVTVYHEIEIGENCLIQSSTVIGADGFGYANDRGNWVKIPQLGRVIIGDRVEIG

ACTTIDRGALDDTVIGNGVIIDNQCQIAHNVVIGDNTAVAGGVIMAGSLKIGRYCMIGGASVINGHMEIC

DKVTVTGMGMVMRPISEPGVYSSGIPLQPNKAWRKTAALVMNIDEMSKRLKAIERKVNQQD

>lcl|NZ\_FO834906.1\_prot\_WP\_002889325.1\_4214 [gene=skp] [locus\_tag=BN49\_RS22810] [protein=molecular chaperone Skp] [protein\_id=WP\_002889325.1] [location=complement(4391100..4391585)] [gbkey=CDS]

MKKWLLAAGLGLAMVTSAQAADKIALVNMNSLFQQVAQKTGVSNTLENEFKGRASELQRMEGDLQSKMQR

LQSMKPGADRTKLEKDVMAQRQTFSQKAQAFEQDRARRSNEERGKLVTRIQTAVQSVAKDQSIDLVVDAN

AVAYNSSDVKDITADVLKQVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529376.1\_4215 [gene=bamA] [locus\_tag=BN49\_RS22815] [protein=outer membrane protein assembly factor BamA] [protein\_id=WP\_016529376.1] [location=complement(4391707..4394136)] [gbkey=CDS]

MAMKKLLIASLLFSSATVYGAEGFVVKDIHFEGLQRVAVGAALLSMPVRPGDTVTDDDISNTIRALFATG

NFEDVRVLRDGDTLLVQVKERPTIASITFSGNKSVKDDMLKQNLEASGVRVGESLDRTTIADIEKGLEDF

YYSVGKYSASVKAVVTPLPRNRVDLKLVFQEGVSAKIQQINIVGNHAFSTDELISHFQLRDEVPWWNVVG

DRKYQKQKLAGDLETLRSYYLDRGYARFNIDSTQVSLTPDKKGIYITVNITEGDQYKFSGVQVTGNLAGH

SAEIEALTKVEPGELYNGAKVTKMENDIKKLLGRYGYAYPRVQSQPEINDSDKTVKLHVNVDAGNRYYVR

KIRFEGNDTSKDAVLRREMRQMEGAWLGSDLVDQGKDRLNRLGFFETVDTDTQRVPGSPDQVDVVYKVKE

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YNDFDANDADLSDYTNKSYGTDITLGFPVNEYNTLRAGVGYVHNSLSNMQPQVAMWRYLNSMGQYPDNTN

DRNSFSANDFTFNYGWTYNKLDRGFFPTEGSRVNLNGKVTIPGSDNEYYKATLDTATYVPIDNDHQWVVL

GRTRFGYGDGIGGKEMPFYENFYAGGSSTVRGFQSNTIGPKAVYFPSSSRHDGDSGYTNDCKSTESAPCK

SDDAVGGNAMAVASLELITPTPFISDKYANSVRTSVFWDMGTVWDTHWDSNAYAGYPDYSDPSNIRMSAG

IAVQWMSPLGPLVFSYAQPFKKYDGDKAEQFQFNIGKTW

>lcl|NZ\_FO834906.1\_prot\_WP\_046043744.1\_4216 [gene=rseP] [locus\_tag=BN49\_RS22820] [protein=sigma E protease regulator RseP] [protein\_id=WP\_046043744.1] [location=complement(4394168..4395520)] [gbkey=CDS]

MLSVLWNLAAFIIALGVLITVHEFGHFWVARRCGIRVERFSIGFGKALWRRMDKQGTEFVIALIPLGGYV

KMLDERVEAVAPEMRHYAFNNKTVGQRAAVIAAGPIANFIFAIFAYWLVFIIGVPGVRPVVGEITPNSVA

AQAQIAKGTELKAIDGIETPDWDAVRLQLVAKIGNPQTIVTVAPFGTNQRQDKIVDLRHWSFEPDKQDPV

TSLGIQPRSAQIDTVLAEVQAGSAAQKAGLQAGDRIVKVDGQPLTQWMTFVNLVRDNPGKALALEIERQG

SALPLTLTPDAKTVKGKAEGFAGVVPKVIPLPEEYKTVRQYGPFAAIAEATDKTWLLMSLTVRMLGKLIT

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ERVQDFSYRIGSILLVLLMGLALFNDFSRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002889318.1\_4217 [gene=cdsA] [locus\_tag=BN49\_RS22825] [protein=phosphatidate cytidylyltransferase] [protein\_id=WP\_002889318.1] [location=complement(4395532..4396389)] [gbkey=CDS]

MLKYRLISAFVLIPIVIAALFLLPPMGFAIVTLVVCMLAAWEWGQLSGFTSTSQRVWLAVLCGLLLAAML

FLLPEYHYDVHQPMVEGSLWASFAWWIVALLLVLSYPASAAFWRHSKVLRLIFGILTIVPFFWGMLALRA

WHYADNHYSGALWLLYVMILVWGADSGAYMFGKMFGKHKLAPKVSPGKTWQGFFGGLLTAAVISWAYGVW

AHLDVTPTVLLVCSVVAALASVLGDLTESMFKREAGIKDSGHLIPGHGGILDRIDSLTAAVPVFACLLLL

VFRTI

>lcl|NZ\_FO834906.1\_prot\_WP\_002889316.1\_4218 [gene=ispU] [locus\_tag=BN49\_RS22830] [protein=(2E,6E)-farnesyl-diphosphate-specific ditrans,polycis-undecaprenyl-diphosphate synthase] [protein\_id=WP\_002889316.1] [location=complement(4396402..4397160)] [gbkey=CDS]

MLSANQTVSEISPTHGCRHVAIIMDGNGRWAKRQGKIRAFGHKAGAKSVRRAVSFAANNGIEALTLYAFS

SENWNRPAQEVSALMELFVWALDSEVKSLHRHNVRLRIIGDTTRFNARLQERIRKAEALTANNTGLTLNI

AANYGGRWDITQGVRLLAKQVQDGTLLPEQITEDMLSQQVCMHELAPVDLVIRTGGEHRISNFLIWQIAY

AELYFTDVLWPDFAEQDFEGALHAFVNRERRFGGTEPGGSHA

>lcl|NZ\_FO834906.1\_prot\_WP\_002889310.1\_4219 [gene=ispC] [locus\_tag=BN49\_RS22835] [protein=1-deoxy-D-xylulose-5-phosphate reductoisomerase] [protein\_id=WP\_002889310.1] [location=complement(4397398..4398600)] [gbkey=CDS]

MKQLTVLGSTGSIGCSTLDVVRHNPGRFSVAALVAGKNVDRMVEQCLEFTPRYAVMDDAQSAERLRTRLH

EHGSRTEVLSGQQAAAEVAALDEVDQVMAAIVGAAGLVPTLAAIRAGKTVLLANKESLVTCGRLFMEAVQ

QSGARLLPVDSEHNAIFQSMPETIQQHLGYADLARNGVSSILLTGSGGPFRETAVAELAAMTPDQACRHP

NWSMGRKISVDSATMMNKGLEYIEARWLFNASAQQMEVLIHPQSVIHSMVRYQDGSVLAQLGEPDMRTPI

AHTMGWPQRLNSGVKPLDFCQLSNLSFSAPDYTRYPCLKLAMDAFDVGQAATTTLNAANEESVAAFLHGD

IRFTDIAAVNLAVLDKMDLQEPQSIDDVLVIDAEARAIAHQQLQRLVAQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002889308.1\_4220 [gene=frr] [locus\_tag=BN49\_RS22840] [protein=ribosome recycling factor] [protein\_id=WP\_002889308.1] [location=complement(4398829..4399386)] [gbkey=CDS]

MISDIRKDAEIRMEKCVEAFKNQISKIRTGRASPSLLDGIVVEYYGTPTPLRQLASVTVEDSRTLKINVF

DRSMSAAVEKAIMASDLGLNPSSAGSDIRVPLPPLTEERRKDLTKIVRGEAEQARVAVRNVRRDANDKVK

ALLKEKEISEDDDRRSQDDVQKMTDAAIKKVDAALADKEAELMQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002889306.1\_4221 [gene=pyrH] [locus\_tag=BN49\_RS22845] [protein=UMP kinase] [protein\_id=WP\_002889306.1] [location=complement(4399537..4400262)] [gbkey=CDS]

MATNAKPVYKRILLKLSGEALQGSEGFGIDASILDRMAQEIKELVELGIQVGVVIGGGNLFRGAGLAKAG

MNRVVGDHMGMLATVMNGLAMRDALHRAYVNARLMSAIPLNGVCDNYSWAEAISLLRNNRVVILSAGTGN

PFFTTDSAACLRGIEIEADVVLKATKVDGVFTADPAKDPSATMYDQLTYSEVLEKELKVMDLAAFTLARD

HKLPIRVFNMNKPGALRRVVMGEKEGTLITE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151930.1\_4222 [gene=tsf] [locus\_tag=BN49\_RS22850] [protein=translation elongation factor Ts] [protein\_id=WP\_004151930.1] [location=complement(4400413..4401264)] [gbkey=CDS]

MAEITASLVKELRERTGAGMMDCKKALTEANGDIELAIENMRKSGAIKAAKKAGNVAADGVIKTKIEGNY

GYILEVNCQTDFVAKDGGFQAFADKVLDAAVAGKISDVEVLKAQFEEERVALVAKIGENINIRRIAVLEG

DVLGSYQHGARIGVLVAAKGADEELVKQLAMHVAASKPEFVKPEDVSAEVVEKEYQVQLDIAMQSGKPKE

IAEKMVEGRMKKFTGEVSLTGQPFVMEPSKSVGQLLKEHNADVTGFIRFEVGEGIEKVETDFAAEVAAMS

KQS

>lcl|NZ\_FO834906.1\_prot\_WP\_002889299.1\_4223 [gene=rpsB] [locus\_tag=BN49\_RS22855] [protein=30S ribosomal protein S2] [protein\_id=WP\_002889299.1] [location=complement(4401384..4402109)] [gbkey=CDS]

MATVSMRDMLKAGVHFGHQTRYWNPKMKPFIFGARNKVHIINLEKTVPMFNEALAELNKIAARKGKILFV

GTKRAASEAVKDAALSCDQFFVNHRWLGGMLTNWKTVRQSIKRLKDLETQSQDGTFDKLTKKEALMRTRE

LDKLENSLGGIKDMGGLPDALFVIDADHEHIAIKEANNLGIPVFAIVDTNSDPDGVDFVIPGNDDAIRAV

SLYLGAVAATVREGRSQDLASQAEESFVEAE

>lcl|NZ\_FO834906.1\_prot\_WP\_011977676.1\_4224 [gene=map] [locus\_tag=BN49\_RS22860] [protein=type I methionyl aminopeptidase] [protein\_id=WP\_011977676.1] [location=4402432..4403226] [gbkey=CDS]

MAISIKTSEDIEKMRVAGRLAAEVLEMIEPYVKPGVSTGELDRICNDYIVNEQKAISACLGYHGYPKSVC

ISVNEVVCHGIPDDGKLLKDGDIVNIDVTVIKDDFHGDTSKMFIVGKPTILGERLCRITQESLYLALRMV

KPGINLRAIGAAIQKFVEAEGFSVVREYCGHGIGRGFHEEPQVLHYDSPETNVVLKPGMTFTIEPMVNAG

KKEIRSMKDGWTVKTKDRSLSAQYEHTIVVTDNGCEILTLRKDDTIPAIISHDE

>lcl|NZ\_FO834906.1\_prot\_WP\_016528860.1\_4225 [gene=glnD] [locus\_tag=BN49\_RS22865] [protein=bifunctional uridylyltransferase/uridylyl-removing protein GlnD] [protein\_id=WP\_016528860.1] [location=4403284..4405947] [gbkey=CDS]

MSNSLPDTASPLLPVPPEHPLSWPQGDLNCAAIKAHIDTFQHWLGEAFDSGIVAEQLIAARTEFIDQLLQ

RLWIACGFESVSDLALVAVGGYGRGELHPLSDVDLLILSRKKLPDDQAQKVGELLTLLWDVKLEVGHSVR

TLEECLLEGLSDLTVATNLIESRLLIGDVALFLELQKHIFSDGFWPSEKFFAAKVEEQNVRHQRYHGTSY

NLEPDVKSSPGGLRDIHTLQWVARRHFGATSMDEMVGFGFLTEAERNELNECLHQLWRIRFALHLELTRY

DNRLLFDRQLSVARRLGYEGDGNQPIEHMMKDFFRVTRRVSELNQMLLQLFEEAILALTEDEKPRPIDDD

FQLRGTLIDLRDDTLFIREPQAILRMFYIMVRNSTITGIYSTTLRHLRHARRHLTQQLCYIPEARTLFLS

MLRHQGAVSRGLLPMHRHSVLWAYMPQWSHIVGQMQFDLFHAYTVDEHTVRVMLKLESFAKEETRSRHPL

CVELWPRLTHPELILIAALFHDIAKGRGGDHSILGAQDVLKFAELHGLNSRETQLVAWLVRHHLLMSVTA

QRRDIQDPEVIKQFAEEVQTENRLRYLVCLTVADICATNETLWNSWKQSLLRELYFATEKQLRRGMQSTP

DMRERVRHHQLQALALLRMDNINEEALHQIWNRCRANYFVRHTPTQLAWHARNLLRHDLNKPMILLSSQA

TRGGTEIFIWSPDRPYLFAAVCGELDRRNLSVHDAQIFTTRDGMAMDTFIVLEPDGSPLSADRHEAIRQG

LEQTITQRSWQPPAPRRQAAKLRHFSVDTEVNFLPTHTDRKSFLELIALDQPGLLARVGQVFADLGISLH

GARITTIGERVEDLFIIATADRRALNNELQQEVQQRLTAALNPNDKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889295.1\_4226 [gene=dapD] [locus\_tag=BN49\_RS22870] [protein=2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase] [protein\_id=WP\_002889295.1] [location=4405978..4406802] [gbkey=CDS]

MQQLQNVIESAFERRADITPANVDTVTREAVNQVIALLDSGALRVAEKIDGQWVTHQWLKKAVLLSFRIN

DNQVIDGAESRYFDKVPMKFADYDEARFQKEGFRVVPPAAVRQGAFIARNTVLMPSYVNIGAYVDEGTMV

DTWATVGSCAQIGKNVHLSGGVGIGGVLEPLQANPTIIEDNCFIGARSEVVEGVIVEEGSVISMGVYLGQ

STKIYDRETGEVFYGRVPAGSVVVSGNLPSKDGKYSLYCAVIVKKVDAKTRGKVGINELLRTID

>lcl|NZ\_FO834906.1\_prot\_WP\_002889292.1\_4227 [locus\_tag=BN49\_RS22875] [protein=DUF3461 family protein] [protein\_id=WP\_002889292.1] [location=4406910..4407296] [gbkey=CDS]

MYDNLKSLGITNPDEIDRYSLRQEANNDILKIYFQKDKGEFFAKSVKFKYPRQRKTVVADGVGQGYKEVQ

EISPNLRYVIDELDQICQRDRTEIDLKRKILDDLRHLESVVTNKISEIEADLEKLTRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002889289.1\_4228 [gene=cdaR] [locus\_tag=BN49\_RS22880] [protein=DNA-binding transcriptional regulator CdaR] [protein\_id=WP\_002889289.1] [location=complement(4407415..4408572)] [gbkey=CDS]

MAGWHLDTKMAQDIVARTMRIIDTNINVMDARGRIIGSGDRERIGELHEGALLVLSQGRVVDIDDAVARH

LHGVRQGINLPLRLEGEIVGVIGLTGEPESLRKYGELVCMTAEMMLEQSRLMHLLAQDSRLREELVMNLI

QAEEHTPALNEWAQRLGIDLNQPRVVAMIEVDSGQLGVDSAMAELQQLQNALTTPDRNNLVAIVSLTEMV

VLKPALNSFGRWDADDHVRRVEQLIARMKENGQLRFRVALGNFFTGPGSIARSYRTARTTMMVGKQRMPE

SRSYFYQDLMLPVLLDSLRGGWQANELARPLARLKAMDNNGLLRRTLQAWFRHNVQPLATSKALFIHRNT

LEYRLNRISELTGLDLGSFDDRLLLYIALQLDEQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004177363.1\_4229 [gene=degP] [locus\_tag=BN49\_RS22885] [protein=serine endoprotease DegP] [protein\_id=WP\_004177363.1] [location=complement(4408739..4410172)] [gbkey=CDS]

MKKTTLAMSALALSLGLALSPLSASAAETASSATNAQQMPSLAPMLEKVMPSVVSINVEGSTTVNTPRMP

RNFQQFFGDNSPFCQDGSPFQSSPFCQGGGQGGQPDGGQQQKFMALGSGVIIDAAKGYVVTNNHVVDNAT

TIKVQLSDGRKFDAKVVGKDPRSDIALIQIQEPKNLTAIKLADSDALRVGDYTVAIGNPFGLGETVTSGI

VSALGRSGLNVENYENFIQTDAAINRGNSGGALVNLNGELIGINTAILAPDGGNIGIGFAIPSNMVKNLT

EQMVKYGQVKRGELGIMGTELNSELAKAMKVDAQRGAFVSQVMPGSAAAKAGIKAGDVITSLNGKAISSF

AALRAQVGTMPIGSKVELGLLRDGKPVTVTVELQQSNQTQVDSSTIFNGIEGAEMSNKGQDKGVVVNNVK

AGTPAAQIGLKKGDVIVGANQQPVKNIADLRKIFDAKPSVLALNIQRGDASIYLLLQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529315.1\_4230 [gene=dgt] [locus\_tag=BN49\_RS22890] [protein=dGTPase] [protein\_id=WP\_016529315.1] [location=complement(4410307..4411821)] [gbkey=CDS]

MAKIDFRNKINWRRRFRSPPRVETERDILRIFESDRGRIVNSPAIRRLQQKTQVFPLERNAAVRTRLTHS

LEVQQVGRYIAKEVLSRLKELRLLEEYGLEELTGPFESVVEMACLMHDIGNPPFGHFGEAAINDWFRQRL

APGDALGQPLTDDRCEVQALRLHDGETSLNALRRKVRQDLCSFEGNAQGIRLVHTLMRMNLTRAQVGCIL

KYTRPAWWSEETPASHSYLMKKPGYYLAEEEYVARLRKELDLAPYNRFPLTWIMEAADDISYCVADLEDA

VEKRIFSAEQLYQHLYDAWGSHEKGSLFSQVVENAWEKSRANYLKQSAEDQFFMYLRVNTLNKLVPYAAR

RFIDNLPAIFTGDFNHALLEDDSDCSQLLELYKNVAMKQVFSHPDVEQLELQGYRVISGLLDIYQPLLKL

SLEDFSELVAQERVRRLPIASRLYQKLSTRHRLAYVEAVNKLARTAPEFALMEYYYRCRLIQDYISGMTD

LYAWDEYRRLMAVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002889282.1\_4231 [gene=mtnN] [locus\_tag=BN49\_RS22895] [protein=5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase] [protein\_id=WP\_002889282.1] [location=4411905..4412603] [gbkey=CDS]

MKIGIIGAMEEEVTLLRDKIENRQTITIGGSEIYTGQLHGVDVALLKSGIGKVAAAMGATLLLERCQPDV

IINTGSAGGLASTLKVGDIVVSDEARYHDADVTAFGYEYGQLPGCPAGFKADEKLVAAAESCIKALDLNA

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LAVAARQSTLMVENLVQNLARG

>lcl|NZ\_FO834906.1\_prot\_WP\_002889279.1\_4232 [gene=btuF] [locus\_tag=BN49\_RS22900] [protein=vitamin B12 ABC transporter substrate-binding protein BtuF] [protein\_id=WP\_002889279.1] [location=4412596..4413396] [gbkey=CDS]

MAKSLSFALAALLLLAPAWLLAAPRVITLSPANTELAFAAGITPVGVSSYSDYPSQAKTIEQVASWQGMN

LERIVALKPDVVLAWRGGNAERQVNQLQSLGIHVLWVQTSTIEEIIATLRELAQWSPQPEKAQQAAQAMQ

QEYDALKARYANAPKKRVFLQFGSAPLFTSGPGSIQDQVLRLCGGENIFATSRVPWPQVSREQVLARQPQ

AIVVTGDASRIAEAQRFWQHQLTISLIALHSDWFERAGPRIILAAKQLCAALDQVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529316.1\_4233 [locus\_tag=BN49\_RS22905] [protein=TRIC cation channel family protein] [protein\_id=WP\_016529316.1] [location=4413433..4414056] [gbkey=CDS]

MLVYWLDIIGTAVFAISGVLLAGKLRMDPFGVLVLGVVTAVGGGTIRDMALANGPVFWVKDPTDLVVAMV

TSMLTILLVRQPRRLPKWILPVLDAVGLAVFVGIGVNKAFLAGSGPLVAVCMGVVTGVGGGIIRDVLARE

IPMILRTEIYATACIVGGIVHATAHDTFHVPLENSAMMGMVVTLVIRLAAIRWHLKLPTFALDDNGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002889275.1\_4234 [gene=erpA] [locus\_tag=BN49\_RS22910] [protein=iron-sulfur cluster insertion protein ErpA] [protein\_id=WP\_002889275.1] [location=complement(4414128..4414472)] [gbkey=CDS]

MSDDVALPLEFTEAAANKVKHLIADEDNPNLKLRVYITGGGCSGFQYGFTFDDQVNEGDMTIEKQGVGLV

VDPMSLQYLVGGSVDYTEGLEGSRFIVTNPNAKSTCGCGSSFSV

>lcl|NZ\_FO834906.1\_prot\_WP\_004191940.1\_4235 [gene=clcA] [locus\_tag=BN49\_RS22915] [protein=H(+)/Cl(-) exchange transporter ClcA] [protein\_id=WP\_004191940.1] [location=complement(4414554..4415972)] [gbkey=CDS]

MKAETPSFEAHQFVRVRRGDAVRRLIQRDKTPLAVLFMAAVVGTLAGLVGVAFEKSVNWVQNQRIGALAQ

VADHWYLVWPLAFILSALLAMVGYFLVRRFAPEAGGSGIPEIEGALEELRPVRWWRVLPVKFVGGMGTLG

AGMVLGREGPMVQLGGNIGRMVLDVFRMRSPEARHTLLATGAASGLSAAFNAPLAGILFIIEEMRPQFRY

NLISIKAVFTGVIMSSIVFRIFNGEAAIIEVGKLSNAPVNTLWLYLVLGMLFGCFGPLFNFLVLRTQDLF

QRIHGGNIKKWVFIGGLIGGLCGLLGLMQPSAVGGGFNLIPIAAAGNFSVGLLLFIFIARVVTTLICFSS

GAPGGIFAPMLALGTLLGTAFGMAAIPLFPAYHLDAGTFAIAGMGALLAASVRAPLTGIVLVLEMTDNYQ

LILPMIITCLGATLLAQFLGGKPLYSTILQRTLAKQEAEQAAKAQQAPRENT

>lcl|NZ\_FO834906.1\_prot\_WP\_002889272.1\_4236 [gene=hemL] [locus\_tag=BN49\_RS22920] [protein=glutamate-1-semialdehyde 2,1-aminomutase] [protein\_id=WP\_002889272.1] [location=4416153..4417433] [gbkey=CDS]

MSKSENLYHAARELIPGGVNSPVRAFTGVGGTPLFIERADGAYLYDVDGKAYIDYVGSWGPMVLGHNHPA

IRNAVIEAASRGLSFGAPTEMEVKMAALVTELVPTMDMVRMVNSGTEATMSAIRLARGFTGRDKIIKFEG

CYHGHADCLLVKAGSGALTLGQPNSPGVPADFAKHTLTCTYNDLASVRAAFEQYPQEIACIIVEPVAGNM

NCIPPQPEFLPGLRALCDEFGALLIIDEVMTGFRVALAGAQAYYGVEPDLTCLGKIIGGGMPVGAFGGRR

EVMDALAPTGPVYQAGTLSGNPIAMAAGFACLNEVAQPGVHETLTELTNQLAQGLLDAARDAGIPLVVNN

VGGMFGIFFTDAETVTCYQDVVKCDVERFKRFFHLMLEEGVYLAPSAFEAGFMSVAHSEEDIDNTIDAAR

RVFAKL

>lcl|NZ\_FO834906.1\_prot\_WP\_004147134.1\_4237 [gene=fhuB] [locus\_tag=BN49\_RS22925] [protein=Fe(3+)-hydroxamate ABC transporter permease FhuB] [protein\_id=WP\_004147134.1] [location=complement(4417570..4419552)] [gbkey=CDS]

MNTRLSPLAIILLAGLLGVAFALSIVNLNVALPYAQWRQALWQPDVDDIAQMLFHYSLLPRLAVALLVGA

GLGLVGVLFQQVLRNPLAEPTTLGVATGAQLGITVTTLWAIPGVLASQFAALAGACLVGALVFGVSWGKR

LSPVTLILAGLVVSLYCGALNQLMVIFHHDQLQSMFLWSTGTLTQTDWSVAQRLWPQLLGGAILTLLLLR

PLTLMGLDDGVARNLGLALSLARLGALTLAIVISALLVNAVGIIGFIGLFAPLLAKMLGARRLLARLLLA

ALIGALLLWLSDQVILWLSRVWREVSTGSVTALIGAPLLLWLLPRLRSISAPVMNGGDNVQPERYHVQWF

VLAGVALLLLAVSVALAFGRDAHGWLWAHGDLLEQLLPWRWPRVLSALFAGVMLAVAGCIIQRLTGNPMA

SPEVLGISSGAAFGVVLMLFFVPGDAFGWLLPAGSLGAAATLLIIMLAAGRGGFSPHRMLLAGMALSTAF

TMLLMMLQASGDPRMAQILTWISGSTYSATPERVVRSGAVMLALLALAPLCRRWLTILPLGGEAARAVGM

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529986.1\_4238 [gene=fhuD] [locus\_tag=BN49\_RS22930] [protein=Fe(3+)-hydroxamate ABC transporter substrate-binding protein FhuD] [protein\_id=WP\_016529986.1] [location=complement(4419549..4420439)] [gbkey=CDS]

MMNPTLITRRRLLIAMTLSPLLWQMRGAQAADVDPQRVVALEWLPAELLLALGVTPYGVADIPNYRLWVN

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MADLLGKTQQAKRHLAEFDALMESLRPRFAGRGDRPLLMISLLDPRHVLVFGENCLFQEVLDRFGIKNAW

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>lcl|NZ\_FO834906.1\_prot\_WP\_002889212.1\_4239 [gene=fhuC] [locus\_tag=BN49\_RS22935] [protein=Fe3+-hydroxamate ABC transporter ATP-binding protein FhuC] [protein\_id=WP\_002889212.1] [location=complement(4420439..4421236)] [gbkey=CDS]

MQEQTPHAETTFALDRVTFRVPGRTLLHPLSLTFPTGKVTGLIGHNGSGKSTLLKMLGRHQPPSAGEVLL

DGQPLESWGSKAFARKVAYLPQQLPPAEGMTVRELVAIGRYPWHGALGRFGAADREKVEEAIALVGLKPL

AHRLVDSLSGGERQRAWIAMLVAQDSRCLLLDEPTSALDIAHQVDVLALVHRLSQQRGLTVIAVLHDINM

AARYCDYLVALRGGEMIAQGTPAELMRSDTLEQIYGIPMGILPHPAGAAPVSFVY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529987.1\_4240 [gene=fhuA] [locus\_tag=BN49\_RS22940] [protein=ferrichrome porin FhuA] [protein\_id=WP\_016529987.1] [location=complement(4421282..4423489)] [gbkey=CDS]

MARPKTAQPNHSLRKVAAVVATAVSGMSVYAQAAEQPKQEETITVVAAPAAQESAWGPAPTIAAKRSATA

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DGMKLQGNNYSEVSMDPYFLERVEVMRGPTSVLYGNSNPGGIVSMVSKRPTTEPLKEVQFKMGTDNLWQT

GFDFSDAIDDAGVWSYRLTGLGRSQDAQQQMAKSTRYAVAPSFSWRPDDKTDFTFLSNFQNDPDAGYYGW

LPREGTVVPYYDANGKAHKLPTDFNEGESDNKISRRQKMVGYSFSHQFDDTFTVRQNLRYADVHTLYRSV

YGNGYVAPGYMNRAYVRSDEHLNTFTVDTQLQSDFATGAVSHTLLTGVDYSRMRNDVDADYGTADPISMS

NPQYGNPNIQVTFPYAVLNRMEQTGLYAQDQMEWDKWVMTLGGRYDYATTSTLTRATNSLAENHDQQFSW

RGGINYLFDNGISPYFSYSESFEPVSGSNSRGQPFDPSRGKQYEAGVKYVPKDMPVVVTAAVYQLTKDKN

LTADPANQAFSIQTGEIRSRGLELEAKAAVNANVNVTAAYSYTDAEYTHDTVFNGKRPAEVPRNMASLWA

DYTFHETALSGLTIGAGARYIGSTVSYYKNDTSTGKKNDAFSVAGYALMDATVKYDLARFGLPGSSVGVN

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529988.1\_4241 [gene=mrcB] [locus\_tag=BN49\_RS22945] [protein=bifunctional glycosyl transferase/transpeptidase] [protein\_id=WP\_016529988.1] [location=complement(4423724..4426273)] [gbkey=CDS]

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RPGEYTVQANSIEMIRRPFDFPDSKEGQVRARLTFDGDHLETIENMDNNRQFGFFRLDPRLITMLQSPNG

EQRLFVKRSGFPDLLVDTLLATEDRHFYEHDGISLYSIGRAVLANLTAGRTVQGASTLTQQLVKNLFLSS

ERSYWRKANEAYMALIVDARYSKDRILELYMNEVYLGQSGDNEIRGFPLASLYYFGRPVEELSLDQQALL

VGMVKGASVYNPWRNPKLALERRNLVLRLLQQQVIDQELYDMLSARPLGVQPRGGVISPQPAFMQMVRQE

LQAKLGDKVKDLSGVKIFTTFDSVAQDAAEKAASEGIPVLKKQRKLADLETAMVVVDRFTGEVRAMVGGA

EPQFAGYNRAMQARRSIGSLAKPATYLTALSQPNQYRLNTWIADAPVTIRLSNGQTWSPQNDDRRFSGQV

MLVDALTRSMNVPTVNLGMALGLPAVVDTWTKLGAPKNQLNAVPSMLLGALNLTPIEVAQAFQTIASGGN

RAPLSALRSVIAEDGTVLYQSYPQAERAVPAQAAYMTLWTMQQVVQRGTGRQLGAKYPGLHLAGKTGTTN

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>lcl|NZ\_FO834906.1\_prot\_4242 [locus\_tag=BN49\_RS31540] [protein=hypothetical protein] [pseudo=true] [partial=3'] [location=4426664..>4426735] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004194926.1\_4243 [gene=gspS] [locus\_tag=BN49\_RS22955] [protein=type II secretion system pilot lipoprotein GspS] [protein\_id=WP\_004194926.1] [location=4426861..4427235] [gbkey=CDS]

MRIPLIFPLCMVALLSGCQQKPASTLSPAISSQAQLEQLSSVAAGTRYLKNKCNRSDLPADETIYRAAVN

VGKARGWGNIDVATLSQNSDRLYQQLLQDSTPEATQCSQFNRQLAPFIASLRSD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530435.1\_4244 [gene=gspB] [locus\_tag=BN49\_RS22960] [protein=type II secretion system assembly factor GspB] [protein\_id=WP\_016530435.1] [location=complement(4427274..4427831)] [gbkey=CDS]

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PVAHAALLPLTAAGEAAPKTPPPAAKASAPAAPEVDSDTLPPLRYSAHVYASLPEKRSIVLNGKAWTEGD

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>lcl|NZ\_FO834906.1\_prot\_WP\_085955203.1\_4245 [locus\_tag=BN49\_RS30600] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_085955203.1] [location=join(4427980..4428448,4428448..4429343)] [gbkey=CDS]

MAKPKYSPETKLAVVNHYLSGKDGEQSTADLFGIERTSVRRWVRAWQFHGAEGLTAKNNHYSDEFKLVVV

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EELRAELRYLRAENAYPKKVESLGSERKKWQKALIISELRHEHALRDLLRAAGMSRSTWYYNMNALKQGD

RYAGLKENIRKIYHYHKGRYGYRRITLALRKQGLRINHKTVQRLMAELSLRSVIRAKKYRAWKGRTGEAA

PNILSRNFGASKANEKWVTDVTEFPVQGKKLYLSSVLDLFNREVIAYSLSERPVMEMVNTMLDGAFPKLR

PGDAPLLHSDQGWHYRMRSYQERLKAHGMTQSMSRKGNCLDNAVMENFFGTLKSECFYLREFRSVSALRK

AVEDYIHYYNNERISLKLKGLSPVEYRTQALRAA

>lcl|NZ\_FO834906.1\_prot\_WP\_023279275.1\_4246 [gene=pulA] [locus\_tag=BN49\_RS22975] [protein=pullulanase-type alpha-1,6-glucosidase] [protein\_id=WP\_023279275.1] [location=complement(4429536..4432844)] [gbkey=CDS]

MLRYTCHALFLGSLVLLSGCDNSSSSSTSGSPGSPGNPGNPGTPGTPDPQDVVVRLPDVAVPGEAVQASA

RQAVIHLVDIAGITSSTPADYATKNLYLWNNETCDALSAPVADWNDVSTTPTGSDKYGPYWVIPLTKESG

CINVIVRDGTNKLIDSDLRVSFSDFTDRTVSVIAGNSAVYDSRADAFRAAFGVALADAHWVDKTTLLWPG

GENKPIVRLYYSHSSKVAADSNGEFSDKYVKLTPTTVNQQVSMRFPHLASYPAFKLPDDVNVDELLQGET

VAIAAESDGILSSATQVQTAGVLDDTYAAAAEALSYGAQLTDSGVTFRVWAPTAQQVELVIYSADKKVIA

SHPMTRDSASGAWSWQGGSDLKGAFYRYAMTVYHPQSRKVEQYEVTDPYAHSLSTNSEYSQVVDLNDSAL

KPEGWDGLTMPHAQKTKADLAKMTIHESHIRDLSAWDQTVPAELRGKYLALTAQESNMVQHLKQLSASGV

THIELLPVFDLATVNEFSDKVADIQQPFSRLCEVNSAVKSSEFAGYCDSGSTVEEVLTQLKQNDSKDNPQ

VQALNTLVAQTDSYNWGYDPFHYTVPEGSYATDPEGTARIKEFRTMIQAIKQDLGMNVIMDVVYNHTNAA

GPTDRTSVLDKIVPWYYQRLNETTGSVESATCCSDSAPEHRMFAKLIADSLAVWTTDYKIDGFRFDLMGY

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LRQNQGVGSGAGVLPNELTTLSDDQARHLADLTRLGMAGNLADFVLIDKDGAVKRGSEIDYNGAPGGYAA

DPTEVVNYVSKHDNQTLWDMISYKAAQEADLDTRVRMQAVSLATVMLGQGIAFDQQGSELLRSKSFTRDS

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>lcl|NZ\_FO834906.1\_prot\_WP\_004219434.1\_4247 [locus\_tag=BN49\_RS31195] [protein=hypothetical protein] [protein\_id=WP\_004219434.1] [location=4433029..4433166] [gbkey=CDS]

MIRHAYRHSPAINNSKANNHLPVSVGYYANVQKNKLAKELKCQFL

>lcl|NZ\_FO834906.1\_prot\_WP\_029497040.1\_4248 [gene=gspC] [locus\_tag=BN49\_RS22985] [protein=type II secretion system protein GspC] [protein\_id=WP\_029497040.1] [location=4433151..4433993] [gbkey=CDS]

MPVSVMGLTNINKGIIKLLPQIVTLIILITAIPQLAKLTWRVVFPVSPEDISALPLTMPPAADPELKNVR

PAFTLFGLAVKNSPTPTDAASLNQVPVSSLKLRLAGLLASSNPARSIAIIEKGNQQVSLSTGDPLPGYDA

RIAAILPDRIIVNYQGRKEAILLFNDSRAPSPPPTAAGNPPLVKRLREQPQNILTYLSISPVLSGDKLLG

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531982.1\_4249 [gene=pulD] [locus\_tag=BN49\_RS22990] [protein=GspD family T2SS secretin variant PulD] [protein\_id=WP\_016531982.1] [location=4434003..4435976] [gbkey=CDS]

MKRLRKMLPALLILTPLLFSPAAAEEFSASFKGTDIQEFINTVSKNLNKTVIIDPSVRGTITVRSYDMLN

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PLLRQLNDNAGAGSVVHYEPSNVLLMTGRAAVIKRLLTIVERVDNAGDRSVVTVPLSWASAAEVVKLVTE

LNKDTSKSALPGSMVANVVADERTNAVLVSGEPNSRQRIIAMIKQLDRQQAVQGNTKVIYLKYAKAADLV

EVLTGISSSLQSDKQSARPVAAIDKNIIIKAHGQTNALIVTAAPDVMNDLERVIAQLDIRRPQVLVEAII

AEVQDADGLNLGIQWANKNAGMTQFTNSGLPISTAIAGANQYNKDGTISSSLASALGSFNGIAAGFYQGN

WAMLLTALSSSTKNDILATPSIVTLDNMQATFNVGQEVPVLTGSQTTSGDNIFNTVERKTVGIKLKVKPQ

INEGDAVLLEIEQEVSSVADSASSTSSDLGATFNTRTVNNAVLVGSGETVVVGGLLDKTVTDTADKVPLL

GDIPVIGALFRSDSKKVSKRNLMLFIRPTIIRDRDEYRQASSGQYTAFNNAQTKQRGKENSEASLSNDLL

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>lcl|NZ\_FO834906.1\_prot\_WP\_023287261.1\_4250 [gene=gspE] [locus\_tag=BN49\_RS22995] [protein=type II secretion system ATPase GspE] [protein\_id=WP\_023287261.1] [location=4435973..4437466] [gbkey=CDS]

MTPAAERRPLLPFAWARAHHLVLLSDGERCEALCRPDTAARALLEARRLADGPMRVSRLAPEAFEKVLVL

SYQRDSAEAHRMMADIGNELDLYTLAEELPDTDDLLDSEDDAPIIRLINAMLTEAIKEKASDIHIETYER

HLQIRFRVDGVLREILRPQRRLAALLISRIKVMASLDIAEKRVPQDGRMALRIGGRAIDVRVSTLPSSHG

ERVVLRLLDKNSVNLDLLTLGMPPALLDRVDALIARPHGIILVTGPTGSGKSTTLYAALSRLDARERNIM

TIEDPVEYELEGIGQTQVNAKVEMTFARGLRAILRQDPDVVLVGEIRDGETAQIAVQASLTGHLVLSTLH

TNSALGAISRLQDMGVEPFLLSTSLLAVMSQRLVRQLCPHCRQPWQADANTARQMAVPVGARLWQPKGCP

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QQTTESV

>lcl|NZ\_FO834906.1\_prot\_WP\_004177382.1\_4251 [gene=gspF] [locus\_tag=BN49\_RS23000] [protein=type II secretion system inner membrane protein GspF] [protein\_id=WP\_004177382.1] [location=4437468..4438682] [gbkey=CDS]

MALFRYQALDAQGKTRRGLQQADSARHARQLLRDKGWLALEVTTADPARRLWAGGSLTRRTSAGDLALLT

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SGHLDGVLNRLADYTEQRQQLRARLLQAMIYPIVLTLVAISVIAILLSTVVPKVVEQFVHLKQALPFSTR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002889054.1\_4252 [gene=gspG] [locus\_tag=BN49\_RS23005] [protein=type II secretion system major pseudopilin GspG] [protein\_id=WP\_002889054.1] [location=4438703..4439125] [gbkey=CDS]

MQRQRGFTLLEIMVVIVILGILASLVVPNLMGNKEKADRQKVVSDLVALEGALDMYKLDNSRYPNTEQGL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004191951.1\_4253 [gene=gspH] [locus\_tag=BN49\_RS23010] [protein=type II secretion system minor pseudopilin GspH] [protein\_id=WP\_004191951.1] [location=4439125..4439640] [gbkey=CDS]

MSQRGFTLLEMMLVLLLIGVSASMVLLAFPSARTQEATQILARFQAQLDFVRERGQQTGQLFGIIIHPER

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>lcl|NZ\_FO834906.1\_prot\_WP\_002889025.1\_4254 [gene=gspI] [locus\_tag=BN49\_RS23015] [protein=type II secretion system minor pseudopilin GspI] [protein\_id=WP\_002889025.1] [location=4439637..4440002] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_023342989.1\_4255 [gene=gspJ] [locus\_tag=BN49\_RS23020] [protein=type II secretion system minor pseudopilin GspJ] [protein\_id=WP\_023342989.1] [location=4439999..4440595] [gbkey=CDS]

MITKMRGFTLIETLLALAILAVLSAAAVMVLQNVIRADGLTREKSQQIAALQRAFRQIADDVTHIIPRRA

RNSDTFFFAGRFQLQSDDWGLAFSRSGWPNPLGILPRSEIQNVSYRLRQQQLERLSFDQQDPLTGSQPTV

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MKNRQRGVALLMVLFILALMMILASAMTERTAVMYQHTAVTLDNLQARWYALAAENMAAALLQRDALDSP

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DDALQVNVNTLRPSQAALLVALFPGDLTLQEAQRLLHNRPRTGWSSVAAFLAQPTLQKTDTTLARPWLTV

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043759.1\_4257 [gene=gspL] [locus\_tag=BN49\_RS23030] [protein=type II secretion system protein GspL] [protein\_id=WP\_046043759.1] [location=4441565..4442758] [gbkey=CDS]

MNKINASPQAMLIVRLAAAQAPLHWQLFAPDEPHHEASGRWPTDDASPFPALAEQYPAWVLIPASDCAFH

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MANLLIWWRQRTPSEQRLLLGLTGLLAACAFWYGLWQPWRAREAQWRQTLVKEQASLRWMTEQAPRLQQL

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>lcl|NZ\_FO834906.1\_prot\_4259 [locus\_tag=BN49\_RS23040] [protein=type II secretion system protein N] [pseudo=true] [location=4443226..4443972] [gbkey=CDS]

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IIAGGAQWRQARLHSPVGSLELAQVNGTFRCTVDGAVALTLRQDSHQLSLSGQGTLSPDGRYLFRGTLQP

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>lcl|NZ\_FO834906.1\_prot\_WP\_004145898.1\_4260 [locus\_tag=BN49\_RS23045] [protein=A24 family peptidase] [protein\_id=WP\_004145898.1] [location=4443969..4444769] [gbkey=CDS]

MTTLAALSLHFPFVWYGFLLLFGLALGSFYNVVIYRLPRMLTQTADDERITLSTPGSSCPQCRQPIAWRD

NIPLLSFLWLGRRARCCQAPIAWSYPLTELATGLLFILAGALLAPGLPLAGGLVLLSFLLILARIDARTQ

LLPDRLTLPLLWAGLLFNLNEVYIALPDAVAGAMAGYLALWSVYWLFRLLTGKEALGYGDFKLLAALGAW

CGWQVLPQVLLLASASGLVWTLLQRLWTRQSLQQPLAFGPWLALAGGGIFLWQQMV

>lcl|NZ\_FO834906.1\_prot\_WP\_023282188.1\_4261 [gene=hrpB] [locus\_tag=BN49\_RS23050] [protein=ATP-dependent helicase HrpB] [protein\_id=WP\_023282188.1] [location=complement(4444817..4447246)] [gbkey=CDS]

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DVQQGLRDDLKLLIMSATLDNDRLQRLLPEAPVVVSEGRAYPVERRFSPLSAHQRFDEAVAVAAAELLRH

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EILHSDLSALLLELLQWGCHVPAALAWLDQPPAVNLAAARRLLEALSALDGERLSAFGRKMAALGNEPRL

AAMLAAAQTDDEAATAAKLAAILEEPPRGGLVDLGAVFSRQQANWQQRAQQLMKRLARRGGQPDAGLMAG

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AARPELAKSSDTVEWDEAQGTLKAWRRTVIGQLVIKTQPLAKPSEAELHQAMLNGIREKGLGVLNWTPEA

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RELPTHYTVPTGSRLAIRYHAENPPALAVRMQEMFGEATTPVIAEGRVPLVLELLSPAQRPLQITRDLSA

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043762.1\_4262 [gene=thpR] [locus\_tag=BN49\_RS23055] [protein=RNA 2',3'-cyclic phosphodiesterase] [protein\_id=WP\_046043762.1] [location=4447319..4447855] [gbkey=CDS]

MSEPKRLFFALELPSAVQKQIVQWRATHFPEDAGRPVAADNLHLTLAFLGEVSAEKQRALAALAGRLRQP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002888848.1\_4263 [gene=sfsA] [locus\_tag=BN49\_RS23060] [protein=DNA/RNA nuclease SfsA] [protein\_id=WP\_002888848.1] [location=4447855..4448571] [gbkey=CDS]

MQFDPPLQPAILLKRYKRFLADVVTPDGRELTLHCPNTGAMTGCAAPGDTVWYSTSDNAKRKYAHTWELT

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EILAWKAELSTTRMTLNKPIAVVLNPGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002888845.1\_4264 [gene=dksA] [locus\_tag=BN49\_RS23065] [protein=RNA polymerase-binding protein DksA] [protein\_id=WP\_002888845.1] [location=4448734..4449189] [gbkey=CDS]

MQEGQNRKTSSLSILAIAGVEPYQEKPGEEYMNEAQLAHFKRILEAWRNQLRDEVDRTVSHMQDEAANFP

DPVDRAAQEEEFSLELRNRDRERKLIKKIEKTLKKVEDEDFGYCESCGVEIGIRRLEARPTADLCIDCKT

LAEIREKQMAG

>lcl|NZ\_FO834906.1\_prot\_WP\_004145903.1\_4265 [gene=gluQRS] [locus\_tag=BN49\_RS23070] [protein=tRNA glutamyl-Q(34) synthetase GluQRS] [protein\_id=WP\_004145903.1] [location=4449249..4450130] [gbkey=CDS]

MTDSRYIGRFAPSPSGELHFGSLIAALGSYLQARANQGIWRVRIEDIDPPREVPGAADTILRQLDHYGLH

WDGDVLWQSQRHEAYREALTWLGEQGLSYYCTCTRARIHAVGGIYDGHCRDLGLGAENAALRLRQTRPVL

QFSDRLRGTLIANEPLAREDFIIHRRDGLFAYNLAVVVDDHFQGITEIVRGADLIEPTVRQISLYQHFGW

QAPDYLHLPLALNGDGNKLSKQNHAPALPEGDPRPEIVRALRFLNQAIPEEWQALSIDDLLAQAVANWQP

AKIEHSQMAPAEL

>lcl|NZ\_FO834906.1\_prot\_WP\_071526609.1\_4266 [gene=pcnB] [locus\_tag=BN49\_RS23075] [protein=polynucleotide adenylyltransferase PcnB] [protein\_id=WP\_071526609.1] [location=4450193..4451587] [gbkey=CDS]

MFTRVANFCRKVLSREEREAEAAVEPTPMTVIPREQHAISRKDISENALKVMYRLNKAGYESWLVGGGVR

DLLLGKKPKDFDVTTNATPDQVRKLFRNCRLVGRRFRLAHVMFGPEIIEVATFRGHHEGHTTDRVTSQRG

QNGMLLRDNIFGSIEEDAQRRDFTINSLYYSVADFTVRDYVGGMKDLQDGVIRLIGNPETRYREDPVRML

RAVRFAAKLNMTISPETAEPLPRLAALLHDVPPARLFEEVLKLLQAGYGYQTYMLLREYSLFQPLFPTIT

RYFTERGDSPMERIISQVLKNTDTRIHNDMRVNPAFLFAVMFWYPLLETAQKIAQESGLAYYDAFALAMN

DVLDEACRTLAIPKRITTLIRDIWQLQLRMSRRQGKRAWKLMEHPKFRAAYDLLELRAGAENNHELQRLT

KWWGEFQVAAPPAQKDMLNDLGDDPAPRRRHRRPRKRAPRQGSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004178602.1\_4267 [gene=folK] [locus\_tag=BN49\_RS23080] [protein=2-amino-4-hydroxy-6-hydroxymethyldihydropteridine diphosphokinase] [protein\_id=WP\_004178602.1] [location=4451584..4452063] [gbkey=CDS]

MTLVYIALGSNLASPLEQVQAAIRALGEIPHSRVVAVSSFYRTPPLGPQDQPDYLNAAVALETALPPETL

LDHTQRIELQQGRVRKAERWGPRTLDLDIMLFGDAVINSERLTVPHYDMKNRGFMLWPLFEIAPDLHFPD

GLALRAVLDNLGAAKPASW

>lcl|NZ\_FO834906.1\_prot\_WP\_002888841.1\_4268 [gene=panB] [locus\_tag=BN49\_RS23085] [protein=3-methyl-2-oxobutanoate hydroxymethyltransferase] [protein\_id=WP\_002888841.1] [location=4452184..4452975] [gbkey=CDS]

MKPTTIALLQKCKQEKKRFATITAYDHSFAKLFADEGINVLLVGDSLGMTVQGHDSTLPVTVEDIAYHTR

AVRRGAPNSLLLADLPFMAYATPEQTFANAAIVMRAGANMVKLEGGAWLADTVRMLAERAVPVCGHLGLT

PQSVNVFGGYKVQGRGDAAQTLFEDALALEAAGAQLLVLECVPVELAKRITDALTIPVIGIGAGNVTDGQ

ILVMHDAFGITGGHIPKFAKNFLAEAGDIRAAVRQYIAEVESGVYPGEEHSFH

>lcl|NZ\_FO834906.1\_prot\_WP\_002888835.1\_4269 [gene=panC] [locus\_tag=BN49\_RS23090] [protein=pantoate--beta-alanine ligase] [protein\_id=WP\_002888835.1] [location=4452987..4453841] [gbkey=CDS]

MLIIESVLLLRQHIRRLRQEGKRIALVPTMGNLHDGHMKLVDEAKASADVVVVSIFVNPMQFDRVDDLAR

YPRTLQDDCEKLNKRHVDFVFAPTPAEVYPQGTEGQTYVDVPGLSTMLEGASRPGHFRGVSTIVSKLFNL

VQPDVACFGEKDFQQLALIRKMVADMGYDIEIIGVPIVRAKDGLALSSRNGYLTADQRKIAPGLYKVLSA

VAEKLAAGDRQLDEIIAIAEQELNEKGFRADDIQIRDADTLLELTDASQRAVILMAAWLGQARLIDNRIV

TLAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002888834.1\_4270 [gene=panD] [locus\_tag=BN49\_RS23095] [protein=aspartate 1-decarboxylase] [protein\_id=WP\_002888834.1] [location=4453934..4454314] [gbkey=CDS]

MMRNMLQGKLHRVKVTQADLHYEGSCAIDQDFLDAAGILENETIHLWNVTNGNRFSTYAIAAERGSRIIS

VNGAAAHCASVGDILIIASFVTMSDEEARSWQPNIAYFEGDNEMKRQAKAIPVQVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004145907.1\_4271 [locus\_tag=BN49\_RS23100] [protein=polysaccharide deacetylase family protein] [protein\_id=WP\_004145907.1] [location=complement(4454350..4455603)] [gbkey=CDS]

MRMLARFLTLLLFLTSLSASASLLSQQGKAVRYMQTTEDAVIWAQVGNHVVSVGNVRAGQILAVVPTAAD

YYEFRFGFGTGFIDKGHLEPVQGKQRVEDRLGDLNKPLSNQNLLTWKDTPLYDAPSVSSAPFGTLANNLR

YPILSKLKDRLNQTWFQIRIGDRLAWVSSLDAQEDHGIPVLTYHHILRDEENTRFRHTSTTTSVRAFTNQ

MTWLRDQGYTTLTLYQLEGYVRNKINLPARAVAITFDDGLKSVNRYAYPVLKQYGFHATAFIISSRIKRH

PQKWDPKSLQFMSISELRQIQDVFDIQSHTHFLHRVDAGRRPILFSRNYHNILFDFARSRRALSQFNPHV

LYLSYPFGGYNATAVQAANDAGFHMAVTTVRGKVKPGDNPFLLKRLYILRTDSLETMSRLISNQPQG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177394.1\_4272 [locus\_tag=BN49\_RS23105] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_004177394.1] [location=complement(4455662..4456102)] [gbkey=CDS]

MLGWVITCHDELAQEMLDRLEQKFGPLAQCRAVNYWRNLSSNMLSRMMCDALHATDSGDGVIFLTDKTGA

APYRAAALMSHKHTHCEVISGVSYPLLERMYLLRGTLSSVAFRQAIVSAGGPMVSSLWHQQQKNPPFRLR

HDAWGN

>lcl|NZ\_FO834906.1\_prot\_WP\_002888827.1\_4273 [locus\_tag=BN49\_RS23110] [protein=ABC transporter permease] [protein\_id=WP\_002888827.1] [location=complement(4456225..4456995)] [gbkey=CDS]

MMQLYWVALKSIWTKEIHRFMRIWVQTLVPPVITMTLYFVIFGNLIGSRIGEMHGFTYMQFIVPGLIMMA

VITNAYANVASSFFSAKFQRNIEELLVAPVPTHVIIAGYVGGGVARGLCVGILVTAVSLFFVPFQVHSWL

FVALTLLLTAVLFSLAGLLNAVFAKTFDDISLIPTFVLTPLTYLGGVFYSLTLLPPFWQGLSHLNPIVYM

ISGFRFGFLGINDVPLATTFAVLVVFIVAFYLLCWSLIQRGRGLRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888823.1\_4274 [locus\_tag=BN49\_RS23115] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_002888823.1] [location=complement(4456992..4457918)] [gbkey=CDS]

MTIALELKQLKKTYPGGVQALRGIDLQVEAGDFYALLGPNGAGKSTTIGIISSLVNKTSGQVNVFGYDLE

KDVVNAKRQLGLVPQEFNFNPFETVQQIVVNQAGYYGVERKEALSRSEKYLKQLDLWEKRNERARMLSGG

MKRRLMIARALMHEPKLLILDEPTAGVDIELRRSMWGFLKDLNDRGTTIILTTHYLEEAEMLCRNIGIIQ

HGELVENTSMKALLSKLKSETFILDLAPKSPVPKLEGYQYQLVDTSTLEVEVLREQGINSVFAQLSAQGV

QVLSMRNKANRLEELFVTLVHERKGESA

>lcl|NZ\_FO834906.1\_prot\_WP\_002888821.1\_4275 [gene=can] [locus\_tag=BN49\_RS23120] [protein=carbonate dehydratase] [protein\_id=WP\_002888821.1] [location=4458103..4458765] [gbkey=CDS]

MNDIDTLISNNALWSKMLVEEDPGFFEKLSQTQKPRFLWIGCSDSRVPAERLTGLEPGELFVHRNVANLV

IHTDLNCLSVVQYAVDVLEVEHIIICGHYGCGGVQAAVENPELGLIDNWLLHIRDIWFKHSSLLGEMPEE

RRLDTLCELNVMEQVYNLGHSTIMQSAWKRGQKVTIHGWAYGIHDGLLRDLDVTAVSRETLEQRYRHGIS

NLKIKHINHR

>lcl|NZ\_FO834906.1\_prot\_WP\_002888819.1\_4276 [gene=hpt] [locus\_tag=BN49\_RS23125] [protein=hypoxanthine phosphoribosyltransferase] [protein\_id=WP\_002888819.1] [location=complement(4458825..4459361)] [gbkey=CDS]

MKHTVEVMIPESEIKARIAELGRQINEHYQNSGSEMVLVGLLRGSFMFMADLCREVQVPHEVDFMTASSY

GSGMSTTRDVKILKDLDEDIRGKDVLIVEDIIDSGNTLSKVREILSLREPKSLAICTLLDKPSRREVNVP

VEYVGFAIPDEFVVGYGIDYAQRYRHLPYIGKVTLLDE

>lcl|NZ\_FO834906.1\_prot\_WP\_012542835.1\_4277 [locus\_tag=BN49\_RS31200] [protein=hypothetical protein] [protein\_id=WP\_012542835.1] [location=complement(4459366..4459485)] [gbkey=CDS]

MALLIPAPKISFCWYTGWLAGHRRGESSGFDDLYLESNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002888816.1\_4278 [locus\_tag=BN49\_RS23135] [protein=glucose/quinate/shikimate family membrane-bound PQQ-dependent dehydrogenase] [protein\_id=WP\_002888816.1] [location=4459566..4461956] [gbkey=CDS]

MAETKSQQSRLLVTLTALFAAFCGLYLLIGGAWLVVLGGSWYYPIAGLVMLGVTVMLFRGKRAALWLYAA

LLLATMIWGVWEVGFDFWALTPRSDILVFFGIWLILPFVWRRLPVPSAGAVGALVVALLISGGMLTWAGF

NDPQEVNGTLSADATPAAPISTVADGDWPAYGRNQEGQRFSPLKQINADNVKNLKEAWVFRTGDLKQPND

PGEITNEVTPIKVGDTLFLCTAHQRLFALDAATGKEKWHFDPQLNADPSFQHVTCRGVSYHEAKADNAPA

DVVADCPRRIILPVNDGRLFAVNADNGKLCETFANKGILNLQTNMPVTTPGMYEPTSPPIITDKTIVIAG

AVTDNFSTREPSGVIRGFDVNTGKLLWAFDPGAKDPNAIPSDEHHFTLNSPNSWAPAAYDAKLDLVYLPM

GVTTPDIWGGNRTPEQERYASSIVALNATTGKLAWSYQTVHHDLWDMDMPSQPTLADIEVNGKTVPVIYA

PAKTGNIFVLDRRNGELVVPAPEKPVPQGAAKGDYVTKTQPFSDLSFRPKKDLTGADMWGATMFDQLVCR

VIFHQLRYEGIFTPPSEQGTLVFPGNLGMFEWGGISVDPNRQVAIANPMALPFVSKLIPRGPGNPMEPPK

DAKGSGTESGVQPQYGVPYGVTLNPFLSPFGLPCKQPAWGYISALDLKTNEVVWKKRIGTPQDSLPFPMP

VKLPFTMGMPMLGGPISTAGNVLFIGATADNYLRAYNMSNGEKLWEARLPAGGQATPMTYEVNGKQYVVI

SAGGHGSFGTKMGDYIVAYALPDDAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004222681.1\_4279 [gene=cueO] [locus\_tag=BN49\_RS23140] [protein=multicopper oxidase CueO] [protein\_id=WP\_004222681.1] [location=complement(4462040..4463638)] [gbkey=CDS]

MQRRDFLKLTAAVGMASALPLWSRAVFAASRPALPIPSLLAADARNRIALRIQAGKTRFGALNATTWGYN

GSLLGPALQLTQGKTVTVDITNQLAEETTLHWHGLEVPGEVDGGPQGVIAPGATRTVSFTPTQRAATCWF

HPHQHGSTGRQVAMGLAGLVLIEDEESGRLLLPKQWGIDDVPVIVQDKKFTAAGEIDYQLDVMSAAVGWF

GDTLLTNGALYPEHAAPRGWLRLRLLNGCNARSLNFATSDKRPLYVVASDGGLLAEPVKVDELPVLMGER

FEVLVDTSDGKPFDLVTLPVSQMGMAIAPFDKPQPVLRVQPLVIPASGKLLDTLAALPALPSLTGLTQRQ

LQLSMDPMLDRMGMQALMEKYGDQAMAGMDHGMMGHGDMSDMGNMHHGDMSMNHGTGMEHGMSSGKGFDF

HNANRINGKAFDMNEPMFAAARGQYERWVISGKGDMMLHPFHIHGTQFRILSENGKPPAAHRRGWKDTVR

VEGDVSEVLVKFDHPAPKEFAYMAHCHLLEHEDTGMMLGFTV

>lcl|NZ\_FO834906.1\_prot\_WP\_002888808.1\_4280 [locus\_tag=BN49\_RS23145] [protein=YacC family pilotin-like protein] [protein\_id=WP\_002888808.1] [location=4463784..4464131] [gbkey=CDS]

MKTLFRTMVLGSLLALSANSYALSESEAEDMADLTAVFVFLKNDCGYQNLPNTQIRRALVFFAQQNQWDL

SNYDSYNMKALGEDSYRDLSGINIPTAKKCKALARDSLSLLAYVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004145917.1\_4281 [locus\_tag=BN49\_RS23150] [protein=hypothetical protein] [protein\_id=WP\_004145917.1] [location=4464378..4464788] [gbkey=CDS]

MNISLTLRVIPLAALLVAGCSNTSSRQPVKPIATPLTSQQQAEQERAASEQARIESCRQALDSLKEVNPQ

QATKLSNDFNALVRAASQYNSVREKVADPTRLGIDSMYQFKSIKLCADIQKTLIDSLVQRGESKQP

>lcl|NZ\_FO834906.1\_prot\_4282 [locus\_tag=BN49\_RS31205] [protein=peptidylprolyl isomerase] [pseudo=true] [partial=3'] [location=4465370..>4465609] [gbkey=CDS]

MTQLAATEKEKQAALEQVKALNADKQPLTTRLAAAEKEKQAVLEQVKALNADKQSLTIRLAAAEKAQQAA

LDQAKALNAD

>lcl|NZ\_FO834906.1\_prot\_WP\_040209737.1\_4283 [locus\_tag=BN49\_RS30610] [protein=FKBP-type peptidyl-prolyl cis-trans isomerase] [protein\_id=WP\_040209737.1] [location=4465787..4466980] [gbkey=CDS]

MATRLAAAEKEKQAVLEQVKALNADKQSLTIRLAAAEKAQQAALDQAKALNADKQPLATRLAAAEKEKQA

VLEQVKALNADKQSLTIRLAAAEKTQQAALDQVKALNADKQSLSTRLAAADKVPHGPANDAAAPKNEPPE

MAAIVAAYRLQADKDNAQLRMKEDEIELLRTQLSVQSKTRSGESAAAKLSASGEQQAYAIGASMGSEALN

VLTTRRTQGVTVDAGLVLQGIEDAFRGQLRLGEQERNKALFDVSQQVYQNLNKIEQKNISAGKKYQQAFA

RKKDVVFKEGVYSRVDYPGKGKISGNDLVTVVIKEMLTDGTVINDMEAKDQALTQKLDAYPPVFREPLKR

LQNHGSVTLVVPPEKAYGSKGLPPKIPPGATMVYSVRIVDSQPEPAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002888741.1\_4284 [gene=speE] [locus\_tag=BN49\_RS23160] [protein=polyamine aminopropyltransferase] [protein\_id=WP\_002888741.1] [location=4467130..4467990] [gbkey=CDS]

MADNPLWHETLHDHFGQYFSVDNVLYHEKTDHQDLIIFDNRAFGRVMALDGVVQTTERDEFIYHEMMTHV

PLLAHGNAKHVLIIGGGDGAMLREVSRHRSIETITMVEIDAGVVSFCRQYLPNHNAGAYDDPRFTLVIDD

GVNFVNQTTQTFDVIISDCTDPIGPGESLFTSAFYEGCKRCLNPGGIFVAQNGVCFLQQDEAVGSHRKLS

HYFRDVSFYQAAIPTYYGGIMTFAWASDNEALRHLSSEIIQARFHKANLTCRYYNPAIHTAAFALPQYLH

DALSAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002888739.1\_4285 [gene=speD] [locus\_tag=BN49\_RS23165] [protein=adenosylmethionine decarboxylase] [protein\_id=WP\_002888739.1] [location=4468015..4468809] [gbkey=CDS]

MKKLKLHGFNNLTKSLSFCIYDICYAKTAEERDGYIAYIDELYNANRLTEILTETCSIIGANILNIARQD

YEPQGASVTILVSEEPVDPKLIDQTEHPGPLPETVVAHLDKSHICVHTYPESHPEGGLCTFRADIEVSTC

GVISPLKALNYLIHQLESDIVTIDYRVRGFTRDINGMKHFIDHEINSIQNFMSDDMKSLYDMVDVNVYQE

NIFHTKMLLKEFDLKHYMFHTRPEELTAEERKVITDLLWKEMREIYYGRNIPAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016531441.1\_4286 [gene=yacL] [locus\_tag=BN49\_RS23170] [protein=protein YacL] [protein\_id=WP\_016531441.1] [location=complement(4468882..4469244)] [gbkey=CDS]

MDYEFLRDITGVVKVRMSMDHEAIGHWFNEEVKGNLTLLDEVEQAARTVKGSERSWQRAGHEYTLWLDGE

EVMIRANQLEFSGDEIEEGMSYYDEESLSLCGVEDFLQVVAAYREFMQQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002888735.1\_4287 [gene=acnB] [locus\_tag=BN49\_RS23175] [protein=bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase] [protein\_id=WP\_002888735.1] [location=complement(4469431..4472028)] [gbkey=CDS]

MLEEYRKHVAERAAMGIVAKPLDATQMAALVELLKNPPAGEEEFLLDLLINRVPPGVDEAAYVKAGFLAA

IAKGEATSPLVTPEKAVELLGTMQGGYNIHPLIDALDDAKLAPIAAKALSHTLLMFDNFYDVEEKAKAGN

EHAKQVMQSWADAEWFLNRPQLAEKITVTVFKVTGETNTDDLSPAPDAWSRPDIPLHALAMLKNPREGIE

PDQPGVVGPIKQIEALQQKGYPLAYVGDVVGTGSSRKSATNSVLWFMGDDIPNVPNKRGGGLCLGGKIAP

IFFNTMEDAGALPIEVDVSNLNMGDVIDVYPFKGEVRNHETNELLASFELKTDVLIDEVRAGGRIPLIIG

RGLTTKAREALGLPHSDVFRQAKDVAESTRGFSLAQKMVGRACGVAGIRPGAYCEPKMTSVGSQDTTGPM

TRDELKDLACLGFSADLVMQSFCHTAAYPKPVDVTTHHTLPDFIMNRGGVSLRPGDGVIHSWLNRMLLPD

TVGTGGDSHTRFPIGISFPAGSGLVAFAAATGVMPLDMPESVLVRFKGKMQPGITLRDLVHAIPLYAIKQ

GLLTVEKKGKKNIFSGRILEIEGLPDLKVEQAFELTDASAERSAAGCTIKLNKEPIVEYLNSNIVLLKWM

IAEGYGDRRTLERRIQGMEKWLADPQLLEADADAEYAAVIDIDLADIKEPILCAPNDPDDARLLSDVQGE

KIDEVFIGSCMTNIGHFRAAGKLLDSHKGQLPTRLWVAPPTRMDAAQLTEEGYYSVFGKSGARIEIPGCS

LCMGNQARVADGATVVSTSTRNFPNRLGTGANVYLASAELAAVASLLGKLPTPEEYQTFVAQVDKTAEDT

YRYLNFNQLDQYTEKADGVIFQTAV

>lcl|NZ\_FO834906.1\_prot\_WP\_032103873.1\_4288 [locus\_tag=BN49\_RS23185] [protein=DUF3300 domain-containing protein] [protein\_id=WP\_032103873.1] [location=4472460..4474067] [gbkey=CDS]

MSLPFKPHIIALLCSAGLLAAAGTLYVQSRTPATIAEPPAQQAPAPAASTTQPVAATYTQAQIDQWVAPI

ALYPDSLLSQVLMASTYPDNVLQAVQWSQDNPAMKGDAAVQAVASQPWDPSVKSLVAFPALLAMMGENPP

WVENLGNAFLAQPHDVMDSVQRLRAIAQQTGTLKSTPQQKVIVTPAAPVSASSSTAATATAHTAAPAPKQ

VIKIEPTNPQVVYVPSYNPSTVYGTWPNSAYPPVYLPPPPGEQFTDSFVKGFGYSLGVATTWALFSSIDW

DDDDHHHHDDDYHHGDYSHNGDNININVNNFNHITGENLPGNHVNWQHNPAYRGHTPYPDNTVAQRFHQT

NVSGGLSATQHAPVDREAQRQAAMTQLQHNVPTATAGNLAANNTSRDAQRQAASAQLKQATQRSNYRGYD

STPTQQQRREAAKTQLKNPTPQQQQRREAARSHEQNRTPQQQQRRQQFQSATPAQRQQTLSHLRANALSG

NESRAPSWQAQQERGLQSRQFSGVNRELRDGTRERLSEHHELRRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531566.1\_4289 [locus\_tag=BN49\_RS23190] [protein=DUF2950 family protein] [protein\_id=WP\_016531566.1] [location=4474079..4474885] [gbkey=CDS]

MRNPLSVALFTLMLSPLAAFAQQQFATPEQAATALAEAISQPNEAALSEVLGDNWQQFLPTDGIDPAAVD

RFQRDWQVKHVIIQQGGKAWLDVGSEAWRLPVPIVKASEGWRFDMAAGEEEILTRAIGRNELSAIAAMHA

YVDAQQDYYHLNHRWAQKIISSEGKKDGLYWPTSPGEAPSPLGPAFSPTVPGSGYHGYRFRIIAGRDDQS

VALLAWPIAWGETGVMSFMIDQQDRVYQANLGEESAAKAQEITRFTPDADAGWQVAEP

>lcl|NZ\_FO834906.1\_prot\_WP\_004177403.1\_4290 [locus\_tag=BN49\_RS23195] [protein=hypothetical protein] [protein\_id=WP\_004177403.1] [location=complement(4474930..4475214)] [gbkey=CDS]

MKRFLTTALVAATFFTGVAYAADANIPWADNSGGTETTHIAAMGQDLNAQHQQVTKTNEGVWAANSGSIS

ADEAALSSTKPAFAGDPSLMPHQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002888731.1\_4291 [gene=lpdA] [locus\_tag=BN49\_RS23200] [protein=dihydrolipoyl dehydrogenase] [protein\_id=WP\_002888731.1] [location=complement(4475379..4476803)] [gbkey=CDS]

MSTEIKTQVVVLGAGPAGYSAAFRCADLGLETVIVERYSTLGGVCLNVGCIPSKALLHVAKVIEEAKALA

EHGIVFGEPKTDIDKIRTWKEKVITQLTGGLAGMAKGRKVKVVNGLGKFTGANTLEVEGENGKTVINFDN

AIIAAGSRPIQLPFIPHEDPRVWDSTDALELKSVPKRMLVMGGGIIGLEMGTVYHALGSEIDVVEMFDQV

IPAADKDVVKVFTKRISKKFNLMLETKVTAVEAKEDGIYVSMEGKKAPAEAQRYDAVLVAIGRVPNGKNL

DAGKAGVEVDDRGFIRVDKQMRTNVPHIFAIGDIVGQPMLAHKGVHEGHVAAEVISGLKHYFDPKVIPSI

AYTEPEVAWVGLTEKEAKEKGISYETATFPWAASGRAIASDCADGMTKLIFDKETHRVIGGAIVGTNGGE

LLGEIGLAIEMGCDAEDIALTIHAHPTLHESVGLAAEVFEGSITDLPNAKAKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004147092.1\_4292 [gene=aceF] [locus\_tag=BN49\_RS23205] [protein=pyruvate dehydrogenase complex dihydrolipoyllysine-residue acetyltransferase] [protein\_id=WP\_004147092.1] [location=complement(4477010..4478908)] [gbkey=CDS]

MAIEIKVPDIGADEVEITEILVKVGDKVEAEQSLITVEGDKASMEVPSPQAGVVKEIKVSVGDKTETGKL

IMIFDSAEGAAAAAPAQEEKKEAAPAAAAPAAAAAAKEVHVPDIGGDEVEVTEIMVKVGDTIAAEQSLIT

VEGDKASMEVPAPFAGTVKEIKINTGDKVSTGSLIMIFEVAGAAPAAAPAQAAAPAAAAPAAAAGVKDVN

VPDIGGDEVEVTEVMVKVGDKVAAEQSLITVEGDKASMEVPAPFAGTVKEIKISTGDKVKTGSLIMVFEV

EGAAPAAAPAQAAAPAPAAAPAQAAKPAAAPAAKAEGKSEFAENDAYVHATPLIRRLAREFGVNLAKVKG

TGRKGRILREDVQAYVKDAVKRAESAPAAAAGGGIPGMLPWPKVDFSKFGEVEEVELGRIQKISGANLSR

NWVMIPHVTHFDKTDITDLEAFRKQQNAEAEKRKLDVKFTPVVFIMKAVAAALEQMPRFNSSLSEDGQRL

TLKKYINIGVAVDTPNGLVVPVFKDVNKKSITELSRELTTISKKARDGKLTAGEMQGGCFTISSIGGLGT

THFAPIVNAPEVAILGVSKSAMEPVWNGKEFVPRLMLPISLSFDHRVIDGADGARFITIINNTLSDIRRL

VM

>lcl|NZ\_FO834906.1\_prot\_WP\_002888700.1\_4293 [gene=aceE] [locus\_tag=BN49\_RS23210] [protein=pyruvate dehydrogenase (acetyl-transferring), homodimeric type] [protein\_id=WP\_002888700.1] [location=complement(4478923..4481586)] [gbkey=CDS]

MSERLHNDVDPIETRDWLQAIESVIREEGVERAQYLIDQLLSEARKGGVKVAAGASAGNYVNTIAVEDEP

EYPGNLDLERRIRSAIRWNAIMTVLRASKKDLELGGHMASYQSSATFYEVCFNHFFRARTEKDGGDLVYF

QGHISPGVYARAFLEGRLTEEQMDNFRQEVHGKGLSSYPHPKLMPEFWQFPTVSMGLGPLGAIYQAKFLK

YLEHRGLKDTSEQTVYAFLGDGEMDEPESKGAITIATREKLDNLVFVINCNLQRLDGPVTGNGKIINELE

GIFGGAGWNVIKVIWGGRWDELLRKDTSGKLIQLMNETVDGDYQTFKSKDGAYVREHFFGKYPETAALVA

DWTDEQIWALNRGGHDPKKVYAALKKAQETKGQPTVILAHTIKGYGMGDTAEGKNIAHQVKKMNMDGVRY

VRDRFNVPVADADLEKLPYVTFPEGSEEHTYLHAQRQKLNGYLPTRQPKFTEKLELPTLADFSALLEEQN

KEISTTIAFVRALNVMLKNKSIKDRLVPIIADEARTFGMEGLFRQIGIYSPNGQQYTPQDREQVAYYKED

EKGQILQEGINELGAGASWLAAATSYSTNNLPMIPFYIYYSMFGFQRIGDLCWAAGDQQARGFLIGGTSG

RTTLNGEGLQHEDGHSHIQSLTIPNCISYDPAYAYEVAVIMHDGLVRMYGEAQENVYYYITTLNENYHMP

AMPEGAEEGIRKGIYKLETIEGSKGKVQLLGSGSILRHVREAAQILAKDYGVGSDVYSVTSFTELARDGQ

DCERWNMLHPLETPRVPYIAQVMNDAPAVASTDYMKLFAEQVRTYVPADDYRVLGTDGFGRSDSRENLRH

HFEVDASYVVVAALGELAKRGEIDKKVVADAIAKFDIDAEKVNPRLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002888699.1\_4294 [gene=pdhR] [locus\_tag=BN49\_RS23215] [protein=pyruvate dehydrogenase complex transcriptional repressor PdhR] [protein\_id=WP\_002888699.1] [location=complement(4481723..4482502)] [gbkey=CDS]

MAYSKIRQPKLSDVIEQQLEFLILEGTLRPGEKLPPERELAKQFDVSRPSLREAIQRLEAKGLLLRRQGG

GTFVQSRLWQSFSDPLVELLSDHPESQFDLLETRHALEGIAAYYAALRSNDEDRDRIRELHQAIERAQQS

GDLDAESGAVVQYQIAVTEAAHNVVLLHLLRCMEPMLAQNVRQNFELLYARREMLPLVSNHRTRIFEAIM

AGEPEQAREASHRHLAFIEEILLDRSREQSRRERSLRRLQQRKDENSGS

>lcl|NZ\_FO834906.1\_prot\_WP\_004147090.1\_4295 [gene=aroP] [locus\_tag=BN49\_RS23225] [protein=aromatic amino acid transporter AroP] [protein\_id=WP\_004147090.1] [location=4483146..4484516] [gbkey=CDS]

MEGQQHGDRLKRGLKNRHIQLIALGGAIGTGLFLGSASVIQSAGPGIILGYAIAGFIAFLIMRQLGEMVV

EEPVAGSFSHFAYKYWGGFAGFASGWNYWVLYVLVAMAELTAVGKYIQFWWPEIPTWASAAVFFIAINAI

NLTNVKVFGEMEFWFAIIKVVAVVAMILFGGWLLFSGNGGPQATVRNLWDQGGFLPHGFYGLVMMMAIIM

FSFGGLELVGITAAEADNPEQSIPKATNQVIYRILIFYVGSLAVLLSLLPWTRVTADTSPFVLIFHELGD

TLVANALNVVVLTAALSVYNSCVYCNSRMLFGLAQQGNAPKALLSVDKRGVPVNTILVSALVTALCVLIN

YLAPESAFGLLMALVVSALVINWAMISLAHMKFRRAKKQQGVVTRFPALFYPLGNWLCLLFMAAVLVIML

MTPGMAISVWLIPVWIAVLGVGYLFKEKAAATIKAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004145929.1\_4296 [locus\_tag=BN49\_RS23230] [protein=MFS transporter] [protein\_id=WP\_004145929.1] [location=4484701..4486107] [gbkey=CDS]

MAENTLSIREKIGYGMGDAGCNIIFGAIMLFVNYFYTDIFGLAPALVGVLLLSVRVIDAVTDPIMGALAD

RTRSKYGRFRPWLLWIAFPYALFSVLMFTTPEWTYNSKVIYAFVTYFLLSITYTAINIPYCSLGTVMTAD

PKERVACQSYRFVMVGIATLLLSLTLLPMADWFGGADKAKGYQMAMTVLAFIGMCMFLFCFATVRERIRP

AVQTNDELKKDLKDVWKNDQWVRILLLTLCNVCPGFIRMAATMYYVTWVMGQSTHFATLFISLGVVGMMI

GSMLAKVLTDRWCKLQVFFWTNIVLAVFSCAFYFFNPHATTLIMVLYFLLNILHQIPSPLHWSLMSDVDD

YGEWKTGKRITGISFSGNLFFLKVGLAVAGAMVGFLLSWYGYDAGAKAQSASALNGIVLLFSVIPGVGYL

ITAGVVRLLKVDRTLMRQIQSDLEKRRSNYSELNEYQELKTSEHVRKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043773.1\_4297 [locus\_tag=BN49\_RS23235] [protein=family 43 glycosylhydrolase] [protein\_id=WP\_046043773.1] [location=4486107..4487057] [gbkey=CDS]

MDNWPTPFIEQRADPFILRHLSHYYFIASVPEYDRLEIRRAVTLEGLRDAEPVVVWRAPQSGPMSQLIWA

PELHEIDGKWYIYFAATHTHDLDALGMFQHRMFVLECADSDPLTGRWQEKGQVVTPFDTFALDATTFTHQ

GKRWYLWAQKSPHIEGNSNLYLAEMANPWTLKGEPVMLSKPEFDWECRGFKVNEGPAVLMHGDKLFISYS

ASATDENYCMGLLWIDRQADPLQPANWHKAPQPVFRTSYENRQYGPGHNSFTQTPEGEDVLVYHARNYTE

IEGDPLYDPNRHTRLKLVSWREDGMPDFGIPPADTL

>lcl|NZ\_FO834906.1\_prot\_WP\_004177406.1\_4298 [gene=ampE] [locus\_tag=BN49\_RS23240] [protein=beta-lactamase regulator AmpE] [protein\_id=WP\_004177406.1] [location=complement(4487293..4488147)] [gbkey=CDS]

MTLFTTLLVLIAERLFKLGEHWQLDHRLEVAFRRIKHFSLPGTLLMTLVAVAVVYIIQRLLQGQLFNIPL

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YRYYLAPLFWFVVGGAWGPLTLIAYSVLRAWQTWLARYQTPHHRLQSGIDGILHIVDWLPVRLVGVVYAL

VGHGEKALPAWFASLGDRHSSQYQVLTRLAQYSLAREPHVDKVATPKAAVSMAKKTSLVVVVIMALLTIY

GTLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002888692.1\_4299 [gene=ampD] [locus\_tag=BN49\_RS23245] [protein=1,6-anhydro-N-acetylmuramyl-L-alanine amidase AmpD] [protein\_id=WP\_002888692.1] [location=complement(4488144..4488707)] [gbkey=CDS]

MQLNEGWLVGARRVPSPHHDCRPDEETPSLLVVHNISLPPGEFGGPWIDALFTGTLDPHAHPFFAEIAHL

RVSAHCLIRRDGEIVQYVPFDKRAWHAGVSCYQGRERCNDFSIGIELEGTDTLAYTDAQYRQLAAVTDLL

IALYPAIAENIAGHSDIAPVRKTDPGPAFDWIKYRALLSAPSEKETS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888684.1\_4300 [gene=nadC] [locus\_tag=BN49\_RS23250] [protein=carboxylating nicotinate-nucleotide diphosphorylase] [protein\_id=WP\_002888684.1] [location=4488841..4489734] [gbkey=CDS]

MSPRRYNPDRRRDVLLERINLDITDAVAHSLREDLGGEVDANNDISAQLLPQDARSHAVVITREDGVFCG

KRWVEEVFIQLAGDDVNITWHVADGDAVKADQPLFELEGPSRILLTGERTALNFVQTLSGVASVVRRYVD

LLAGTKTQLLDTRKTLPGLRTALKYAVLCGGGANHRLGLFDAFLIKENHIIASGSIRQAVEKAFWLHPDV

PVEVEVETLDELEQALKAGADIIMLDNFTTDLMREAVKITAGQAALEVSGNVTFDTIREFADTGVDYISV

GALTKHVQALDLSMRFR

>lcl|NZ\_FO834906.1\_prot\_WP\_002888683.1\_4301 [gene=ppdD] [locus\_tag=BN49\_RS23255] [protein=prepilin peptidase-dependent pilin] [protein\_id=WP\_002888683.1] [location=4489916..4490347] [gbkey=CDS]

MDKQRGFTLIELMVVIGIIAILSAIGIPAYQNYLRKAALTDLLQTFVPYRTAIELCALDHGGLTPCDGGS

NGIPSPTTTRYLSAMSVAKGVVTLTGQESLNGLGVTLTPTWDNAEGVTGWQRVCTITGNSALQQACEDVF

RVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531569.1\_4302 [gene=gspE] [locus\_tag=BN49\_RS23260] [protein=type II secretion system protein GspE] [protein\_id=WP\_016531569.1] [location=4490358..4491743] [gbkey=CDS]

MKTEQLIPLCRRYHALLLHSDEQTISIAVVNTPPAELMEALRFATQKRIDIECWRQEQMDKRLQAQEKQA

QLAQNDGPENIAERVNQILEQALRQRASDIHIEPTETHLRIRLRVDGVLHALPLLAPELAAPVIARLKVL

ASLDIAEHRLPQDGQFALNLAGRPLSFRIATLPCRYGEKIVLRLLHQVDQALDLEALGLSSSQLAAFRQA

LNQPQGLLLVTGPTGSGKTVTLYSALQARNREQVNICSVEDPLEIPIAGMNQTQINPRAGLTFHSVLRAL

LRQDPDIVMVGEIRDAETAEIALKAAQTGHLVLSTLHTNSTSETLTRLQQMGIARWMISSALSLVIAQRL

VRKLCPHCRRNAGSAADLPHSLWPRPLPRWQAAGCEHCYHGYYGRLALFEVLPVTPGLRQGIVQGLNAIE

IESLARAAGMMTLFESGCQAIEQGLTSLEEVVRVLGIPHGD

>lcl|NZ\_FO834906.1\_prot\_WP\_004182933.1\_4303 [gene=hofC] [locus\_tag=BN49\_RS23265] [protein=protein transport protein HofC] [protein\_id=WP\_004182933.1] [location=4491733..4492938] [gbkey=CDS]

MATKRLWRWRGIDVQGAPCQGMLWQTKRLEVLQHLQQQRVIPLAVRRCAVKQSLWHPRYSCETIRQLATL

LQAGLPLAEGLSLLAQQQSHAQWQALLEALGRELAQGVAFSAALAQWPQAFPPLYLAMISTGELTGKLDI

CCLQLANQQQEQQRLASKVKKALRYPLIVLSLALLVVLGMLYFVLPEFTAIYQTFSTPLPLLTRMVVAAG

DMLSRGWPLLLASLLSPLLLNQLIRRRSDWLLRRQRLLNALPLIGSLIGGQQLSLIFTILALTQSAGISF

LQGLQSVEESLSCPLWRQRLAQARALIVQGEPIWQALSRCGGFTPLCLQLIRTGESAGALDQMLENLAHH

HRQQTYQRADSLAAHLEPMMLVITGSLVGILVVAMYLPVFHLGDAIGGAGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004145938.1\_4304 [locus\_tag=BN49\_RS23270] [protein=GMP reductase] [protein\_id=WP\_004145938.1] [location=complement(4492975..4494018)] [gbkey=CDS]

MRIEEDLKLGFKDVLIRPKRSTLKSRSDVELEREFTFKHSGLTWSGVPIIAANMDTVGTFSMAKALATFG

ILTAVHKHYTAEEWLAFTQGASADVLKHVMVSTGTSDADFEKTQQILSQNPQLNFVCIDVANGYSEHFVQ

FVAKAREAWPQKTIIAGNVVTGEMCEELILSGADIVKVGIGPGSVCTTRVKTGVGYPQLSAVIECADAAH

GLGGQIISDGGCTMPGDVAKAFGGGADFVMLGGMLAGHEESGGTIVEENGEKFMLFYGMSSESAMTRHVG

GVAKYRAAEGKTVKLPLRGPVENTARDILGGLRSACTYVGASRLKELTKRTTFIRVQEQENRVFNSL

>lcl|NZ\_FO834906.1\_prot\_WP\_032103863.1\_4305 [gene=coaE] [locus\_tag=BN49\_RS23280] [protein=dephospho-CoA kinase] [protein\_id=WP\_032103863.1] [location=4494362..4494982] [gbkey=CDS]

MGYTVALTGGIGSGKSTVADAFAQLGVKVIDADVIARQVVEPGTPALQAIVGHFGPQMIAPDGTLNRRLL

REKIFAHVEEKAWLNALLHPLIQQETRRQMQAATSPYILWVVPLLVENRLSGQADRVLVVDVPKETQIER

TMLRDKVSREHAEHILAAQATRQQRLAVADDVIENTGTPDAVASDVARLHEKYLTLASQAASQENL

>lcl|NZ\_FO834906.1\_prot\_WP\_004178596.1\_4306 [gene=zapD] [locus\_tag=BN49\_RS23285] [protein=cell division protein ZapD] [protein\_id=WP\_004178596.1] [location=4494982..4495725] [gbkey=CDS]

MHTPVLFEHPLNEKMRTWLRIEFLIQQMAFRPQIASHADALHFFRNAGDLLDVLERGEVRTDLVKELERQ

QRKLQSWAEVPGVDQERINELRHQLKQSSSTLMAAPRIGQFLREDRLIALVRQRLSIPGGCCSFDLPTLH

IWLHMPQAHRDEQVASWLASLDPLVQSLSLILDLIRNSALFRKQTSLNGFYQDNGEDADLLRLRLDLAHQ

LYPQISGHKSRFAIRFLALDSEYGIVPERFDFELACC

>lcl|NZ\_FO834906.1\_prot\_WP\_002888644.1\_4307 [gene=yacG] [locus\_tag=BN49\_RS23290] [protein=DNA gyrase inhibitor YacG] [protein\_id=WP\_002888644.1] [location=4495735..4495929] [gbkey=CDS]

MSEETIVNCPTCGKTVVWGEQSPFRPFCSKRCQLIDLGEWAAEEKRIPSAGDLSDSDDWSEQQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002888641.1\_4308 [gene=mutT] [locus\_tag=BN49\_RS23295] [protein=8-oxo-dGTP diphosphatase MutT] [protein\_id=WP\_002888641.1] [location=complement(4495982..4496374)] [gbkey=CDS]

MKKLQIAVGIIRNPQGEIFITQRAADAHMANKLEFPGGKIESDETPEQALIRELQEEVGITVTASSLFDK

LEYQFPDRHITLWFFLVESWQGEPWGKEGQPGRWMAGPTLDPAAFPPANEPVISKLIAQG

>lcl|NZ\_FO834906.1\_prot\_WP\_020805137.1\_4309 [gene=secA] [locus\_tag=BN49\_RS23300] [protein=preprotein translocase subunit SecA] [protein\_id=WP\_020805137.1] [location=complement(4496433..4499138)] [gbkey=CDS]

MLIKMLTKVFGSRNDRTLRRMRKVVNIINGMEPAMEKLSDDELKAKTTEFRARLEKGETLESLIPEAFAV

VREASKRVFGMRHFDVQLLGGMVLNDRCIAEMRTGEGKTLTATLPAYLNALTGKGVHVVTVNDYLAQRDA

ENNRPLFEFLGMTVGINMSGLPAPAKREAYAADITYGTNNEYGFDYLRDNMAFSPEERVQRKLHYALVDE

VDSILIDEARTPLIISGPAEDSSEMYRKVNKIIPHLIRQEKEDSDTFTGEGHFSVDEKARQVNLTERGLV

LIEELLVQEGIMDEGESLYSPTNIMLMHHVTAALRAHALFTRDVDYIVKDGEVIIVDEHTGRTMQGRRWS

DGLHQAVEAKEGVEIQNENQTLASITFQNYFRLYEKLAGMTGTADTEAFEFSSIYKLDTVVVPTNRPMIR

KDMADLVYMTEAEKIQAIIEDIKTRTAAGQPVLVGTISIEKSEVVSRELTKAGIKHNVLNAKFHASEADI

VAQAGYPSAVTIATNMAGRGTDIMLGGSWQAEVAALENPTPEQIEKIKADWQVRHDAVLAAGGLHIIGTE

RHESRRIDNQLRGRAGRQGDAGSSRFYLSMEDALMRIFASDRVSGMMRKLGMKPGEAIEHPWVTKAIANA

QRKVESRNFDIRKQLLEYDDVANDQRRAIYTQRNELLDVSDVSETINSIREDVFKATIDAHIPPQSLEEM

WDIEGLQERLKNDFDLDLPIKEWLDKEPELHEETLRERILQSAVETYQRKEEVVGAEMMRHFEKGVMLQT

LDSLWKEHLAAMDYLRQGIHLRGYAQKDPKQEYKRESFSMFAAMLESLKYEVISTLSKVQVRMPEEVEAM

EQQRREEAERLAQMQQLSHQSDDEAAAQDLAAQTGERKVGRNDPCPCGSGKKYKQCHGRLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888635.1\_4310 [gene=secM] [locus\_tag=BN49\_RS23305] [protein=secA translation cis-regulator SecM] [protein\_id=WP\_002888635.1] [location=complement(4499201..4499698)] [gbkey=CDS]

MSGLLTRWRQFGRRYFWPHLLLGMVAASLGLPALSNGHETAAPAKATASNHNPSKVNFSQLALLETNRRP

SFTVDYWHQHAIRTVIRHLSFAMAPQALPVAEETSPLQAQHLALLDTLSALLTQDSTPPVVIRQAGYIPS

SYSAFRVSAWISQVAGIRAGPQRLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888632.1\_4311 [gene=lpxC] [locus\_tag=BN49\_RS23310] [protein=UDP-3-O-acyl-N-acetylglucosamine deacetylase] [protein\_id=WP\_002888632.1] [location=complement(4500021..4500938)] [gbkey=CDS]

MIKQRTLKRIVQATGVGLHTGKKVTLTLRPAPANTGVIYRRTDLNPPVDFPADAKSVRDTMLCTCLVNEH

DVRISTVEHLNAALAGLGIDNIIVEVDAPEIPIMDGSAAPFVYLLLDAGIDELNCAKKFVRIKETVRVED

GDKWAEFKPYNGFSLDFTIDFNHPAIDASTQRYTLNFSADAFMRQISRARTFGFMRDIEYLQSRGLCLGG

SFDCAIVVDDYRVLNEDGLRFEDEFVRHKMLDAIGDLFMCGHNIIGAFTAYKSGHALNNKLLQAVLAKQE

AWEYVTFEDDAKLPMAFRAPSMVLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002888628.1\_4312 [gene=ftsZ] [locus\_tag=BN49\_RS23315] [protein=cell division protein FtsZ] [protein\_id=WP\_002888628.1] [location=complement(4501039..4502190)] [gbkey=CDS]

MFEPMELTNDAVIKVIGVGGGGGNAVEHMVRERIEGVEFFAVNTDAQALRKTAVGQTIQIGSGITKGLGA

GANPEVGRNAADEDREALRAALDGADMVFIAAGMGGGTGTGAAPVVAEVAKDLGILTVAVVTKPFNFEGK

KRMAFAEQGITELSKHVDSLITIPNDKLLKVLGRGISLLDAFGAANDVLKGAVQGIAELITRPGLMNVDF

ADVRTVMSEMGYAMMGSGVASGEDRAEEAAEMAISSPLLEDIDLSGARGVLVNITAGFDLRLDEFETVGN

TIRAFASDNATVVIGTSLDPDMNDELRVTVVATGIGMDKRPEITLVTNKQVQQPVMDRYQQHGMSPLTQE

QKPAAKVVNDNTPQTAKEPDYLDIPAFLRKQAD

>lcl|NZ\_FO834906.1\_prot\_WP\_002888625.1\_4313 [gene=ftsA] [locus\_tag=BN49\_RS23320] [protein=cell division protein FtsA] [protein\_id=WP\_002888625.1] [location=complement(4502253..4503515)] [gbkey=CDS]

MIKATDRKLVVGLEIGTAKVAALVGEVLPDGMINIIGVGSCPSRGMDKGGVNDLESVVKCVQRAIDQAEL

MADCQISSVYLALSGKHISCQNEIGMVPISEEEVTQDDVENVVHTAKSVRVRDEHRVLHVIPQEYAIDYQ

EGIKNPVGLSGVRMQAKVHLITCHNDMAKNIVKAVERCGLKVDQLIFAGLAASYSVLTEDERELGVCVVD

IGGGTMDIAVYTGGALRHTKVIPYAGNVVTSDIAYAFGTPPSDAEAIKVRHGCALGSIVGKDENVEVPSV

GGRPPRSLQRQTLAEVIEPRYTELLNLVNEEILQLQEQLRQQGVKHHLAAGIVLTGGAAQIEGLAACAQR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002888624.1\_4314 [gene=ftsQ] [locus\_tag=BN49\_RS23325] [protein=cell division protein FtsQ] [protein\_id=WP\_002888624.1] [location=complement(4503512..4504342)] [gbkey=CDS]

MSQAALNTRNHEEEASSSRRSNGTRLAGIVFLLAVLFTVLVSGWMVLGWMEDAQRLPLSKMVVTGERHYT

RNDDIRQAILALGSPGTFMTQDVNIIQSQIERLPWIKQASVRKQWPDELKIHLVEYVPIARWNDQHMVDA

EGNAFSVPADRTSKQNLPMLYGPEGSENEVLQGYRDMGQVLAKDKFTLKVAAMTARRSWQLTLNNDIKLN

LGRGDTMKRLQRFMELYPVLQQQAQTDGKRISYVDLRYDSGAAVGWVPAPAEETNQQQNQAQAEQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016529358.1\_4315 [locus\_tag=BN49\_RS23330] [protein=D-alanine--D-alanine ligase] [protein\_id=WP\_016529358.1] [location=complement(4504344..4505264)] [gbkey=CDS]

MADKIAVLFGGTSAEREVSLNSGAAVLAGLREGGVDAHPVDPRDVDITQLKKQGFKKAFIALHGRGGEDG

TLQGLLELIQLPYTGSGVMASAISMDKLRSKWLWQGAGLPVAPWVALTRAQFAAGLSTDVEQQIAALGLP

VIIKPSREGSRVGMSKVSESCDLASALALAFQHDDEVLVEKWLSGPEFTVAIVGEEILPSIRIQAAGTFY

DYEAKYLSDETQYFCPGFEDPARESAIQNLVLKAWNVLGCKGWGRIDVMLDSDGQFYLLEANTSPGMTSH

SLVPMAARQAGMSFSQLVVRILDLAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529359.1\_4316 [gene=murC] [locus\_tag=BN49\_RS23335] [protein=UDP-N-acetylmuramate--L-alanine ligase] [protein\_id=WP\_016529359.1] [location=complement(4505257..4506732)] [gbkey=CDS]

MNTQDLAKLRSIVPEMRRVRHIHFVGIGGAGMGGIAEVLANEGYQISGSDLAPNPVTQQLSQLGATIYFN

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YAEAGLDPTFVNGGLVKAAGVHARLGHSRYLIAEADESDASFLHLQPMVAIVTNIEADHMDTYHGDFENL

KQTFINFLHNLPFYGRAVMCVDDPVIRELLPRVGRQITTYGFSEDADVRVEDYRQVGAQGHFRLVRQDKA

ILQVTLNAPGRHNALNAAAAVAVATEEGIDDRAILRALESFQGTGRRFDFLGEFPLAEVNGKPGSAMLID

DYGHHPTEVDATIKAARAGWPDKNLVMVFQPHRYTRTRDLYDDFANVLTQVDALLMLDVYPAGEAPIPGA

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G

>lcl|NZ\_FO834906.1\_prot\_WP\_002888566.1\_4317 [gene=murG] [locus\_tag=BN49\_RS23340] [protein=undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase] [protein\_id=WP\_002888566.1] [location=complement(4506780..4507850)] [gbkey=CDS]

MSGQEKRLMVMAGGTGGHVFPGLAVAHHLMDQGWQVRWLGTADRMEADLVPKNGIEIDFIRISGLRGKGI

KAQLLAPVRIFNAWRQARAIMKRFQPDVVLGMGGYVSGPGGLAAWSLGIPVVLHEQNGIAGLTNKWLAKI

AKKVMQAFPGAFPHADVVGNPVRTDVLALPLPGQRLVGRQGPIRVLVVGGSQGARVLNQTMPQVAAKLGA

TVTIWHQSGKGGQQTVQQAYAAAGQPQHKVTEFIDDMAAAYAWADVVVCRSGALTVSEIAAAGLPALFVP

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AVALAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002888565.1\_4318 [gene=ftsW] [locus\_tag=BN49\_RS23345] [protein=cell division protein FtsW] [protein\_id=WP\_002888565.1] [location=complement(4507847..4509121)] [gbkey=CDS]

MRFSLPRLRMPQLSLPRLRLPRLPGMFIFAWLFAALKGWVMGSRPKDNDSLVMYDRMLLWLTFGLAAIGF

IMVTSASMPVGQRLANDPFLFAKRDGLYIVLAFALAMITLRLPMDFWQRHSTAMLIASIVMLLIVLVVGS

SVNGASRWIALGPLRIQPAEFTKLSLFCYIANYLVRKADEVRNNLRGFLKPMGVIFVLAILLLAQPDLGT

VVVLFVTTLAMLFLAGAKLWQFIAIIGMGISAVVLLILAEPYRIRRVTSFWNPWEDPFGSGYQLTQSLMA

FGRGEMWGQGLGNSVQKLEYLPEAHTDFIFAIIGEELGYIGVVLALLMVFFVAFRAMSIGRKALEIDHRF

SGFLACAIGIWFSFQALVNVGAAAGMLPTKGLTLPLISYGGSSLLIMSTAIMLLLRIDYETRLEKAQAFT

RGVR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530382.1\_4319 [gene=murD] [locus\_tag=BN49\_RS23350] [protein=UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase] [protein\_id=WP\_016530382.1] [location=complement(4509121..4510437)] [gbkey=CDS]

MADYQGKKVVIIGLGMTGLSCVDFFMARGVTPRVMDTRVAPPGLDKLPESVECHVGGLNDTWLLAADLIV

ASPGIALAHPSLSAAADAGVEIVGDIELFCREAQAPIIAITGSNGKSTVTTLVGEMAKAAGVNVGMGGNI

GLPALMLLDTDRELYVLELSSFQLETTSSLQAVAATILNVTEDHMDRYPLGLQQYRAAKLRIYENAKTCV

VNADDALTMPVRGADERCISFGVDVGDYHLNRQQGETWLRVKGEKVLNVKEMPLTGQHNYSNALAALALA

DAAGLPRASSLKALTTFTGLAHRFQLVLDHNGVRWINDSKATNVGSTEAALNGLQLDGTLYLLLGGDGKS

ADFTPLKRYLGGDRIRLYCFGRDGAELAELRPEVAVQTETMEQAMRQIAPLVKAGDMVLLSPACASLDQF

KNFEQRGEMFARLAKELG

>lcl|NZ\_FO834906.1\_prot\_WP\_002888562.1\_4320 [gene=mraY] [locus\_tag=BN49\_RS23355] [protein=phospho-N-acetylmuramoyl-pentapeptide-transferase] [protein\_id=WP\_002888562.1] [location=complement(4510440..4511522)] [gbkey=CDS]

MLVWLAEHLVKYYSGFNVFSYLTFRAIVSLLTALFISLWMGPRMIARLQKLAFGQVVRNDGPESHFSKRG

TPTMGGIMILTAITVSVLLWAYPSNPYVWCVLTVLIGYGIIGFVDDYRKVVRKDTKGLIARWKYFWMSVI

ALGVAFALYLAGKDTPATELVVPFFKDVMPQLGLFYILLAYFVIVGTGNAVNLTDGLDGLAIMPTVFVAA

GFALVAWATGNMNFANYLHIPYLRHAGELVIVCTAIVGAGLGFLWFNTYPAQVFMGDVGSLALGGALGII

AVLLRQEFLLVIMGGVFVVETLSVILQVGSFKLRGQRIFRMAPIHHHYELKGWPEPRVIVRFWIISLMLV

LIGLATLKVR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043775.1\_4321 [gene=murF] [locus\_tag=BN49\_RS23360] [protein=UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase] [protein\_id=WP\_046043775.1] [location=complement(4511516..4512874)] [gbkey=CDS]

MIRFTLSQLAAIAHGERQGSDVAIDEVTTDTRKVTAGCLFVALKGERFDAHDFAEQAKAAGAGALLVSRP

LACDLPQVIVNDTRQAFGELAAWVRQQVPTRVVALTGSSGKTSVKEMTAAILSQCGNTLYTAGNLNNDIG

VPMTLLRLTKEHQYAVIELGANHQGEIAWTVSLTRPEAALVNNLAAAHLEGFGSLAGVAKAKGEIYTGLP

ENGIAILNADNNDWLNWQAVIGDRKVWRFSPNAANSDFTATNVQITSHGTEFTLQTPTGNADVLLPLPGR

HNIANALAATSLAMAVGADLAAVKAGLAQLQAVPGRLFPIRLTESQLLLDDSYNANVGSMTAAVQVLSEM

PGFRTMVVGDMAELGAESAACHREVGEAAKAAGLDCVLSVGALSADISRASGVGEHFNDKAAVVARLREL

LAEHKIMTILVKGSRSAAMEEVVRALQETGTC

>lcl|NZ\_FO834906.1\_prot\_WP\_046043777.1\_4322 [gene=murE] [locus\_tag=BN49\_RS23365] [protein=UDP-N-acetylmuramoyl-L-alanyl-D-glutamate--2,6-diaminopimelate ligase] [protein\_id=WP\_046043777.1] [location=complement(4512871..4514358)] [gbkey=CDS]

MADRNLRDLLAPWVPNAPERILREMTLDSRVAASGDLFIAVQGHQADGRRYIPQAIAQGVAAIIAEAQGE

AKDGEIREMHGVPVIYLSQLNERLSALAGRFYHQPSQQLRLVGVTGTNGKTTTTQLLAQWAKLLGETSAV

MGTVGNGLLDKVVPTENTTGSAVDVQHVLSSLVGQGATFGAIEVSSHGLVQHRVAALQFAASVFTNLSRD

HLDYHGDMEHYEAAKWLLYSTHHCGQAIVNADDEVGRRWLAKLPDAVAVSMEDHINPNCHGRWLKATAVN

YHDSGATIQFDSSWGKGEIESRLMGAFNVSNLLLALATLLALGYPLADLLKTAARLQPVCGRMEVFSAPG

KPAVVVDYAHTPDALEKALQAARLHCSGKLWCVFGCGGDRDKGKRPLMGAIAEEFADIVVVTDDNPRTEE

PRAIINDILAGMLDAGQAKVMEGRAEAVTNAVMQAKENDVVLVAGKGHEDYQIVGNRRLDYSDRVTVARL

LGAVA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532398.1\_4323 [locus\_tag=BN49\_RS23370] [protein=peptidoglycan glycosyltransferase FtsI] [protein\_id=WP\_016532398.1] [location=complement(4514345..4516111)] [gbkey=CDS]

MKAAPKTPKAKRQEEQANFISWRFALLCGCILLALAFLLGRVAWLQVISPDMLVRQGDMRSLRVQEVSTA

RGMITDRSGRPLAVSVPVKAIWADPKELHDAGGVTLDTRWKALADALNMPLDQLATRINTNPRMRFIYLA

RQVNPDMADYIKKLKLPGIHLREESRRYYPSGEVTAHLIGFTNVDSQGIEGVEKSFDKWLTGQPGERIVR

KDRYGRVIEDISSTDSQAAHNLALSIDERLQALVYRELNNAVAFNKAESGSAVLVDVNTGEVLAMANSPS

YNPNNFAGTAKDTMRNRAITDVFEPGSTVKPMVVMTALQRGIVNENTVLNTVPYRINGHEIKDVARYSEL

TLTGVLQKSSNVGVSKLALAMPSSVLVDTYSRFGLGKATNLGLVGERSGLYPQKQRWSDIERATFSFGYG

LMVTPLQLARVYATIGSYGIYRPLSITKVDPPVPGERVFPESLVRTVVHMMESVALPGGGGVKAAIKGYR

IAIKTGTAKKVGPDGRYINKYIAYTAGVAPASHPRFALVVVINDPQAGKYYGGAVSAPVFGAIMGGVLRT

MNIEPDALATGEKSEFVINQGEGTGGRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888550.1\_4324 [gene=ftsL] [locus\_tag=BN49\_RS23375] [protein=cell division protein FtsL] [protein\_id=WP\_002888550.1] [location=complement(4516127..4516492)] [gbkey=CDS]

MIGRVTEALSKVKGSIGSNERHALPGVIGDDLLRFGKLPLCLFICIIITAITVVTTAHHTRLLTAQREQL

VLERDALDIEWRNLILEENALGDHSRVERIATEKLQMQHVDPSQENIVVQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002888547.1\_4325 [gene=rsmH] [locus\_tag=BN49\_RS23380] [protein=16S rRNA (cytosine(1402)-N(4))-methyltransferase RsmH] [protein\_id=WP\_002888547.1] [location=complement(4516489..4517430)] [gbkey=CDS]

MMENYKHTTVLLDEAVNGLNIRPDGIYIDGTFGRGGHSRLILSRLGAEGRLLAIDRDPQAIAVAQTIDDP

RFSIVHGPFSQLAEYVGERNLTGKIDGILLDLGVSSPQLDDAERGFSFMRDGPLDMRMDPTRGQSAAEWL

QTAEEDDIAWVIKTFGEERFGKRIARAIVERNRIQPMTRTKELAEVIAAAMPVKDKHKHPATRTFQAVRI

WVNSELEEIEQALKSSLSVLAPGGRLSIISFHSLEDRIVKRFMREQSRGPQVPAGIPMTEAQLKKLGGRE

LRALGKLMPGEEEVAENPRARSSVLRIAERTNA

>lcl|NZ\_FO834906.1\_prot\_WP\_002888541.1\_4326 [gene=mraZ] [locus\_tag=BN49\_RS23385] [protein=division/cell wall cluster transcriptional repressor MraZ] [protein\_id=WP\_002888541.1] [location=complement(4517433..4517891)] [gbkey=CDS]

MFRGATLVNLDSKGRLAVPTRYREGLIEDAAGQLVCTIDIHHPCLLLYPLPEWEVIEQKLSRLSSMNPVE

RRVQRLLLGHASECQMDNAGRLLIAPVLRQHAGLTKEVMLVGQFNKFELWDETTWYQRVKEDIDAEQSAT

GELSERLQDLSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004145952.1\_4327 [gene=cra] [locus\_tag=BN49\_RS23390] [protein=catabolite repressor/activator] [protein\_id=WP\_004145952.1] [location=complement(4518527..4519531)] [gbkey=CDS]

MKLDEIARLAGVSRTTASYVINGKAKQYRVSDKTVEKVMAVVREHNYHPNAVAAGLRAGRTRSIGLVIPD

LENTSYTRIANYLERQARQRGYQLLIACSEDQPDNEMRCIEHLLQRQVDAIIVSTSLPPEHPFYQRWAND

PFPIVALDRALDREHFTSVVGADQDDAEMLAAELRTFPGETVLYLGALPELSVSFLREQGFRKAWQDDPR

EVHYLYANSYEREAAAQLFEKWLETHPMPQALFTTSFPLLQGVMDVTLRREGKLPSELAIATFGDNELLD

FLQCPVLAVAQRHRDVAERVLEIVLASLDEPRKPKPGLSRIRRNLYRRGSLNRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002888536.1\_4328 [gene=ilvN] [locus\_tag=BN49\_RS23395] [protein=acetolactate synthase small subunit] [protein\_id=WP\_002888536.1] [location=complement(4519712..4520203)] [gbkey=CDS]

MRRILSVLLENESGALSRVIGLFSQRGYNIESLTVAPTDDPTLSRMTIQTVGDEKAIEQIEKQLHKLVDV

LRVSELGQGAHVEREIMLVKVQASGYGREEVKRNTEIFRGQIIDVTPSIYTVQLAGTSDKLDAFLASLRD

VARIVEVARSGVVGLSRGDKIMR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529268.1\_4329 [gene=ilvI] [locus\_tag=BN49\_RS23400] [protein=acetolactate synthase 3 large subunit] [protein\_id=WP\_016529268.1] [location=complement(4520206..4521930)] [gbkey=CDS]

MEMLSGAEMVVQSLVDQGVKQVFGYPGGAVLDIYDALHTLGGIDHVLVRHEQAAVHMADGLARATGEVGV

VLVTSGPGATNAITGIATAYMDSIPLVILSGQVATSLIGYDAFQECDMVGISRPVVKHSFLVKQTEDIPG

VLKKAFWLAASGRPGPVVVDLPKDILNPAKKLPYVWPDAVSMRSYNPTTSGHKGQIKRALQTLVAASKPV

VYVGGGAINAHCEPQLRELVEKLKLPVASSLMGLGAFPATHSQALGMLGMHGTYEANMTMHHSDVIFAVG

VRFDDRTTNNLAKYCPNATVLHIDIDPTSISKTVPADVPIVGDARLVLEQMLELLEQEEAQQPLDDIRDW

WQQIEQWRARHCLRYDDQSDKIKPQAVIDTIWRLTQGDAYVTSDVGQHQMFAALYYPFDKPRRWINSGGL

GTMGFGLPAALGVKMALPDEMVVCVTGDGSIQMNIQELSTALQYELPVLVLNLNNRYLGMVKQWQDMLYS

GRHSQSYMESLPDFVRLAEAYGHVGIRISEPQELETKLAEALEQVRQRRLVFVDVTVDGSEHVYPMQIRG

GGMDEMWLSKTERT

>lcl|NZ\_FO834906.1\_prot\_WP\_004192013.1\_4330 [gene=leuO] [locus\_tag=BN49\_RS23405] [protein=transcriptional regulator LeuO] [protein\_id=WP\_004192013.1] [location=complement(4522325..4523293)] [gbkey=CDS]

MTAELDMLIETPEYKSAPGQEVVKPQLRMVDLNLLTVFDAVMQEQNITRAAHTLGMSQPAVSNAVSRLKV

MFNDELFVRYGRGIQPTARAYQLFGSVRQALQLVQNELPGSGFEPLSSERVFHLCVCSPLDNILTSVIFN

KVAEIAPNIHLVFKSALNQNTEHQLRYQETEFVIGYEEFRRPEFACVPLFKDEMVLVASRNHPRISGPMM

EADIYREEHAAVALDRYASFSLPWYDTADKQARIAYQGNAMVSVLNVVSQTQMVAIAPRWLADEFADKLA

LQILPLPLKVNSRTCYLSWHEAAGRDKGHQWMEELLVDICKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004222662.1\_4331 [gene=leuL] [locus\_tag=BN49\_RS29505] [protein=leu operon leader peptide] [protein\_id=WP\_004222662.1] [location=4523907..4523993] [gbkey=CDS]

MIRTARITSLLLLNACHLRGRLLGDVQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004178594.1\_4332 [gene=leuA] [locus\_tag=BN49\_RS23415] [protein=2-isopropylmalate synthase] [protein\_id=WP\_004178594.1] [location=4524089..4525660] [gbkey=CDS]

MSQQVIIFDTTLRDGEQALQASLSVKEKLQIALALERMGVDVMEVGFPVSSPGDFESVQTIARTIKNSRV

CALARCVEKDIDVAAESLKVAEAFRIHTFIATSPMHIATKLRSTLDEVIERAIYMVKRARNYTDDVEFSC

EDAGRTPIADLARVVEAAINAGATTINIPDTVGYTMPFEYANIISGLYDRVPNIDKAIISVHTHDDLGIA

VGNALAAVHAGARQVEGAMNGIGERAGNCALEEVIMAIKVRKDIMNVHTNINHHEIWRTSQTVSQICNMP

IPANKAIVGTGAFAHSSGIHQDGVLKNRENYEIMTPESIGLNQVQLNLTSRSGRAAVKHRMEEMGYQESD

YNLDHLYDAFLKLADKKGQVFDYDLEALAFINKQQEEPEHFRLDYFNVQSGSSDIATASIKLVCGDEIKT

EAANGNGPVDAIYQAINRVTDYNIELVKYGLSAKGHGKDALGQVDIVVDYNGRRFHGVGLATDIVESSAK

AMVHVLNNIWRAAEVEKELQRKAQNKENNKETV

>lcl|NZ\_FO834906.1\_prot\_WP\_002888487.1\_4333 [gene=leuB] [locus\_tag=BN49\_RS23420] [protein=3-isopropylmalate dehydrogenase] [protein\_id=WP\_002888487.1] [location=4525660..4526751] [gbkey=CDS]

MSKNYHIAVLPGDGIGPEVMNQAMKVLEAVRQRFAMHITTSQYDVGGAAIDRQGTPLPQATVAGCEQADA

ILFGSVGGPKWEHLPPAEQPERGALLPLRKHFKLFSNLRPAKLYQGLEEFCPLRADIAANGFDILCVREL

TGGIYFGQPKGREGSGQHEKAFDTEVYHRFEIERIARIAFESARKRRHKVTSIDKANVLQSSILWREIVS

EIGKEYPDVELAHMYIDNATMQLIKDPSQFDVLLCSNLFGDILSDECAMITGSMGMLPSASLNEQGFGLY

EPAGGSAPDIAGKNIANPIAQILSLALLLRYSLDADEAATAIENAINRALEEGVRTGDLARGTAAVSTDE

MGDIIARYVAEGV

>lcl|NZ\_FO834906.1\_prot\_WP\_004177417.1\_4334 [gene=leuC] [locus\_tag=BN49\_RS23425] [protein=3-isopropylmalate dehydratase large subunit] [protein\_id=WP\_004177417.1] [location=4526754..4528154] [gbkey=CDS]

MAKTLYEKLFDAHVVYEAQNETPLLYIDRHLVHEVTSPQAFDGLRAHGRQVRQPGKTFATMDHNVSTQTK

DINASGEMARIQMQELIKNCKEFGVELYDLNHPYQGIVHVMGPEQGVTLPGMTIVCGDSHTATHGAFGAL

AFGIGTSEVEHVLATQTLKQGRAKTMKIEVQGKAAPGITAKDIVLAIIGKTGSAGGTGHVVEFCGEAIRD

LSMEGRMTLCNMAIEMGAKAGLVAPDETTFNYVRGRLHAPKGKDFDDAVAYWKTLKTDDGATFDTVVTLQ

AAEIAPQVTWGTNPGQVISVTDNIPDPASFSDPVERASAEKALAYMGLKSGIPLTEVAIDKVFIGSCTNS

RIEDLRAAAEIAKGRKVAPGVQALVVPGSGPVKAQAEAEGLDKIFIEAGFEWRLPGCSMCLAMNNDRLNP

GERCASTSNRNFEGRQGRGGRTHLVSPAMAAAAAVTGHFADIRNLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002888481.1\_4335 [gene=leuD] [locus\_tag=BN49\_RS23430] [protein=3-isopropylmalate dehydratase small subunit] [protein\_id=WP\_002888481.1] [location=4528165..4528770] [gbkey=CDS]

MAEKFTQHTGLVVPLDAANVDTDAIIPKQFLQKVTRTGFGAHLFNDWRFLDDKGQQPNPEFVLNFPEYQG

ASILLARENFGCGSSREHAPWALTDYGFKVVIAPSFADIFYGNSFNNQLLPVTLSDEQVDELFKLVQANP

GITFEVDLEAQVVKAGDKTYSFKIDDFRRHCMLNGLDSIGLTLQHEAAISDYERKLPAFMN

>lcl|NZ\_FO834906.1\_prot\_WP\_016529137.1\_4336 [locus\_tag=BN49\_RS23435] [protein=FAD-dependent oxidoreductase] [protein\_id=WP\_016529137.1] [location=4529166..4531199] [gbkey=CDS]

MSHYPHLFSPLTINGMTLKNRIIMPPMGTNMATLNGEVSQEQLEYYELRAKGGTGLITIENICIDFPFAS

NGTTQLRIDNDQYIPRLFKLTETLHKHGACVSIQLNHAGASAYAYRLEGQTPLSSSTTPSKKHGNIPRPM

THEEIYHAVEKFGDAAERVRRAGFDCVEIHAGHSYLISQFLSPLFNKRTDEFGGSVENRTRILSLIVDKV

RACVGPRFPVSLRISADDFLKGGNTLEDSLRILELCQEKVDIINVSAAQNDNLNLQIDQMSLEDGWKRYL

SRAVRDKFHKPTVIAGNIRTPQVAEDILASGDADLIAIGRGLIAEPEWVQKVQGGKERLMRKCISCNIGC

ADHRIARSRPLRCSINPDIIHGDAYKMRRVNRDTNVVVIGAGTAGMEAACTAAEVGCHTWLLEAKNHVGG

LANEISRLPEKKRIADFPQFMKNRIASLDNLMLQIGKRADVASVSALRPHLIVNATGSTPLLPPIEGLRE

NIDVENGKIFSITGMIDNLAKFTDIKGKRIAVVGAGAVGLDVIEYFTARGAQAVLIEMQDAAGRDLDIIT

KNAMLTMLDEHQVEQHMNTQLMAVAADHFQVKNTQQTFDIPFDYGFVCLGMRANRTGLDEIERWANANNV

KIMNIGDSVMARRIIDGVREGRNVLDALEDMGALGSREAQRIPFLTY

>lcl|NZ\_FO834906.1\_prot\_WP\_002888460.1\_4337 [locus\_tag=BN49\_RS23440] [protein=shikimate dehydrogenase] [protein\_id=WP\_002888460.1] [location=4531211..4532074] [gbkey=CDS]

MAERITGHTELIGLIATPIRHSMSPTMHNEAFAHLGLDYVYLAFEVGNQELKDVVQGFRAMKLRGFNVSM

PNKTEICQYLDKLSPAAQLVGAVNTVVNDDGVLTGHITDGTGYMRALSEAGIDIIGKKMTVLGAGGAATA

LCVQAALDGVKAISIFNRRDKFFANAEETVAKIRHNTDCEIHLFDLDDHDKLRAEIDSSVILTNATGVGM

KPFEGQMLLPDDSFLRPDLIVSDVVYNPRKTHLLEVAEKKGCRTLNGLGMMLWQGARAFEIWTGKQMPVD

YIKSILF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529138.1\_4338 [locus\_tag=BN49\_RS23445] [protein=MFS transporter] [protein\_id=WP\_016529138.1] [location=4532085..4533299] [gbkey=CDS]

MKNKYIPTAAGLYLNYLIHGMGVLLITLNMAHLQEQWGTDKAGVSIVISSLGIGKLATIVTGFLSDRFGR

KPFIYLGILSYLIFFVGILLTKNIYLAYVFGIMAGLANSFLDSGTYPALMESFPHSASRANVLIKAFVSA

GQFLLPFIISFLIWANLWFGWSFVIAAALFVLSGIYLLKMPFPDSQASKKEEAPTAQAETAVQPQANKLD

MVIFTLYGYIGMATFYLVSQWLAQYGQFVVGLPYASAIKLLSIYTVGSLVCVFVTAAFVKEVFSSAIAMI

IYTGLSMISLLLVCLFPTPMMVTGFAFVIGFAAAGGVLQLGATIMAMSFPNGKGKETGIFYTAGSIASFT

IPLITAKLSQISIASIMWFDFLIAVIGFVIALYIGYRQLQARAAQKVSRTAVTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177420.1\_4339 [gene=aroD] [locus\_tag=BN49\_RS23450] [protein=type I 3-dehydroquinate dehydratase] [protein\_id=WP\_004177420.1] [location=4533330..4534085] [gbkey=CDS]

MTNAVTVKNITFQEGETLICVPLIGKTLDEILGNAHGLVDAGADIIEWRVDHFAQVREMAQVMAALAEIR

GALKALPLLFTFRSKKEGGETELSDEAYFALNREAARSGLVDVIDIELFNDEAQIRALVDDAHAAGVKVI

MSNHDFHKTPAQEDIIYRLRRMQDLGADLPKIAVMPQSPQDVLTLLAATLTMKEKYATRPLITMSMGKSG

GVSRVTGRLFGSAMTFGTVGQASAPGQIAIAKLREVMDILS

>lcl|NZ\_FO834906.1\_prot\_4340 [locus\_tag=BN49\_RS23455] [protein=LysR family transcriptional regulator] [pseudo=true] [location=complement(4534123..4535020)] [gbkey=CDS]

MNLKQLYYFKRLSETEHYTEAASSLCITQPSLSHAISELEKELGVALFARQGRNVKITQNGKRFLPYVED

ALASLENGRMILQKNGAENKENIRIAFIYTMGEYVVPQLINKYSLSPECHNVTFSFTQGTSLTLLQELKA

GKVDLAICSYIADEPDIDFIPVIQQELVVVTAKDHPLARLYEHEVDLVETIHYPYIYFSENSGLRPFIDN

VFMQQKLVPEIACYVDEDTAMAGLVSIDYGIAIMPRITALSYYNVHILKIKNTIPPPLYLSGDHERQGAL

SGAGVI\*KCGYPRQPEDLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004147047.1\_4341 [locus\_tag=BN49\_RS23460] [protein=MFS transporter] [protein\_id=WP\_004147047.1] [location=4535252..4536562] [gbkey=CDS]

MSMSNSQEVLTSTSGAKKRSRVRIVILLLLSVGTMINYLDRTILGIVAPQLSKEIHIDPAMMGIIFSAFA

WTYALAQIPGGMFLDRFGNKLTYALSIFFWSLFTLLQSFTLGLKSLLLLRLGLGVSEAPCFPANSRIVST

WFPQHERARATATYTVGEYIGLAAFSPLLFLILEHHGWRTLFFLTGGLGILFTLVWWRFYHEPHESRTAN

QAELEYIGANGINNKIQNVPFNWRDARRLLGCRQILGASLGQFAGNTTLVFFLTWFPSYLANERHLPWLH

VGFFATWPFLAAAIGILFGGWISDRLLKRTGSVNISRKLPIISGLLLSSCIIAANWVSANSTVIIIMSVA

FFGQGMVGLGWTLISDIAPENMAGLTGGIFNFCANMASIIAPLIIGVIISATGNFFYALIYVGLTALIGV

IAYIFIIGDIKRIELK

>lcl|NZ\_FO834906.1\_prot\_4342 [locus\_tag=BN49\_RS23465] [protein=sugar efflux transporter] [pseudo=true] [location=complement(4536596..4537780)] [gbkey=CDS]

MLWLMTMGRRLNGVYAAFMLVAFMMGVAGALQAPTLSLFLSREVGAQPFWVGLFYTVNAIAGILVSLWLA

KRSDSRGDRRRLIMFCCLMAVGNALLFAFNRHYLTLITCGVMLASIANAAMPQLFALAREYADSSAREVV

MFSSVMRAQLSLAWVIGPPLAFMLALNYGFTTMFSIAAGIFVISLALIAIKLPSVPRVEQPSEEAAALAQ

AGGWQDKNVRMLFIASTLMWTCNTMYIIDMPLWISSDLGLPDSLAGILMGTAAGLEIPAMILAGYYVKRF

GKRKMMVAAVAAGVLFYAGLILFHGRTALLALQLFNAIFIGIIAGIGMLWF\*DLMPGRAGAATTLFTNSI

STGVILAGVMQGALSQSYGHASVYWTIAAISLVTLFLTSKVKDI

>lcl|NZ\_FO834906.1\_prot\_WP\_002888448.1\_4343 [locus\_tag=BN49\_RS23475] [protein=glucose uptake inhibitor SgrT] [protein\_id=WP\_002888448.1] [location=complement(4538048..4538200)] [gbkey=CDS]

MMRSTAKSFYQRYFSATQEASWLARLMAGRQQEILGELMQWGVTSTTSDH

>lcl|NZ\_FO834906.1\_prot\_WP\_046043784.1\_4344 [gene=sgrR] [locus\_tag=BN49\_RS23480] [protein=HTH-type transcriptional regulator SgrR] [protein\_id=WP\_046043784.1] [location=4538288..4539943] [gbkey=CDS]

MSSGRLQQQFIRLWQCCDGKSQETTLNELAEMLSCSRRHMRTLLNMMESRGWLTWEAEAGRGKRSRLTFL

YTGLALQQQRAEDLLEQDRIDQLVQLVGDKAAVRQMLVSHLGRSFRQGRHILRVLYYRPMKNLLPGSALR

RSETHIARQIFSALTRVNEENGELEADIAHHWQQLTPTHWRFFLRPGIHFHHGRELEMADVIASLQRSNA

LPLYSHIERIESPTAWTLDIHLRQPDRWLPWLLGQVPAMVLPQEWQTMNHFSSMPVGTGPYAVVRNNQNQ

LKIHAFEDYFGYRALIDEVNVWVLPEISEEPNGGLTLQGNTESEKAVESRLEEGCYYLLFDSRSPLGAND

AVRRWLSYLFQPANLLYHAGEHYQGNWFPAYGLLPRWHHASNHPCEKPAGLETVTLTYYRDHVEHRVIGG

IMRDLLAAHQVKLEIQELEYDAWHRGEVVSDIWLNSVNFTLPIEFSLFAYLYEVPLIQRCIPIDWQADAC

RWRAGEFNPATWSQRLLAGQHIVPLIHHWLMIQGQRSMRGVRMNTLGWFDFKSAWFAPPEP

>lcl|NZ\_FO834906.1\_prot\_WP\_004178584.1\_4345 [gene=thiB] [locus\_tag=BN49\_RS23485] [protein=thiamine ABC transporter substrate binding subunit] [protein\_id=WP\_004178584.1] [location=4540233..4541216] [gbkey=CDS]

MLKKLLPLLALVAMPALAKPVLTVYTYDSFSADWGPGPAVKKAFEAECGCELKFVALEDGVSLLNRLRME

GKNSKADVVLGLDNNLLEAAAQSKLFAKSNVPASAVSVPGGWDNDTFVPYDYGYFAFVYDKNKLANPPKS

LKELVEGPQKWRVIYEDPRTSTPGLGLLLWMQKVYGDQAPEAWQKLAAKTVTVTKGWSEAYGLFLKGESD

LVLSYTTSPAYHMIEEKKDNYAAASFAEGHYLQVEVAARTAASKQPELAEKFLKFMVSPGFQNAIPTGNW

MYPVTKVTLPAGFDTLVKPQTTLSFTPQQVASERQTWISAWQRAVSR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043786.1\_4346 [gene=thiP] [locus\_tag=BN49\_RS23490] [protein=thiamine/thiamine pyrophosphate ABC transporter permease ThiP] [protein\_id=WP\_046043786.1] [location=4541192..4542802] [gbkey=CDS]

MATRRQPLNLRGLMPGLFAATLLCAVALAAFLALWFSAPGAGWQSVFSDSYLWHVVRFSFWQASLSALIS

VGPAIFLARALYRRRFPGRTLLLRLCAMTLILPVLVAVFGILSVYGRQGWLASLFHALGWQWEFSPYGLQ

GILLAHVFFNMPMATRLLLQALENIPGEQRQIAAQLGMRGYAFFRLVEWPWLRRHIPAVAALIFMLCFAS

FATVLSLGGGPKATTIELAIYQALSFDYDPARAAMLALIQMLCCLGLVLLSQRLSKAVAIGVSHVRGWRD

PDDRLHSRLSDGLLIGAALLLLLPPLLAVIVDGINRNMLDVLAQPALWQALSTSLHIAIAAGLLSVTLTM

MLLWSSRELRSRQRPLAGQAMELSGMLILAMPGIVLATGFFLLLNNTIGLPESADGIVIFTNALMAIPYA

LKVLENPMRDIAARYSMLCQSLGIEGFARLRVVELRALRRPLAQALAFACVLSIGDFGVVALFGNEAFRT

LPFYLYQQIGAYRSQDGAVTALLLLLLCFLLFTLIEKLPGRDAKTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004145970.1\_4347 [gene=thiQ] [locus\_tag=BN49\_RS23495] [protein=thiamine ABC transporter ATP-binding protein ThiQ] [protein\_id=WP\_004145970.1] [location=4542786..4543487] [gbkey=CDS]

MLKLNDVTWLYQHLPMRFTLDVARGERIAVLGPSGAGKSTLLNLIAGFLPPASGSLLINGEAHNATPPAQ

RPVSMLFQENNLFNHLTIRQNISLGIHPGLKLSREQQAQVTAIAGQMGIDALLERLPGELSGGQRQRAAL

ARCLVRQQPVLLLDEPFSALDPALRQEMLSLVADVCEQQQLTLLMVSHSVEDAARIAPRSMVVAEGRIVW

DGATAELLSGHSSASHLMGISAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002888373.1\_4348 [locus\_tag=BN49\_RS23500] [protein=DedA family protein] [protein\_id=WP\_002888373.1] [location=complement(4543474..4544241)] [gbkey=CDS]

MQALLEHFITQSTVYSLLAVMLVAFLESLALVGLILPGTVMMAGLGALIGGGEVNFWQAWLAGIVGCLLG

DWISFWLGWRFKKPLHRWSFMKKNRALLEKTEHALHQHSMITILIGRFVGPTRPLVPMVAGMLDLPVAKF

VLPNIIGCLLWPPLYFLPGILAGAAIDIPADENSASFKWLLLGAALLAWLAGWLCWRLWRSAKTSGDRLT

RWLPRGRLLWLSPLMVALAATALTFVFRHPLMPVYLAILHKVIAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145972.1\_4349 [gene=araC] [locus\_tag=BN49\_RS23505] [protein=arabinose operon transcriptional regulator AraC] [protein\_id=WP\_004145972.1] [location=complement(4544370..4545215)] [gbkey=CDS]

MAETQNDPLLPGYSFNAHLVTGLTPIEAQGYLDFFIDRPLGMKGYILNLTIRGEGVINNHGEQFVCRPGD

MLLFPPGEIHHYGRHPDASEWYHQWVYFRPRAYWHEWLNWPTIFAQTGFFRPDEQWQARFGELFGQIVDA

GQGAGRYSELLAINLLEQLLLRRMEAINESLHPPLDNRVRDACQYISDHLADSHFDIASVAQHVCLSPSR

LSHLFRQQLGVSVLGWREDQRISQAKLLLSTTRMPIATVGRNVGFEDQLYFSRVFKKCTGASPSEFRAGC

E

>lcl|NZ\_FO834906.1\_prot\_WP\_004177423.1\_4350 [gene=araB] [locus\_tag=BN49\_RS23515] [protein=ribulokinase] [protein\_id=WP\_004177423.1] [location=4545553..4547262] [gbkey=CDS]

MAIAIGLDFGSDSVRALAVECASGAELATSVEWYPRWREGQYCDGANNRFRHHPRDYIESMEAALKSVLA

SLSAEQRADVVGIGVDSTGSTPAPVDAEGNVLALREEFADNPNAMFVLWKDHTAVEEAEAITRLCHQPGK

EDYSRYIGGIYSSEWFWAKILHVTREDSAVAQAAASWVELCDWVPALLSGTTRPQDLRRGRCSAGHKSLW

HESWGGLPPASFFDELDPIINQHLAWPLFTDTWTADVPVGTLSAEWAQRLGLSQSVAISGGAFDCHMGAV

GAGAQPNALVKVIGTSTCDILIADKESVGERTVKGICGQVDGSVVPHFIGMEAGQSAFGDIYAWFGRILG

WPLEQLAQQQPALREQIKASQKQLLPALTEAWANNPSLEHLPVVLDWFNGRRTPNANQRLKGVITDLNLA

TDAPALFGGLIAATAFGARAIMECFTEQGIPVNNVMALGGIARKNQVIMQACCDVLNRPLQIVASDQCCA

LGAAIFAAVAAGVYEDIPAAQQRMASQVETTLQPRPAQAQRFEQLYQRYQQWSVSAEQHYLPSAAKAEKA

PQSQAALTH

>lcl|NZ\_FO834906.1\_prot\_WP\_004177424.1\_4351 [gene=araA] [locus\_tag=BN49\_RS23520] [protein=L-arabinose isomerase] [protein\_id=WP\_004177424.1] [location=4547273..4548775] [gbkey=CDS]

MTIFDNYEVWFVIGSQHLYGPEALRQVTKHAEHVVNSLNAEAKLPCKLVLKPLGTTPDEITHICRDANYD

DKCAGLVVWLHTFSPAKMWINGLTILNKPLLQFHTQYNAALPWDSIDMDFMNLNQTAHGGREFGFIGARM

RQQHSVVTGHWQDKEAHQRIGGWMRQAVSKQDTRHLKVCRFGDNMREVAVTDGDKVAAQIKFGFSVNTWA

VGDLVQVVNSISDGDISALVDEYESSYRLTPAAQVHGEKRQNVLDAARIELGMKRFLEQGGFHAFTTTFE

DLHGLKQLPGLAVQRLMQQGYGFAGEGDWKTAALLRIMKVMSTGLQGGTSFMEDYTYHFDNGNDLVLGSH

MLEVCPTIATAEKPILDVQPLGIGGKADPARLIFNTQTGPAIVASLIDLGDRFRLLVNTIETVPTPHDLP

KLPVANALWKAQPDLRTASEAWIIAGGAHHTVFSHALNLDDMRQFAELHDIELTVIDNDTRLPSFKDALR

WNEVYYGSKR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531719.1\_4352 [gene=araD] [locus\_tag=BN49\_RS23525] [protein=L-ribulose-5-phosphate 4-epimerase] [protein\_id=WP\_016531719.1] [location=4548913..4549608] [gbkey=CDS]

MLEDLKRQVLEANLALPKHNLVTLTWGNVSAVDREKGVFVIKPSGVDYRVMTADDMVVVSLESGEVVEGN

KKPSSDTPTHRLLYQAFPTLGGIVHTHSRHATIWAQAGQSIPATGTTHADYFYGPVPCTRLMTDAEINGD

YEWETGNVIVETFRQQRIDPAQMPGVLVHSHGPFAWGKNAEDAVHNAIVLEEIAYMGIFCRQLAPQLPAM

QQTLLDKHYLRKHGAKAYYGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043788.1\_4353 [gene=polB] [locus\_tag=BN49\_RS23530] [protein=DNA polymerase II] [protein\_id=WP\_046043788.1] [location=4549784..4552141] [gbkey=CDS]

MTQPRAGFLLTRHWRDTPQGTELSFWLATDDGPLQVTLPPQESVAFIPEAQRAQAERLLQGEKGLRFAPL

ALKDFHRQPIVGLYCRAHRQLMRLEKMLRDSGVTVYEGDIRPPERYLMERFITAPVWVEGETRGSQLVNA

RMKPNPDYRPPLKWVSLDIETSRHGELYCIGLEGCGQRVVYMLGPEPETPPDVDFELVFIASRPLLLEKL

NAWFAEHDPDVLIGWNVVQFDLRVLQKHAERYRIPLRLGRGNSELEWREHGFKNGVFFAQANGRLIIDGI

DALKSAFWNFSSFSLEAVARELLGEGKAIDTPWDRMDEIDRRFHEDKPALAIYNLQDCELVTRIFHKTEI

MPFLLERATVNGLPADRHGGSVAAFSHLYFPRMHRLGYVAPNLGDVPPQASPGGYVMDSRPGLYDSVLVL

DYKSLYPSIIRTFLIDPVGLVEGLAQPDDQHSIEGFLGARFSRDKHCLPGIVSQIWHGRDEAKRQHNKPL

SQALKIIMNAFYGVLGTSACRFFDPRLASSITMRGHAIMRQTKALIEAKGYDVIYGDTDSTFVWLKRPHS

EAQAAEIGRELVSDVNAWWSQELSKSQLTSALELEYETHFCRFLMPTIRGADTGSKKRYAGMIQEGDAQR

MVFKGLETVRTDWTPLAQQFQQELYLRIFRNQPYQDYVRETIARLMNGELDEQLVYRKRLRRPLAEYQRN

VPPHVRAARLADEHNLKLGRTQQYQQRGTIKYVWTTSGPEPVDYQQSPLDYDHYLTKQLQPVAEGILPFV

NDDFATIVTGQLGLF

>lcl|NZ\_FO834906.1\_prot\_WP\_004178574.1\_4354 [gene=rapA] [locus\_tag=BN49\_RS23535] [protein=RNA polymerase-associated protein RapA] [protein\_id=WP\_004178574.1] [location=4552329..4555235] [gbkey=CDS]

MPFTLGQRWISDTESELGLGTVVALDARMVTLLFPAIGENRLYSRNDSPITRVMFNPGDTITSHEGWQLH

VDKVNEENGLLSYTGTRLDTQEANVTLREVLLDSKLVFSKPQDRLFAGQIDRMDRFALRYRARKFQSEQY

RMPWSGLRGQRTSLIPHQLHIAHDVGRRHAPRVLLADEVGLGKTIEAGMILHQQLLSGAAERVLIVVPET

LQHQWLVEMLRRFNLRFSLFDDERYAEAQHDAYNPFETEQLVICSLDFVRRSKQRLEHLCDAEWDLMVVD

EAHHLVWSEEAPSREYQAIEQLAERVPGILLLTATPEQLGMESHFARLRLLDPNRFHDFEQFVEEQQNYR

PVADAVALLLAGNKLSDSELNTLGDLIGEQDIEPLLQAANSDREDAQAARQELISMLMDRHGTSRVLFRN

TRNGVKGFPKRELHTIRLPLPTQYQTAIKVSGIMGARKTAEERARDMLYPEQIYQEFEGDTGTWWNFDPR

VEWLMGYLTSHRSQKVLVICAKAATALQLEQVLREREGIRAAVFHEGMSIIERDRAAAWFAEEDTGAQVL

LCSEIGSEGRNFQFASNLVMFDLPFNPDLLEQRIGRLDRIGQAHDIQIHVPYLEKTAQSVLVRWYHEGLD

AFEHTCPTGRTVYDSVHDELINYLAAPESTDGFDDLIKSCRQQHDALKAQLEQGRDRLLEIHSNGGEKAQ

ALAESIEEQDDDTSLIAFSMNLFDIVGINQDDRGENLIVLTPSDHMLVPDFPGLPEDGCTITFERDVALS

REDAQFITWEHPLIRNGLDLILSGDTGSSTISLLKNKALPVGTLLLELIYVVEAQAPKQLQLNRFLPATP

VRMLLDKNGNNLAAQVEFESFNRQLSAVNRHTGSKLVNAVQQDVHAILQQGEAQIAKAAQGLIDAARNEA

DEKLTAELSRLEALKAVNPNIRDDELAAIESNRQQVMDALAQAGWRLDALRLIVVTHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002888348.1\_4355 [gene=rluA] [locus\_tag=BN49\_RS23540] [protein=bifunctional tRNA pseudouridine(32) synthase/23S rRNA pseudouridine(746) synthase RluA] [protein\_id=WP\_002888348.1] [location=4555248..4555907] [gbkey=CDS]

MAMENYNPPQDPWLVILYQDEHIMVVNKPSGLLSVPGRLEEHKDSVMTRIQRDFPQAESVHRLDMATSGV

IVVALNKAAERELKRQFREREPKKQYVARVWGHPQPAEGLVDLPLICDWPNRPKQKVCYETGKAAQTEYE

VLEYAEDNTARVRLKPITGRSHQLRVHMLALGHPILGDRFYATPEALAMAPRLLLHAETLTITHPAYGNA

MTFRAPIDF

>lcl|NZ\_FO834906.1\_prot\_WP\_002888347.1\_4356 [gene=citX] [locus\_tag=BN49\_RS23545] [protein=citrate lyase holo-[acyl-carrier protein] synthase] [protein\_id=WP\_002888347.1] [location=complement(4555982..4556521)] [gbkey=CDS]

MSVDTPAQAGVSIDALLAAKEQRAARQADWLAHYQQPVISLTLVTPGAVKDSIRYRNMMGVALQACDQLL

WKHRWQTLDRQVLWLPTGPEALWCVAHPASEIKAMCSTLEQSHPLGRLWDIDVICPQNGLVGRQSLGESQ

RRCLLCDEPAHACARSRRHDTDLVVARVEQMIDAWFARD

>lcl|NZ\_FO834906.1\_prot\_WP\_002888345.1\_4357 [locus\_tag=BN49\_RS23555] [protein=2-hydroxycarboxylate transporter family protein] [protein\_id=WP\_002888345.1] [location=complement(4556701..4558065)] [gbkey=CDS]

MSTTDNAFSATLEPIDTPKTTLKQRWWHIMDNWKVGIVPLPLFLLAGGLIALDCLGGKLPSDIVVMVATL

AFFGFACGEFGKRLPVLGKLGAAAICATFIPSALVHYGLLPDVVIESTTKFYKSTNILYLYICCIIVGSI

MSMNRTTLIQGFLKIFFPMLCGEVVGMLVGIGVGTLLGMEPFQVFFFIVLPIMAGGVGEGAIPLSMGYAA

LMHMEQGVALGRVLPMVMLGSLTAIVISGCLNQLGKRFPHLTGEGQLMPNRSHETRSLSESEGVSGKTDV

GTLASGALLAVLLYMMGMLGHKLIGLPAPVGMLFLAVLLKLANVVSPRLQEGSQMVYKFFRTAVTYPILF

AVGVAITPWQELVNAFTLTNLLVIVSTVSALVATGFLVGKKIGMHPIDVAIVSCCQSGQGGTGDVAILTA

GNRMSLMPFAQIATRIGGAINVSLGLLFLSHYLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002888340.1\_4358 [locus\_tag=BN49\_RS23560] [protein=sensor histidine kinase] [protein\_id=WP\_002888340.1] [location=4558390..4560015] [gbkey=CDS]

MKLSFQYKLFISLVAFFSVLFIALGIYYYFDASRQLYQEMSARAKIQAEEIALMPNLRQQVSRHDPQAIQ

AFMQQIAAHSDASFIVIGDRQGVHLFHSVHPEWVGTRLVGGDNQAVLEGKSITTIRKGGLGVSLRSKTPI

VDDAGRVIGIVSVGYLTSYLDSITLTKVINIFIAAVLLLIALFIFSWYFTRSIKKQIFSLEPREIGLLVR

QQKAMMESIFEGVIVIDRQRRIEVINHAARSLLGLSQPARQLRGQSIDSVISPQPFFASGDMLERDTHDE

LCRFNQLTVLASRVRIMLENTLQGWVITFRDRNEINALTAQLSQVKRYVDNLRIMRHEQLNRMTTLSGLL

HMGHYDEAIRYIQAQSEHAQELLDFISSHFHSPTLCGLLLGKATRAREKGVALSFDPACRIDRPLPSLME

SELISIIGNLLDNAIEATQRAELPHEPVEVLIQLNARELIIEVADRGVGIRPDIRERIFERGVTTKTRGD

HGIGLYLIEHYVTQAGGTIEVADNAPRGTIFTLFIPADAHACPQPEAHDAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888337.1\_4359 [locus\_tag=BN49\_RS23565] [protein=response regulator] [protein\_id=WP\_002888337.1] [location=4560005..4560703] [gbkey=CDS]

MHHDLVDVLIIEDESELARLHAELVQKHPRLRLAGMAASLAQARQLLHATPPQLVLLDNYLPDGKGVTLM

TDPALATSQCSVIFITAASDMETCSQAIRNGAFDYILKPVSWKRLSQSLERFIQFYDQQREWKIVDQQNV

DSLYQLQAKNYRVDSGSKGIEEKTLALVQGLFSDREAHCFSVDEVVSAAGLSKTTARRYLEHGVETGFLE

VEMLYGKIGHPRRLYRRAKVKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888332.1\_4360 [gene=djlA] [locus\_tag=BN49\_RS23570] [protein=co-chaperone DjlA] [protein\_id=WP\_002888332.1] [location=complement(4560736..4561563)] [gbkey=CDS]

MQYLGKVIGVAVALLMGGGFWGVVLGFLVGHMFDRARSRRLNLFANQQERQSLFFSTTFEVMGHLTKSKG

RVTEADIHVANVLMDRMNLHGASRTAAQQAFRDGKADNYPLREKMRQLRSVCFGRFDLIRMFLEIQLQAA

FADGELHPNEREVLFVIADELGISRAQFDQFLRMMQGGAQFGGGSQQRSYGQHGGNAGWQQAQRGPTLED

ACNVLGVKPTDDAATVKRAYRKLMNEHHPDKLVAKGLPPEMMEMAKQKAQEIQKAWELIKEQRGF

>lcl|NZ\_FO834906.1\_prot\_WP\_004147026.1\_4361 [gene=lptD] [locus\_tag=BN49\_RS23575] [protein=LPS assembly protein LptD] [protein\_id=WP\_004147026.1] [location=4561807..4564155] [gbkey=CDS]

MKKRIPSLLATMIASALYSQQGLAADLATQCMLGVPSYDRPLVEGRPGDLPVTINADHAKGNYPDNAVFT

GNVDINQGNSRLRADEVQLHQQQAAGQAQPVRTVDALGNVHYDDNQVILKGPKAWSNLNTKDTNVWQGDY

QMVGRQGRGTADLMKQRGENRYTILENGSFTSCLPGSDTWSVVGSEVIHDREEQVAEIWNARFKLGSVPI

FYSPYLQLPVGDKRRSGFLIPNAKYSTKNGVEFSLPYYWNIAPNFDATITPHYMNKRGGVMWENEFRYLT

QLGSGLTEFDYLPSDKVYEDDHSSDSNSRRWLFYWNHSGVIDQVWRLNADYTKVSDPDYFNDFSSKYGSS

TDGYATQKFSAGYVNQNFDATVSTKQFQVFDRESSNSYSAEPQLDVNYYQNDVGPFDTHLYGQVAHFVNS

NNNMPEATRVHFEPTINLPLSNGWGSLNTEAKLLATHYQQSNLDKYNAANGTDYKESVSRVMPQFKVDGK

MVFERDLQEGFTQTLEPRVQYLYVPYRDQSEIGNYDSTLLQSDYTGLFRDRTYSGLDRIASANQVTTGLT

SRVYDAAAVERFNISVGQIYYFTESRTGDDNINWENNDTTGSLVWAGDTYWRIADEWGLRGGIQYDTRLD

NVATGNGTIEYRRDENRLVQLNYRYASPEYIQATLPSYSTAAQYKQGISQVGMTASWPIVDRWSVVGAYY

YDTNTRKAANQMLGVQYNSCCYAIRLGYERKVNGWNSNDNGGESKYDNTFGINIELRGLSSNYGLGTQQM

LRSNILPYQSSL

>lcl|NZ\_FO834906.1\_prot\_WP\_002888329.1\_4362 [gene=surA] [locus\_tag=BN49\_RS23580] [protein=peptidylprolyl isomerase SurA] [protein\_id=WP\_002888329.1] [location=4564210..4565496] [gbkey=CDS]

MKNWKTLLLGIAMIANTSFAAPQVVDKVAAVVNNGVVLESDVDGLMQSVKLNAGQAGQQLPDDATLRHQI

LERLIMDQIVLQMGQKMGVKISDDQLDQAIANIAKQNNMTLDQMRSRLAYEGINYNTYRNQIRKEMLISE

VRNNEVRRRITVLPQEVEALAKQIGDQNDASTELNLSHILIPLPENPTSDEVAAAQEQANSIVEQARNGA

NFGKLAITYSADQQALKGGQMGWGRIQELPGIFAQALSTAKKGDIVGPIRSGVGFHILKVNDLRGGTQNI

SVTEVHARHILLKPSPIMNDAQAQAKLEQIAAEIKSGKITFAQAAKTYSEDPGSANQGGDLGWATPDIFD

PAFRDALMRLNKGQTSGPVHSSFGWHLIELLDSRQVDRTDAAQKDRAYRMLMNRKFSEEAATWMQEQRAS

AYVKILSN

>lcl|NZ\_FO834906.1\_prot\_WP\_002888327.1\_4363 [gene=pdxA] [locus\_tag=BN49\_RS23585] [protein=4-hydroxythreonine-4-phosphate dehydrogenase PdxA] [protein\_id=WP\_002888327.1] [location=4565502..4566491] [gbkey=CDS]

MPETRKVVITPGEPAGIGPDLVVQLAQRDWPVELVICADGALLTDRAKRLGLPLSLLPYDPAQPPVPQRA

GTLTLLNVPLNVPAEPGVLNVQNGAYVVETLARACDGCLSGEFAALVTGPVHKGNINDAGIAFTGHTEFF

EERAKASKVVMMLATEELRVALVTTHLPLKAISEAITPELLREIITILDHDLRTKFGIAQPHVLVCGLNP

HAGEGGHMGTEEIDTIIPVLEEMRAKGMNLSGPLPADTLFQPKYLDHADAVLAMYHDQGLPVLKYQGFGR

GVNITLGLPFIRTSVDHGTALELAGQGKADVGSFITALNLAIKMIVNTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002888324.1\_4364 [gene=rsmA] [locus\_tag=BN49\_RS23590] [protein=16S rRNA (adenine(1518)-N(6)/adenine(1519)-N(6))-dimethyltransferase RsmA] [protein\_id=WP\_002888324.1] [location=4566488..4567309] [gbkey=CDS]

MNNRVHQGHLARKRFGQNFLNDQFVIDSIVSAINPQKGQAMVEIGPGLAALTEPVGERLDQLTVIELDRD

LAARLQTHPFLGPKLTIYQQDAMTMNFGELAEKMGQPLRVFGNLPYNISTPLMFHLFSYTDAIADMHFML

QKEVVNRLVAGPNSKAYGRLSVMAQYYCQVIPVLEVPPSAFTPPPKVDSAVVRLVPHSTMPYPVKEIRVL

SRITTEAFNQRRKTIRNSLGNLFSVEVLTELGIDPAMRAENISVAQYCLMANWLSDNLPTKES

>lcl|NZ\_FO834906.1\_prot\_WP\_002888323.1\_4365 [gene=apaG] [locus\_tag=BN49\_RS23595] [protein=Co2+/Mg2+ efflux protein ApaG] [protein\_id=WP\_002888323.1] [location=4567312..4567689] [gbkey=CDS]

MIHSPRVCVQVQSVYIESQSSPEEERYVFAYTVTIRNLGRSQVQLLGRYWLITNGHGRETEVQGEGVVGE

QPHIPAGGEYQYTSGAVIETPLGTMQGHYEMIDIDGAPFRIEIPVFRLAVPTLIH

>lcl|NZ\_FO834906.1\_prot\_WP\_002888321.1\_4366 [gene=apaH] [locus\_tag=BN49\_RS23600] [protein=bis(5'-nucleosyl)-tetraphosphatase (symmetrical) ApaH] [protein\_id=WP\_002888321.1] [location=4567694..4568542] [gbkey=CDS]

MSTYLIGDVHGCYDELIALLAQVEFDPRRDTLWLTGDLVARGPGSLEVLRYVKSLGDSVRLVLGNHDLHL

LAVFAGISRNKPKDRLKPLLEAPDADELLNWLRRQPLLQVDEEKKLVMAHAGITPQWDLETAQQCARDVE

AVLSSDSYPFFLDAMYGDMPNHWSNELSGLARLRFISNAFTRMRYCFPNGQLDMYSKEAPEDAPAPLKPW

FAIPGPVSNAYSIAFGHWASLEGRGTPEGIYALDTGCCWGGELTCLRWEDKQYFTQPSNRQKSLDEGEAV

AS

>lcl|NZ\_FO834906.1\_prot\_WP\_002888320.1\_4367 [gene=folA] [locus\_tag=BN49\_RS23605] [protein=type 3 dihydrofolate reductase] [protein\_id=WP\_002888320.1] [location=complement(4568746..4569225)] [gbkey=CDS]

MISLIAALAVDRVIGMENAMPWNLPADLAWFKRNTLNKPVVMGRLTWESIGRPLPGRKNIVISSKPGSDD

RVQWVSSVEEAIAACGDVEEIMVIGGGRVYEQFLPKAQKLYLTHIDAEVEGDTHFPDYDPDEWESVFSEF

HDADAQNSHSYCFEILERR

>lcl|NZ\_FO834906.1\_prot\_WP\_004145992.1\_4368 [gene=kefC] [locus\_tag=BN49\_RS23610] [protein=glutathione-regulated potassium-efflux system protein KefC] [protein\_id=WP\_004145992.1] [location=complement(4569399..4571264)] [gbkey=CDS]

MDSHTLIQALIYLGAAALIVPIAVRLGLGSVLGYLIAGCIIGPWALRLVTDAEAILHFAEIGVVLMLFVI

GLELDPQRLWKLRASVFGGGALQMVACGVLIGLFCMLLGLRWQVAELIGMTLALSSTAIAMQAMNERNLT

VSQMGRSAFAVLLFQDIAAIPLVAMIPLLAASGGATSLMAFALSALKVAAALALVVVLGRYLTRPLLRFV

ARSGLREVFSAVALFLVFGFGLLLEEVGLSMAMGAFLAGVLLASSEYRHALESDIEPFKGLLLGLFFIGV

GMSIDFGTLVTHPLRIVILLVGFLAIKMLMLWLIARPLGVPRAQRRWFAVLLGQGSEFAFVVFGAARMAD

VLDGEWAKALTLAVALSMAATPILLVLLTRLEKSSSGQARDADEIDEEQPRVIVAGFGRFGQIAGRLLLS

SGVKMVILDHDPDHVDTLRKFDMKVFYGDATRVDLLESAGAEKAEVLINAIDDPHVSLELVARVKEHFPH

LQIISRARDVDHYIQLRQAGVEAPERETFEAALKSGRMTLEALGLGAYEARERADLFRRFNLQMVEEMVA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002888068.1\_4369 [gene=kefF] [locus\_tag=BN49\_RS23615] [protein=glutathione-regulated potassium-efflux system oxidoreductase KefF] [protein\_id=WP\_002888068.1] [location=complement(4571257..4571790)] [gbkey=CDS]

MILIIYAHPYPQHSHANKRMLEQAGTLEGVEIRSLYQLYPDFNIDVAAEQAALARADLVIWQHPMQWYSV

PPLLKLWMDKVLSHGWAYGHNGIALRGKSLMWAVTTGGGESHFDIGSFPGFPVLAQPLQATALYCGMKWL

PPFAMHCTFICDDETLQAQARRYRQRLIDWQEAHQNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002888059.1\_4370 [locus\_tag=BN49\_RS23620] [protein=YgdI/YgdR family lipoprotein] [protein\_id=WP\_002888059.1] [location=complement(4571922..4572155)] [gbkey=CDS]

MRNNILVASALAATAIMFVAGCSSNQSIKTTDGKTIVTSGKPQVDDDTGLVSYKNAETGRVEQINRDQVK

SMDELDN

>lcl|NZ\_FO834906.1\_prot\_WP\_002888056.1\_4371 [gene=carB] [locus\_tag=BN49\_RS23625] [protein=carbamoyl-phosphate synthase large subunit] [protein\_id=WP\_002888056.1] [location=complement(4572325..4575549)] [gbkey=CDS]

MPKRTDIKSILILGAGPIVIGQACEFDYSGAQACKALREEGYRVILVNSNPATIMTDPEMADATYIEPIH

WEVVRKIIEKERPDAVLPTMGGQTALNCALELERQGVLAEFGVTMIGATADAIDKAEDRRRFDIAMKKIG

LDTARSGIAHTMEEALAVAADVGFPCIIRPSFTMGGTGGGIAYNREEFEEICERGLDLSPTNELLIDESL

IGWKEYEMEVVRDKNDNCIIVCSIENFDAMGIHTGDSITVAPAQTLTDKEYQIMRNASMAVLREIGVETG

GSNVQFAVNPKNGRLIVIEMNPRVSRSSALASKATGFPIAKVAAKLAVGYTLDELMNDITGGRTPASFEP

SIDYVVTKIPRFNFEKFAGANDRLTTQMKSVGEVMAIGRTQQESLQKALRGLEVGATGFDPKVSLDDPEA

LTKIRRELKDAGAERIWYIADAFRAGLSVDGVFNLTNIDRWFLVQIEELVRLEEKVAEVGINGLDADFLR

TLKRKGFADARLAKLAGVREAEIRKLRDQYDLHPVYKRVDTCAAEFATDTAYMYSTYEEECESNPSVDRD

KIMVLGGGPNRIGQGIEFDYCCVHASLALREDGYETIMVNCNPETVSTDYDTSDRLYFEPVTLEDVLEIV

RIEKPKGVIVQYGGQTPLKLARALEAAGVPVIGTSPDAIDRAEDRERFQHAVDRLKLKQPANATVTAIEQ

AVEKAKEIGYPLVVRPSYVLGGRAMEIVYDEQDLRRYFQTAVSVSNDAPVLLDRFLDDAIEVDVDAICDG

EMVLIGGIMEHIEQAGVHSGDSACSLPAYTLSKEIQDVMREQVQKLAFELQVRGLMNVQFAVKDNEVYLI

EVNPRAARTVPFVSKATGVPLAKVAARVMAGKTLAQQGVTKEIIPPYYSVKEVVLPFNKFPGVDPLLGPE

MRSTGEVMGVGRTFAEAFAKAQLGSNSTMKKQGRALLSVREGDKERVVDLAAKLLKFGFELDATHGTAIV

LGEAGINPRLVNKVHEGRPHIQDRIKNGEYTYIINTTAGRQAIEDSKLIRRSALQYKVHYDTTLNGGFAT

AMALNADATEKVISVQEMHAQITK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177433.1\_4372 [gene=carA] [locus\_tag=BN49\_RS23630] [protein=glutamine-hydrolyzing carbamoyl-phosphate synthase small subunit] [protein\_id=WP\_004177433.1] [location=complement(4575567..4576715)] [gbkey=CDS]

MIKSALLVLEDGTQFHGRAIGATGTAVGEVVFNTSMTGYQEILTDPSYSRQIVTLTYPHIGNVGTNAADE

ESSQVHAQGLVIRDLPLIASNFRSTEDLSSYLKRHNIVAIADIDTRKLTRLLREKGAQNGCIIAGDSPDA

QLALEKAKAFPGLNGMDLAKEVTTAETYSWTQGSWTLAGDLPEAKAESELPFHVVAYDFGAKRNILRMLV

DRGCRLTVVPAKTSAADVLALNPDGIFLSNGPGDPAPCDYAIEAIEKFLETDIPVFGICLGHQLLALASG

AKTIKMKFGHHGGNHPVKDIDNNVVMITAQNHGFAVDEATLPANLRVTHKSLFDGTLQGIHRTDKPAFSF

QGHPEASPGPHDAAPLFDHFIELIELYRQSAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004151369.1\_4373 [gene=dapB] [locus\_tag=BN49\_RS23645] [protein=4-hydroxy-tetrahydrodipicolinate reductase] [protein\_id=WP\_004151369.1] [location=complement(4577173..4577994)] [gbkey=CDS]

MHDAQIRVAIAGAGGRMGRQLIQAALQMEGVALGAALEREGSSLVGSDAGELAGAGKAGVAVQSSLAAVK

DDFDVLIDFTRPEGTLNHLAFCREHGKGMVIGTTGFDDAGKQAIRDAAQDIAIVFAANFSVGVNVLLKLL

EKAAKVMGDYTDIEIIEAHHRHKVDAPSGTALAMGEAIAGALNKDLKDCAVYSREGYTGERVPGTIGFAT

VRAGDIVGEHTAMFADIGERIEITHKASSRMTFANGAVRSALWLKGKKNGLFDMRDVLDLNSL

>lcl|NZ\_FO834906.1\_prot\_WP\_004222628.1\_4374 [gene=citG] [locus\_tag=BN49\_RS23650] [protein=triphosphoribosyl-dephospho-CoA synthase CitG] [protein\_id=WP\_004222628.1] [location=complement(4578223..4579131)] [gbkey=CDS]

MSDVLINPARVRRVKPLSAEEVVSAVERALLTEVRLTPKPGLVDIRNAGAHWDMDLASFEASTAVVAPWM

EKFFIMGHDTAAVAPEQVLMMLRPVGMACENDMLEATGGVNTHRGAIFAFGLLSAAAGRLVSKGEPIEQH

RLCDQVARFCRGMVMQELSSAGGERLSKGEAHFLRYGLSGARGEAESGFLTVRTQAMPVFTRMMEETGDS

NLALLQTLLHLMAWNDDTNLVSRGGLAGLNFVQQEAQRLLWQGGVLADGGLEALRQFDDELIARHLSPGG

SADLLAVTWFLSAFPAGALFPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016532426.1\_4375 [gene=citF] [locus\_tag=BN49\_RS23655] [protein=citrate lyase subunit alpha] [protein\_id=WP\_016532426.1] [location=complement(4579150..4580676)] [gbkey=CDS]

MKETVAMLNQQYVMPNGLTPYAGVTAKSPWLASESEKRQRKICDSLETAIRRSGLQNGMTISFHHAFRGG

DKVVNMVVAKLAEIGFRDLTLASSSLIDAHWPLIEHIKNGVIRQIYTSGLRGKLGEEISAGLMENPVQIH

SHGGRVQLIQSGELSIDVAFLGVPCCDEFGNANGFSGKSRCGSLGYARVDAEHAKCVVLLTEEWVDYPNY

PASIAQDQVDLIVQVDEVGDPQKITAGAIRLTSNPRELLIARQAAKVFEHSGYFKEGFSLQTGTGGASLA

VTRFLEDKMRRNGITASFGLGGITGTMVDLHEKGLIKTLLDTQSFDGDAARSLAQNPNHVEISTNQYASP

GSKGASCERLNVVMLSALEIDIDFNVNVMTGSNGVLRGASGGHSDTAAGADLTIITAPLVRGRIPCVVEK

VLTRVTPGASVDVLVTDHGIAVNPARQDLIDNLRSAGIPLMTIEELQQRAELLTGKPQPIEFTDRVVAVV

RYRDGSVIDVIRQVKNSD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151372.1\_4376 [gene=citE] [locus\_tag=BN49\_RS23660] [protein=citrate (pro-3S)-lyase subunit beta] [protein\_id=WP\_004151372.1] [location=complement(4580687..4581556)] [gbkey=CDS]

MKPRRSMLFIPGANAAMLSTSFVYGADAVMFDLEDAVSLREKDTARLLVYQALQHPLYQDIETVVRINPL

NTPFGLADLEAVVRAGVDMVRLPKTDSKEDIHELEAHVERIERECGREVGSTKLMAAIESALGVVNAVEI

ARASPRLAAIALAAFDYVMDMGTSRGDGTELFYARCAVLHAARVAGIAAYDVVWSDINNEEGFLAEANLA

KNLGFNGKSLVNPRQIELLHQVYAPTRKEVDHALEVIAAAEEAETRGLGVVSLNGKMIDGPIIDHARKVV

ALSASGIRD

>lcl|NZ\_FO834906.1\_prot\_WP\_009309208.1\_4377 [gene=citD] [locus\_tag=BN49\_RS23665] [protein=citrate lyase acyl carrier protein] [protein\_id=WP\_009309208.1] [location=complement(4581553..4581846)] [gbkey=CDS]

MEMKIDALAGTLESSDVMVRIGPAAQPGIQLEIDSIVKQQFGAAIEQVVRETLAQLGVKQASVVVDDKGA

LECVLRARVQAAALRAAQQTQLQWSQL

>lcl|NZ\_FO834906.1\_prot\_WP\_004222626.1\_4378 [gene=citC] [locus\_tag=BN49\_RS23670] [protein=[citrate (pro-3S)-lyase] ligase] [protein\_id=WP\_004222626.1] [location=complement(4581877..4582905)] [gbkey=CDS]

MTLILKRVQLLKDKPRREAIDRFLRQHQLSLEADCEMAIIAEYQQRLVGCGAIAGNVLKCIAIDPSLQGE

GLSLKLLTELLTLAYELGRSELFLFTKPCNAALFSGAGFWPIAQAGDRAVLMENSRERLTRYCRQLAMYR

QPGRKIGAIVMNANPFTLGHRWLVEQAASQCDWLHLFVVKEDASCFSYHDRFKLIEQGITGIDKVTLHPG

SAYLISRATFPGYFLKEQGVVDDCHSQIDLQLFRERLAPALQITHRFVGTEPLCPLTRNYNQRMKSLLEA

PGDAPPIEVVELARIEKNGGPVSASRVRELYRQRNWQAVAALVPPGTLSFLMQLAESEHQTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151375.1\_4379 [gene=citS] [locus\_tag=BN49\_RS23675] [protein=citrate/sodium symporter CitS] [protein\_id=WP\_004151375.1] [location=4583162..4584502] [gbkey=CDS]

MTNMSQAPATEKKGVSDLLGFKIFGMPLPLYAFALITLLLSHFYNALPTDIVGGFAIMFIIGAIFGEIGK

RLPIFNKYIGGAPVMIFLVAAYFVYAGIFTQKEIDAISNVMDKSNFLNLFIAVLITGAILSVNRRLLLKS

LLGYIPTILMGIVGASIFGIAIGLVFGIPVDRIMMLYVLPIMGGGNGAGAVPLSEIYHSVTGRSREEYYS

TAIAILTIANIFAIVFAAVLDIIGKKHTWLSGEGELVRKASFKVEEDEKAGQITHRETAVGLVLSTTCFL

LAYVVAKKILPSIGGVAIHYFAWMVLIVAALNASGLCSPEIKAGAKRLSDFFSKQLLWVLMVGVGVCYTD

LQEIINAITFANVVIAAIIVIGAVLGAAIGGWLMGFFPIESAITAGLCMANRGGSGDLEVLSACNRMNLI

SYAQISSRLGGGIVLVIASIVFGMMI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151376.1\_4380 [locus\_tag=BN49\_RS23680] [protein=oxaloacetate decarboxylase subunit gamma] [protein\_id=WP\_004151376.1] [location=4584658..4584909] [gbkey=CDS]

MTDNAVLLGEGFTLMCLGMGFVLVFLLLLIFAIRGMSLAVNRLFPEPPAAPKPAPAAVAPADDFARLKPA

IVAAIHHHRRLHP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043795.1\_4381 [gene=oadA] [locus\_tag=BN49\_RS23685] [protein=sodium-extruding oxaloacetate decarboxylase subunit alpha] [protein\_id=WP\_046043795.1] [location=4584925..4586715] [gbkey=CDS]

MTVAITDVVLRDAHQSLFATRLRLDDMLPVAAQLDDVGYRSLECWGGATFDACIRFLGEDPWVRLRELKK

AMPKTPLQMLLRGQNLLGYRHYADDVVERFVERAVKNGMDVFRVFDAMNDPRNMQAALQAVRRHGAHAQG

TLSYTTSPAHTLQTWLDLTEQLLETGVDSVAIKDMSGILTPHAAFELVSEIKKRYDVTLHLHCHATTGMA

EMALLKAIEAGVDGVDTAISSMSATYGHPATEALVATLAGTQYDTGLDIHRLENIAAYFREVRKKYHAFE

GQLKGTDSRILVSQVPGGMLTNLEGQLKQQSAAHRLDDVLAEIPRVREDLGFIPLVTPTSQIVGTQAVLN

VLGGERYKTIAKETAGILKGEYGRTPAPVNAALQARVLDGADPVTCRPADLLKPELAALEADVRRQAQEK

GITLAENAIDDVLTVALFPQIGLKFLENRHNPAAFEPVPQAEAAQPVAKAEKPAASGVYTVEVEGKAFVV

KVSDGGDVSQLTAAAPAPAPAPAPASAPAAAAPAGAGTPVTAPLAGTIWKVLASEGQTVAAGEVLLILEA

MKMETEIRAAQAGTVRGIAVKAGDAVAVGDTLMTLA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043797.1\_4382 [locus\_tag=BN49\_RS23690] [protein=sodium ion-translocating decarboxylase subunit beta] [protein\_id=WP\_046043797.1] [location=4586731..4587927] [gbkey=CDS]

MESLNALIQGMGLMHLGAGQAIMLLVSLLLLWLAIAKKFEPLLLLPIGFGGLLSNIPEAGLALTALESLL

AHHDPAQLAVIAAKLHCAPDVHAIKAALALALPSVQGQMESLAVDMGYSAGVLAIFYKVAIGSGIAPLVI

FMGVGAMTDFGPLLANPRTLLLGAAAQFGIFATVLGALTLNYFGIISFTLPQAAAIGIIGGADGPTAIYL

SGKLAPELLGAIAVAAYSYMALVPLIQPPIMKALTTDKERKIRMVQLRTVSKREKILFPAVLLLLVALLL

PDAAPLLGMFCFGNLMRESGVVERLSDTVQNALINIVTIFLGLSVGAKLVADKFLQPQTLGILVLGVIAF

CVGTAAGVLMAKLMNVFSRHKINPLIGSAGVIGSAIAAGVMLKYVLAM

>lcl|NZ\_FO834906.1\_prot\_WP\_016529045.1\_4383 [locus\_tag=BN49\_RS23695] [protein=sensor histidine kinase] [protein\_id=WP\_016529045.1] [location=4588099..4589727] [gbkey=CDS]

MYTRKITHWFARRSFQNRIFLLILFTSTIVMLAMSWYLTDITEERLHYQVGQRALIQAMQISAMPELVEA

VQKRDLARIKALIDPMRSFSDATYITVGDASGQRLYHVNPDEIGKSMEGGDSDEALINAKSYVSVRKGSL

GSSLRGKSPIQDATGKVIGIVSVGYTIEQLENWLSLQISSLLIPMAIMLLLLLFCARRFSLHIKKQMLNM

EPQQLSQLLIQQSVLFESVFEGLIAIDSDYKITAINQTARRLLNLSQPEPTLIGKRISSVISQEVFFYDA

PQTNKKDEIVTFNQIKVIASRMAVILNNEPQDWVISFRSKDDINTLSLQLSQVQQYADNLRAVQHEHRNL

ISTIAGLLFLKRYNQALELIQQQSESHQKVIDFIARNFQDNHLAGLLIGKYYRAKELGLELIFDPACFVD

RLPTALSHNEWISIVGNLLDNAYNASLRQPQGSKQIECLINSDGQEVIIEIADQGCGIDEALRDRIFERG

VTSSASKDHGIGLWLVRSYVEQAGGSIVVENNIPFGTIFTLYIPLTRDEHHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004222618.1\_4384 [locus\_tag=BN49\_RS23700] [protein=response regulator] [protein\_id=WP\_004222618.1] [location=4589720..4590424] [gbkey=CDS]

MDSITTLIVEDEPMLAEILVDNIKQFPQFDVIGIADKLESARKQLRLYQPQLILLDNFLPDGKGIDLIRH

AVSTHYKGRIIFITADNHMETISEALRLGVFDYLIKPVHYQRLQHTLERFARYRSSLRSSEQASQLHVDA

LFNIQAREQTEPASAPLRGIDESTFQRVLQLFADPTVVHTADSLARILGSSKTTARRYLEQGVKNDFLEA

EISYGKVGRPERIYHGKQTYPEQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002887990.1\_4385 [locus\_tag=BN49\_RS23705] [protein=hypothetical protein] [protein\_id=WP\_002887990.1] [location=complement(4590430..4591059)] [gbkey=CDS]

MTERVYYTSDATDGRAQIIACTAEADGRYAIELDRTLFHPQGGGQPADRGWIAGQVVETVVVRGERVLHI

LSQPLPLGEVEMKIDASARQLHARLHSAGHLLGLAGEQLGWQPVKAHHWPGEGRITFASRNSAALPDASA

LLALVKAWQAQDLPRQVTFADGMRKVGFGELPAYPCGGTHVARLAELGDIVISQIKMKKGQLVVSYTLA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529044.1\_4386 [locus\_tag=BN49\_RS23710] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016529044.1] [location=4591152..4592081] [gbkey=CDS]

MNLNLLPDLALFVQIVDQGSFSAVARQNGITPSAVSRSVSRLEREMGCKLLQRTTRKLRLSDAGETIYQH

AQQMLEAARQAMDSAGSRQTVAQGKLTLSVPKAVGRFVIHPLMMAFFHRYPQVDVCLRLEDRPLDFIDDG

IDLALRITDTPSPGLHGKPLMPIRHVICATEAYLQQHGTPYTPQDLRAHSCISLGETPADARWKFRREGK

TETVQTYGRYAANHTAVRLDAVRQHLGIGSLPLFTAREALAKGDIVQVLPEWEFISSYSGDLWLLWAGDK

HMPARMRAMIDYLSETVPALSAGSTEPAK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529043.1\_4387 [locus\_tag=BN49\_RS23715] [protein=DUF805 domain-containing protein] [protein\_id=WP\_016529043.1] [location=complement(4592029..4592394)] [gbkey=CDS]

MTYGQAYLSGWKETFNFSGRASRQQFWTFFLINVLIAAAPVAAWSLATLVDPHYGILSFVVIPFAALWLL

LMAIPLLAVGCRRMHDIGRSGIWFVLGVIIPWFAIISLALCCLRSAPAPSR

>lcl|NZ\_FO834906.1\_prot\_WP\_002887981.1\_4388 [gene=rihC] [locus\_tag=BN49\_RS23720] [protein=ribonucleoside hydrolase RihC] [protein\_id=WP\_002887981.1] [location=complement(4592425..4593339)] [gbkey=CDS]

MRLPIILDTDPGIDDAAAIAAALFAPELDLQLMTTVAGNVSVEKTTRNALQLLHFWNADVPLAQGASMPL

VRPLRDAASVHGESGMEGYDFVEHQRQPLAKPAFQAIRDALMHAAEPITLVAIGPLTNIALLLTQYPECV

FNIRRLVIMGGSAGRGNFTPNAEFNIAIDPEAAAKVFHSGLEIVMCGLDVTNRALLAADYLATLPTLNQT

GKMLHALFSHYRSGSMSSGLRMHDLCAIAWLARPELFTLQPCFVAVETQGTWTAGTTVVDIEGRLGQPAN

AQVALDIDVEGFQRWAAEVIALAP

>lcl|NZ\_FO834906.1\_prot\_WP\_002887979.1\_4389 [gene=ispH] [locus\_tag=BN49\_RS23725] [protein=4-hydroxy-3-methylbut-2-enyl diphosphate reductase] [protein\_id=WP\_002887979.1] [location=complement(4593406..4594356)] [gbkey=CDS]

MQILLANPRGFCAGVDRAISIVENALTLYGAPIYVRHEVVHNRYVVDSLRKRGAIFIEQISEVPDGAILI

FSAHGVSQAVRNEAKSRDLTVFDATCPLVTKVHMEVARASRRGEESILIGHAGHPEVEGTMGQYNNPQGG

MYLVESPEDVLKLEVKNDARLSFMTQTTLSVDDTSDVIDALRARFPKIVGPRKDDICYATTNRQEAVRAL

AEQADVVLVVGSKNSSNSNRLAELAQRMGKAAYLIDDASDIQEAWVKDAACVGVTAGASAPDILVQNVIT

RLQELGGGEAVPLEGREENIVFEVPKELRVDVREVE

>lcl|NZ\_FO834906.1\_prot\_WP\_002887976.1\_4390 [gene=fkpB] [locus\_tag=BN49\_RS23730] [protein=FKBP-type peptidyl-prolyl cis-trans isomerase] [protein\_id=WP\_002887976.1] [location=complement(4594358..4594807)] [gbkey=CDS]

MSKSVQSNSAVLVHFTLKLDDGSTAESTRSNGKPALFRLGDTSLSEGLEQQLLGLKEGEKKAFSLEPDAA

FGVPSPDLIQYFSRREFIDAGEPEIGAIMLFTAMDGSEMPGVIREVNGDSITVDFNHPLAGRTVHFDIEV

LEIDPALEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002887973.1\_4391 [gene=lspA] [locus\_tag=BN49\_RS23735] [protein=signal peptidase II] [protein\_id=WP\_002887973.1] [location=complement(4594923..4595423)] [gbkey=CDS]

MSKSICSTGLRWLWVVVAVLIIDLGSKFLILQNFALGETVPLFPSLNLHYARNYGAAFSFLADSGGWQRW

FFSGIAIGICVVLTVLMYRSKATQKLNNIAYALIIGGALGNLFDRLWHGFVVDMIDFYVGDWHFATFNLA

DSAICIGAALIVLEGFLPKPTVKEQA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531349.1\_4392 [gene=ileS] [locus\_tag=BN49\_RS23740] [protein=isoleucine--tRNA ligase] [protein\_id=WP\_016531349.1] [location=complement(4595423..4598239)] [gbkey=CDS]

MSDYKSTLNLPETGFPMRGDLAKREPGMLARWTDDDLYGIIRAAKKGKKTFILHDGPPYANGSIHIGHSV

NKILKDIIVKSKGLTGYDSPYVPGWDCHGLPIELKVEQEYGKPGEKFTAAEFRAKCREYAAEQIDGQRKD

FIRLGVLGDWSHPYLTMDFKTEANIIRALGKIIGNGHLHKGAKPVHWCVDCRSALAEAEVEYYDKTSPSI

DVAFHAVDKAAVLAKFGVADVNGPVSLVIWTTTPWTLPANRAISLSPEFDYALVQVDGQALILAKDLVES

VMKRLGVTDYRILAAVQGSELELMRFKHPFLDFDVPAILGDHVTLDAGTGAVHTAGGHGPDDYTISQKYG

LEIANPVGPDGAYLPGTWPSLDGINVFKANDIIVEMLRDSGALLHVEKMQHSYPCCWRHKSPIIFRATPQ

WFVSMDQKGLRAQSLKEIKGVQWIPDWGQARIESMVANRPDWCISRQRTWGVPMSLFVHKETHELHPRTL

ELMEEVAKRVEVDGIQAWWDLDSRVILGDDADSYEKVPDTLDVWFDSGSTHSSVVDVRPEFAGHAADMYL

EGSDQHRGWFMSSLMISTAMKGKAPYRQVLTHGFTVDGQGRKMSKSIGNTVSPQDVMNKLGADILRLWVA

STDYTGEMAVSDEILKRAADSYRRIRNTARFLLANLNGFDPAKDMVKPEEMVVLDRWAVGCAQAAQEDIL

KAYESYDFHEVVQRLMRFCSIEMGSFYLDIIKDRQYTAKADSVARRSCQTALFHIVEALVRWMAPIMSFT

ADEIWGYLPGEREKYVFTGEWYEGLFGLADDEAMNDDFWDELLKVRGEVNKVIEQARADKKVGGSLEAAV

TLYADADLAAKLNALGDELRFVLLTSGANVADYASASADAQQSELLKGLKVALSKAEGEKCPRCWHYTTD

IGKVAEHAEICGRCVSNVAGDGEQRKFA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887969.1\_4393 [gene=ribF] [locus\_tag=BN49\_RS23745] [protein=bifunctional riboflavin kinase/FAD synthetase] [protein\_id=WP\_002887969.1] [location=complement(4598283..4599221)] [gbkey=CDS]

MKLIRGIHNLSQAPHGCVLTIGNFDGVHRGHQALLQRLREEGRQRGLPVVVMIFEPQPLELFAADKAPAR

LTRLREKLGYLAESGVDYVLCVRFDRRFAALTAQDFISELLVRRLGVQFLAVGDDFRFGAGRQGDFLLLQ

KAGAEYGFDVTSTQTFCEGGVRISSTAVRQALADDDLLLAETLLGHPFSISGRVVHGDELGRTIGFPTAN

LPLRRQVSPVKGVYAVEVTGLGDKPIAGVANIGTRPTVAGVRQQLEVHLLDVVMDLYGRHINVILRKKIR

NEQRFASLDELKAQIARDELTARELFGLTSQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887965.1\_4394 [gene=rpsT] [locus\_tag=BN49\_RS23750] [protein=30S ribosomal protein S20] [protein\_id=WP\_002887965.1] [location=4599551..4599814] [gbkey=CDS]

MANIKSAKKRAVQSEKARKHNASRRSMMRTFIKKVYAAIEAGDKAAAQKAFNEMQPIVDRQAAKGLIHKN

KAARHKANLTAQINKLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887961.1\_4395 [gene=nhaR] [locus\_tag=BN49\_RS23760] [protein=transcriptional activator NhaR] [protein\_id=WP\_002887961.1] [location=complement(4599934..4600830)] [gbkey=CDS]

MSHINYNHLYYFWHVYKEGSVVGAAEALFLTPQTITGQIKALEERLQGKLFKRKGRGLEPSELGELVFRY

ADRMFTLSQEMLDIVNYRKESNLLFDVGVADALSKRLVSGVLDAAVVESEQIHLRCFESTHELLLEQLSQ

HKLDMIISDCPIDSTQQEGLFSVKIGECSVSFWCMNPAPTKPFPACLEERRLLIPGRRSMLGRKLLNWIN

VQGLKVEILGEFDDAALMKAFGAAHNAIFVAPTLYAHDFYHDESIVEIGRMDSVMEEYHAIFAERMIQHP

AVQRICNRDYSSLFTEPR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043800.1\_4396 [gene=nhaA] [locus\_tag=BN49\_RS23765] [protein=Na+/H+ antiporter NhaA] [protein\_id=WP\_046043800.1] [location=complement(4600885..4602060)] [gbkey=CDS]

MKHLQRFFSSDASGGIVLIIAAALAMVMANTSVTSGLYHSFLETPVLLRVGALEINKNMLLWINDALMAV

FFLLIGLEVKRELIQGSLASRRQAVFPVIAALGGMIVPALVYLAFNAQDPVAREGWAIPAATDIAFALGV

LALLGSRVPTALKIFLMALAIIDDLGAIVIIALFYTHDLSMLSLGVAAAAIAVLVALNLSGVRRTGIYIL

VGAVLWTAVLKSGVHATLAGVIVGFMIPLEEKHGKSPAKALEHVLHPWVAFMILPLFAFANAGVSLQGVT

LAGLTSLLPLGIMAGLFIGKPLGISLFCWLALKLKWASLPEGTTCKQIMAVGILCGIGFTMSIFIATLAF

GSVDPALINWAKLGILIGSVLSAVVGYLILRQRVTDTRLAV

>lcl|NZ\_FO834906.1\_prot\_WP\_002887955.1\_4397 [gene=dnaJ] [locus\_tag=BN49\_RS23770] [protein=molecular chaperone DnaJ] [protein\_id=WP\_002887955.1] [location=complement(4602238..4603371)] [gbkey=CDS]

MAKQDYYEILGVSKTAEEREIKKAYKRLAMKYHPDRNQGDKEAEAKFKEIKEAYEILTDAQKRAAYDQYG

HAAFEQGGMGGGGGFGGGADFSDIFGDVFGDIFGGGRGRQRAARGADLRYNMELTLEEAVRGVTKEIRIP

TLEECDVCHGSGAKAGSKPQTCPTCHGAGQVQMRQGFFAVQQTCPHCQGRGTLIKDPCNKCHGHGRVEKT

KTLSVKIPAGVDTGDRIRLAGEGEAGEHGAPAGDLYVQVQVKQHAIFEREGNNLYCEVPINFTMAALGGE

IEVPTLDGRVNLKIPGETQTGKLFRMRGKGVKSVRGGAQGDLLCRVVVETPVGLNEKQKQLLKELQESFG

GPTGENNSPRSKSFFDGVKKFFDDLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_004146997.1\_4398 [gene=dnaK] [locus\_tag=BN49\_RS23775] [protein=molecular chaperone DnaK] [protein\_id=WP\_004146997.1] [location=complement(4603459..4605375)] [gbkey=CDS]

MGKIIGIDLGTTNSCVAIMDGTTARVLENAEGDRTTPSIIAYTQDGETLVGQPAKRQAVTNPQNTLFAIK

RLIGRRFQDEEVQRDVSIMPYKIVAADNGDAWLDVKGTKTAPPQISAEVLKKMKKTAEDYLGEPVTEAVI

TVPAYFNDAQRQATKDAGRIAGLEVKRIINEPTAAALAYGLDKEVGNRTIAVYDLGGGTFDISIIEIDEV

DGEKTFEVLATNGDTHLGGEDFDTRLINYLVDEFKKDQGIDLRNDPLAMQRLKEAAEKAKIELSSAQQTD

VNLPYITADATGPKHMNIKVTRAKLESLVEDLVNRSIEPLKVALQDAGLSVSDINDVILVGGQTRMPMVQ

KKVAEFFGKEPRKDVNPDEAVAIGAAVQGGVLTGDVKDVLLLDVTPLSLGIETMGGVMTALISKNTTIPT

KHSQVFSTAEDNQSAVTIHVLQGERKRASDNKSLGQFNLDGINPAPRGMPQIEVTFDIDADGILHVSAKD

KNSGKEQKITIKASSGLNEEEIQKMVREAEANAESDRKFEELVQTRNQGDHLLHSTRKQVEEAGDKLPAD

DKTAIESALTALESSLKGEDKADIEAKMQALAQASQKLMEIAQQQHAQQQAGSADAQASNAKDDDVVDAE

FEEVKDKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004222594.1\_4399 [locus\_tag=BN49\_RS23780] [protein=DUF2541 family protein] [protein\_id=WP\_004222594.1] [location=4605761..4606165] [gbkey=CDS]

MKSLYRLSVGLILGVSFITSAAANDHKILGVIAMPRNETNDLTLTLPVCRVVKRIQLSADRGDIQLSGAT

VYFKASRGASHTLNVPAGIKEGSTTGWININSDNDNKRCVKKIAFSGHTVHSSDMASLKIIGDD

>lcl|NZ\_FO834906.1\_prot\_WP\_004146011.1\_4400 [gene=msyB] [locus\_tag=BN49\_RS23785] [protein=acidic protein MsyB] [protein\_id=WP\_004146011.1] [location=4606193..4606942] [gbkey=CDS]

MHINYLEDDDLAFLPECSEAHLEAFTRILTHGENGKPRLSSTLLRNETFLAMEGHPERYRRNWQLIAGEL

QHFGGDSIANTLRRHGKFYRAILLDVCKRLKAKVDKQLSTPQIEQQLLAHFLQHSWNKLNAEQKAQFLAA

VECRSHELDSLMAHLLRHRKLSEGVTLLLDERLTAILRTHAAVSVIGHGLVRGAGLGGPLGAALNSVKAV

SGSAYRVTIPAVLHIACLRQMLQPPSDTAEIGEKYPARS

>lcl|NZ\_FO834906.1\_prot\_WP\_004177461.1\_4401 [gene=satP] [locus\_tag=BN49\_RS23790] [protein=acetate uptake transporter] [protein\_id=WP\_004177461.1] [location=4607031..4607597] [gbkey=CDS]

MGNTKLANPAPLGLMGFGMTTILLNLANSGLFAFDVAILAMGIFYGGIAQIFAGLLEYKKGNTFGLTAFT

SYGSFWLTLVAILLMPKMGLADAPNAHFLGMYLGLWGVFTLFMFFGTLKAARMLQFVFLSLTVLFALLAI

GHLVDNEGIVKVAGWVGLICGASAIYLAMGEVLNEQFGRTVLPIGEPR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529692.1\_4402 [locus\_tag=BN49\_RS23795] [protein=MFS transporter] [protein\_id=WP\_016529692.1] [location=complement(4607660..4608964)] [gbkey=CDS]

MSYANRPLNRQDYKTLTLAALGGALEFYDFIIFVFFAAVVGELFFPADIPEWLRQVQTFGIFAAGYLARP

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FVAEHVPEKRIGIACGTLTAGLTVGILLGSVVATLINTSLTPQGIHDGGWRIPFLLGGVFGLIAMYLRRW

LQETPIFLEMQQRKALLQELPVKAVALKHQKAVVISMLLTWLLSAGVVVVILMSPVWLQKHYGFAPAITL

QANSIATIMLCIGCLLAGLAADRFGASRTFIVGSLLLAVASWAFYHLAGASPQRLFLLYGTVGLCVGVVG

AVPYVMVRAFPAEVRFTGISFSYNLSYAIFGGLTPIAVTMLMGVSPMAPAWYVLALSLMGLGLGIWLRQE

LTAPTGMLEGELQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002887898.1\_4403 [gene=mog] [locus\_tag=BN49\_RS23800] [protein=molybdopterin adenylyltransferase] [protein\_id=WP\_002887898.1] [location=complement(4609084..4609671)] [gbkey=CDS]

MNTLRIGLVSISDRASSGVYQDKGIPALEEWLARALTTPFELQTRLIPDEQAIIEQTLCELVDEMGCHLV

LTTGGTGPARRDVTPDATLAIADREMPGFGEQMRQVSLHFVPTAILSRQVGVIRKQALILNLPGQPKAIQ

ETLEGVKDADGNVLVHGIFASVPYCVQLLEGPYVETDGRVVEAFRPKSARRETLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002887897.1\_4404 [gene=tal] [locus\_tag=BN49\_RS23805] [protein=transaldolase] [protein\_id=WP\_002887897.1] [location=complement(4609771..4610724)] [gbkey=CDS]

MTDKLTSLRQYTTVVADTGDIAAMKLYQPQDATTNPSLILGAAQIPEYRKLIDDAVAWARSQSSDRAQQI

LDASDKLAVNIGLEILKLIPGRISTEVDARLSYDTEASIAKAKRIIKLYNDAGISNDRILIKLASTWQGI

RAAEQLEKEGINCNLTLLFSFAQARACAEAGVFLISPFVGRILDWYKANTDKKEYAPAEDPGVVSVSEIY

EYYKQHGYETVVMGASFRNVGEILELAGCDRLTIAPALLKELSESEGAVERKLVYTGEVKARPERITESE

FLWQHNQDPMAVDKLAEGIRKFAIDQEKLEKMIDELL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043803.1\_4405 [locus\_tag=BN49\_RS23810] [protein=sodium:alanine symporter family protein] [protein\_id=WP\_046043803.1] [location=4610927..4612336] [gbkey=CDS]

MPDFLSFINEILWGSVMIYLLLGAGIWFSWQTRGIQFRYVRKFGRSLKKSLHPQPGGLTSFQALCTSLAA

RVGSGNLAGVTLAIAAGGPGAVFWMWVSALLGMASSFAECSLAQLYKERDSRGQFRGGPAWYMARGLGMR

WMGVLFSILLLLAYGFIFNTVQANSVAHALRYAFDLPAAVSGGVLAVVVLLAILRGLRGVARLMQWIVPF

MALLWIATSLLIGLWHITALPTIFATIFRCAFGWQEAAAGAVGYTISQALTSGFQRGMFSNEAGMGSSPN

AAAAAASWPPHPAAQGIVQMIGVFIDTIVICTASAIIVMLAPRPDNEYTLNGIQDLQHAMSVLVGGWGAG

FIALIVLLFAFSSIVANYVYAENNLVFLRLDKPRYIWGLRILTVLMVLLGTMVSLPVVWQSADIIMALMA

MTNLTAILLLSPTVRIIASDYLRQRRLGIQPTFDATRYPDIDQQLAPGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887869.1\_4406 [gene=yaaA] [locus\_tag=BN49\_RS23815] [protein=peroxide stress protein YaaA] [protein\_id=WP\_002887869.1] [location=4612435..4613208] [gbkey=CDS]

MLILISPAKTLDYQSPLATTRYTQPELLEYSQQLIGIARKLSAPQIGKLMSISDKLADLNATRFHDWHPD

FTPQNARQAILAFKGDVYTGLQAETLTEDDFDFAQQHLRMLSGLYGVLRPLDLMQPYRLEMGIRLENPRG

KDLYQFWGDTITEKLNQALRDQGDDIVINLASDEYFKSVKTPKLQGQLIKPVFLDEKNGKFKVISFYAKK

ARGLMSRYIIENRLTQPEQLKAFNSEGYFFDADASEKGELVFKRHEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002887866.1\_4407 [locus\_tag=BN49\_RS23820] [protein=hypothetical protein] [protein\_id=WP\_002887866.1] [location=complement(4613277..4613654)] [gbkey=CDS]

MRILSLFLVVFALTGCSGTTIGGNEDKLTPAYLKQHLIVGKTTKAEVRQYFGAPDSGHTTVTASGKESWY

YSVDKGINLVSLAGSMIPVTGASQAADAVDKSSQKDSNSLMIFFDEKGVVENWVR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529383.1\_4408 [gene=thrC] [locus\_tag=BN49\_RS23825] [protein=threonine synthase] [protein\_id=WP\_016529383.1] [location=complement(4613968..4615248)] [gbkey=CDS]

MKLYNLKDHNEQVSFAQAVTQGLGKHQGLFFPHDLPEFSLTEIDDMLAQDFVTRSAKILSAFIGDEIPQD

VLQQRVRSAFAFPAPVSKVQEDVGCLELFHGPTLAFKDFGGRFMAQMLTHIAGDKPVTILTATSGDTGAA

VAHAFYGLPNVKVVILYPRGKISPLQEKLFCTLGGNIETVAIDGDFDACQALVKQAFDDEELKATLGLNS

ANSINISRLLAQICYYFEAAAQLPQEARNQLVISVPSGNFGDLTAGLLAKSLGLPIKRFIAATNANDTVP

RYLQGGEWAPKATQATLSNAMDVSQPNNWPRVEELFRRKIWRLSELGYAAVDDETTKAAMRELKAIGYIS

EPHAAIAWRALRDQLQPGEYGLFLGTAHPAKFKESVEEILQETLPLPKELADRADLPLLSHNLPADFAAL

RKLMMG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887853.1\_4409 [gene=thrB] [locus\_tag=BN49\_RS23830] [protein=homoserine kinase] [protein\_id=WP\_002887853.1] [location=complement(4615252..4616181)] [gbkey=CDS]

MVKVYAPASSANMSVGFDVLGAAVTPVDGTLLGDNVTVEAAEQFSLQNLGRFASKLPTAPQENIVYQCWE

SFCREIGKTVPVAMTLEKNMPIGSGLGSSACSVVAALVAMNEFCGKPLNETRMLALMGEMEGRISGSIHY

DNVAPCYLGGMQLMIEENGIISQQVPGFDEWLWVLAYPGIKVSTAEARAILPAQYRRQDCIAHGRHLAGF

IHACYTRQPQLAAKLMKDVIAEPYRTKLLPGFSEARQAAMEMGAQACGISGSGPTLFALCDKPDTAQRVA

DWLGAHYLQNQEGFVHICRLDTAGARVVG

>lcl|NZ\_FO834906.1\_prot\_WP\_025861072.1\_4410 [gene=thrA] [locus\_tag=BN49\_RS23835] [protein=bifunctional aspartate kinase/homoserine dehydrogenase I] [protein\_id=WP\_025861072.1] [location=complement(4616183..4618645)] [gbkey=CDS]

MRVLKFGGTSVANAERFLRVADILESNARQGQVATVLSAPAKITNHLVAMIEKTIGGQDALPNIADAERI

FAELLQGLADAQPAFPLAQLKAFVEQEFAQIKHVLHGISLLGQCPDSVNAALICRGEKLSIAIMAGLLEA

RGHKVSVINPVEKLLAVGHYLESTVDIAESTRRIAASQIPADHMILMAGFTAGNEKGELVVLGRNGSDYS

AAVLAACLRADCCEIWTDVDGVYTCDPRQVPDARLLKSMSYQEAMELSYFGAKVLHPRTIAPIAQFQIPC

LIKNTGNPQAPGTLIGASRDEDDLPVKGISNLNNMAMFNVSGPGMKGMVGMAARVFATMSRAGISVVLIT

QSSSEYSISFCVPQSDCVRAKRAMEDEFYLELKEGLLEPLAIMERLAIISVVGDGMRTLRGISAKFFAAL

ARANINIVAIAQGSSERSISVVVSNDDATTGVRVTHQMLFNTDQVIEVFVIGVGGVGGALLEQIKRQQGW

LKNKHIDLRVCGVANSQALLTSVHGLNLENWSAELAEAKEPFNLGRLIRLVKEYHLLNPVIVDCTSSQAV

ADQYADFLREGFHVVTPNKKANTSSLDYYHQLRHAASSSRRKFLYDTNVGAGLPVIENLQNLLNAGDELR

HFSGILSGSLSFIFGKLDEGVSFSAATAMAREMGYTEPDPRDDLSGVDVARKLLILARETGRELELADII

VESALPPDFDASGDVETFMARLPSLDDGFASRVAKARDEGKVLRYVGNIEEDGTCRVKIAAVDGNDPLFK

VKNGENALAFYSHYYQPLPLVLRGYGAGNDVTAAGVFADLLRTLSWKLGV

>lcl|NZ\_FO834906.1\_prot\_WP\_004222578.1\_4411 [gene=thrL] [locus\_tag=BN49\_RS29525] [protein=thr operon leader peptide] [protein\_id=WP\_004222578.1] [location=complement(4618727..4618795)] [gbkey=CDS]

MNRIGMITTIITTTITTGNGAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887846.1\_4412 [locus\_tag=BN49\_RS23845] [protein=tRNA/rRNA methyltransferase] [protein\_id=WP\_002887846.1] [location=complement(4619007..4619693)] [gbkey=CDS]

MRLTIILVGPARAENVGAAARAMKTMGFRELRIVDSEAHLAPPARWVAHGSGDILDGITTYPTLAEALHD

VDFTVATTARSRARFHYYATPQQLLPLLEEKAQWMNHTALVFGREDAGLTNEELALADVLTGVPMAADYP

SLNLGQSVMVYCYQLASLMQQTAPAAAAADHHQLQALRTRTLALLSRLGVEDDAKLADWLSQRLGLLQQR

DTAMLHRLLHDIEKNLPE

>lcl|NZ\_FO834906.1\_prot\_WP\_004146984.1\_4413 [locus\_tag=BN49\_RS30625] [protein=hypothetical protein] [protein\_id=WP\_004146984.1] [location=complement(4620090..4620230)] [gbkey=CDS]

MTKVRNCVLDALSINVNNIISLVVGTFPLDPTVSKTADILTILTAT

>lcl|NZ\_FO834906.1\_prot\_WP\_002887843.1\_4414 [gene=arcA] [locus\_tag=BN49\_RS23850] [protein=two-component system response regulator ArcA] [protein\_id=WP\_002887843.1] [location=4620326..4621042] [gbkey=CDS]

MQTPHILIVEDELVTRNTLKSIFEAEGYDVFEATDGAEMHQILSENDINLVIMDINLPGKNGLLLARELR

EQADVALMFLTGRDNEVDKILGLEIGADDYITKPFNPRELTIRARNLLSRTMNLGTVSEERRSVESYKFN

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>lcl|NZ\_FO834906.1\_prot\_WP\_004182878.1\_4415 [gene=creD] [locus\_tag=BN49\_RS23855] [protein=cell envelope integrity protein CreD] [protein\_id=WP\_004182878.1] [location=complement(4621104..4622462)] [gbkey=CDS]

MLKSPLFWKITTLIGCIVLLSLPLMMVRELINERADYRSEVVDAIEQSTSGSQKLAGPLIAIPITETLTR

MENQKEVNYQRSWVYYWLPESLAVTGKQTVESRRVGIYSGQVWHNALQIKASFDPLRLAALRKTNIVLGQ

PRLVVSVGDARGIGAIHAPEVNGNVLSVEPGLGISGDGAGIHMPMPALAEDNKPLEIAFSLDLNGTGEFS

LVPLGRNSELQLTSNWPHPGFLGSFLPTQREVSAAGYRAHWQSSWFANDMGSYFKDDMEIPWSRLPAFSA

DVMSLADQYQLTDRATKYAILLIGLTFMAFFVFESLTRRPLHPMQYLLVGLSLVLFYLVLLALSEHIGFT

AAWLAASLSGAVMNGIYLQAVLRGWRNSLLFVAALLLLDGVMWFLLHSEDSALLLGTGVLALALSVLMFL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887823.1\_4416 [gene=creC] [locus\_tag=BN49\_RS23860] [protein=two-component system sensor histidine kinase CreC] [protein\_id=WP\_002887823.1] [location=complement(4622523..4623947)] [gbkey=CDS]

MRIGMRLLLGYFLIVAIAAWFVLSIFVQEVKPGVRRATEGTLNDTATLLAALAREDLLAANPQQGRLAQA

FHQLNQQPLNANIGGIKKVRNEYRVYLTDARGKVVFDSSGQATGQDYSRWNDVWLTLRGQYGARSTRSDP

HDEASSVMYIAAPVMDKGRIIGVLSVGKPNLAMTPVIKRSERRILWAGGALLGIALLIGGGVVWWINFSI

GKLVRYADSVTAERPLPLPEVGSSELRKLAQALESMRVKLEGKNAIENYVYDLTHELKSPLAAIRGAAEI

LREGPPPEVAARFTDNILAQNTRMQLLVERLLQQARLESRLEIKQHPVSIDALYQRLTEERNIALAAKAI

TLRWRESGMLVNGDGELLAQALGNLLDNAIDFTPQGGEIALAAEKRNEEVQLSVIDNGCGIPDYALERIF

ERFYSLPREDGHKSSGLGLAFVREVARLHHGDINLHNRPEGGVVATLRLHRPFT

>lcl|NZ\_FO834906.1\_prot\_WP\_004182877.1\_4417 [gene=creB] [locus\_tag=BN49\_RS23865] [protein=two-component system response regulator CreB] [protein\_id=WP\_004182877.1] [location=complement(4623947..4624636)] [gbkey=CDS]

MQQPRIWLVEDEQSIADTLVYMLQQEGFQVSVFGRGLPALEAAAHQAPDVAILDVGLPDISGFELCRRLL

TRYPALPVLFLTARSDEVDKLLGLEIGADDYIAKPFSPREVCARVRTVLRRLQKFAAPSPVVRVGEFVLD

EQAAAISWFGQPLNLTRYEFLLLKTLLHAPGRVFSRQQLMELVWSDAWESLDRTVDTHIKTLRAKLRAVN

PEKAPINTHRGMGYSLGRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887814.1\_4418 [gene=creA] [locus\_tag=BN49\_RS23870] [protein=protein CreA] [protein\_id=WP\_002887814.1] [location=complement(4624649..4625122)] [gbkey=CDS]

MKYKKFAMGLLLLAGSQLAQAEQIGSVDTVFKWLGPDHKIVVEAFDDPDVQNVTCYISRAKTGGIKGGLG

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GSPKNAISAVPIMPWNK

>lcl|NZ\_FO834906.1\_prot\_WP\_002887812.1\_4419 [gene=robA] [locus\_tag=BN49\_RS23875] [protein=MDR efflux pump AcrAB transcriptional activator RobA] [protein\_id=WP\_002887812.1] [location=4625331..4626200] [gbkey=CDS]

MDQAGIIRDLLSWLEGHLDQPLSLDNVAAKAGYSKWHLQRMFKDVTGHAIGAYIRARRLSKSAVALRLTA

RPILDIALQYRFDSQQTFTRAFKKQFSLTPALYRRSPDWSSFGMRPPLRLGEFTLPKHEFITLPPTQLLG

VTQSYTCKLEEISDFRNQMRVQFWRDFLGNSPSIPPVLYGLHEPRPSLEKDDEQEVFYTTALTPEMANGH

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CEYLIPIRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002887811.1\_4420 [gene=gpmB] [locus\_tag=BN49\_RS23880] [protein=2,3-diphosphoglycerate-dependent phosphoglycerate mutase GpmB] [protein\_id=WP\_002887811.1] [location=complement(4626197..4626844)] [gbkey=CDS]

MLQVYLVRHGETQWNAERRIQGQSDSPLTAHGERQAWQVGERARTLGITHIITSDLGRTRRTAEIIAEAC

GCSVIADARLRELDMGVLEKRHIDSLSEEEEGWRRQLVNGTPDGRIPQGESMQELSERMHAALASCLELP

AGSRPLLVSHGIALGCLVSTILGLPAYAERRLRLRNCSISRVDYQQSPWLASGWVVETAGDVSHLDAPAM

DELQR

>lcl|NZ\_FO834906.1\_prot\_WP\_004178555.1\_4421 [gene=yjjX] [locus\_tag=BN49\_RS23885] [protein=inosine/xanthosine triphosphatase] [protein\_id=WP\_004178555.1] [location=4626958..4627473] [gbkey=CDS]

MHHVVSATTNPAKIQAILQAFDEIFGEGSCHIESVAVESGVPEQPFGSEETRAGARNRVANARLARPNAD

FWVAIEAGIDDDSTFSWVVIESASQRGEARSATLPLPDVILEQVRAGEALGPVMSQYTGIDQIGRKEGAI

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887809.1\_4422 [gene=trpR] [locus\_tag=BN49\_RS23890] [protein=trp operon repressor] [protein\_id=WP\_002887809.1] [location=complement(4627460..4627789)] [gbkey=CDS]

MTQQSPYSAAVAEQRHQEWLRFVALLQQAYAEDLHLPLLQLMLTPDEREALGTRVRIIEELLRGEMSQRE

LKNELGAGIATITRGSNSLKSAPVELRQWLEQTLLASDK

>lcl|NZ\_FO834906.1\_prot\_WP\_002887806.1\_4423 [gene=sltY] [locus\_tag=BN49\_RS23895] [protein=murein transglycosylase] [protein\_id=WP\_002887806.1] [location=complement(4627878..4629815)] [gbkey=CDS]

MEKAKKMTWHLLAASVGLLTLSQLAHADSLDEQRSRYAQIKQAWDNRQMDVVDQLMPTLSTYPLYPYLQY

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SVGQSQEAWSGAKELWLTGKNQPGACEPLFSAWRDSGQQDPLAYLERIRLAMKAGNIGLVKSLAQQMPAN

YQSIASAVVALANDPNSVLTFARTTGATDFTRQMAAVAFASVARQDVENARLMIPSLVQAQQLNEDQTQE

LRDIVAWRLMGSDVTEEQAIWRDDAIMRSQSTPLVERRVRMALGTGDRHGLNTWLARLPMEAKEKDEWRY

WQADLLLERGRDEEAQAILRSLMQQRGFYPMVAAQRLGEEYTFRIDKASGTIDPALASGPEMARVRELMY

WNMDNTARTEWANLVTSRTKSQQAQLARYAFDQHWWDLSVQATIAGKLWDQLEERFPLAYNDLFARYVSG

KDIPQSYAMAIARQESAWNPKVRSPVGASGLMQIMPGTATHTVSMFSIPGYSGPSQLLDPETNINIGTSY

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887805.1\_4424 [gene=ettA] [locus\_tag=BN49\_RS23900] [protein=energy-dependent translational throttle protein EttA] [protein\_id=WP\_002887805.1] [location=4630044..4631711] [gbkey=CDS]

MAQFVYTMHRVGKVVPPKRHILKNISLSFFPGAKIGVLGLNGAGKSTLLRIMAGIDTEIEGEARPQPGIK

IGYLPQEPQLNPEHTVRESVEEAVAEVVNALKGLDEVYAKYAEPDADFDKLAAQQGKFEEIIQAHDGHNL

NVQLERAADALRLPDWDAKIANLSGGERRRVALCRLLLEKPDMLLLDEPTNHLDAESVAWLERFLHDFEG

TVVAITHDRYFLDNVAGWILELDRGEGIPWEGNYSSWLEQKDQRLAQEASQEAARRKSIEKELEWVRQGA

KGRQSKGKARLARFEELNNVEYQKRNETNELFIPPGPRLGDKVLEVSHLRKSYGDRVLIDDLSFSVPKGA

IVGIIGPNGAGKSTLFRMMSGQEQPDSGTITLGETVKLASVDQFRDAMDNSKTVWEEVSGGLDIMKIGNT

EMPSRAYVGRFNFKGVDQGKRVGELSGGERGRLHLAKLLQVGGNVLLLDEPTNDLDIETLRALENALLEF

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887802.1\_4425 [gene=nadR] [locus\_tag=BN49\_RS23905] [protein=multifunctional transcriptional regulator/nicotinamide-nucleotide adenylyltransferase/ribosylnicotinamide kinase NadR] [protein\_id=WP\_002887802.1] [location=complement(4631805..4633037)] [gbkey=CDS]

MSSFDYLKSAIKQKGCTLQQVAEASGMTKGYLSQLLNAKIKSPSAQKLEALHRFLGLEFPRRQKSVGVVF

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AFNEEGMEPYPHGWDVWSHGIRAFMSEKGIEPNRIYTSEEADAPQYLEHLGIETVLIDPKRTFMNISGGQ

IRENPFRYWEYIPTEVKPFFVRTVAILGGESSGKSTLVNKLANIFNTTSAWEYGRDYVFSHLGGDEMALQ

YSDYDKIALGHAQYIDFAVKYANKVAFIDTDFVSTQAFCLKYEGREHPFVQALIDEYRFDLVILLENNTP

WVADGLRSLGSSVDRKEFQSLLVSLLKENEIEFVHVKESDYDARFLRCVELVKQLMGEQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887800.1\_4426 [gene=radA] [locus\_tag=BN49\_RS23910] [protein=DNA repair protein RadA] [protein\_id=WP\_002887800.1] [location=complement(4633059..4634441)] [gbkey=CDS]

MAKAPKRAFVCNECGADYPRWQGQCSACHAWNTITEMRIAASPQVARNERLSGYAGNAGVSKVQKLSDIS

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AHRLGLPTANLNMLSETSIEQICQIADEEKPQLMVIDSIQVMHMADVQSSPGSVAQVRETAAYLTRFAKT

RGVAIVMVGHVTKDGSLAGPKVLEHCIDCSVLLDGDADSRFRTLRSHKNRFGAVNELGVFAMTEQGLREV

SNPSAIFLSRGDEITSGSSVMVVWEGTRPLLVEIQALVDHSMMSNPRRVAVGLEQNRLAILLAVLHRHGG

LQMADQDVFVNVVGGVKVTETSADLALLLAMVSSLRDRPLPQDLVVFGEVGLAGEIRPVPSGQERISEAA

KHGFRRAIVPAANVPKKVPEGMQIFGVKKLSDALSVFDDL

>lcl|NZ\_FO834906.1\_prot\_WP\_004177487.1\_4427 [gene=serB] [locus\_tag=BN49\_RS23915] [protein=phosphoserine phosphatase] [protein\_id=WP\_004177487.1] [location=complement(4634451..4635422)] [gbkey=CDS]

MPNSLTWCDLPEDVSLWPGLPLSLSGDEVMPLDYHAGRSGWLLYGRGLDKRRLTAWQRELGAALVIVASW

VVEDYQVIRLAGSLTPRATRLAHEAGLDVAPLGKIPHLRTPGLLVMDMDSTAIQIECIDEIAKLAGTGEL

VSEVTERAMRGELDFTASLRQRVATLKDADASILLQVRDALPLMPGLAQLVLKLETLGWKVAIASGGFTF

FAEYLRDKLHLDAVFANELEIRDGKLTGNVLGDIVDAKYKANTLRKLAEKYEIPTAQTVAIGDGANDLPM

IKAAGLGIAYHAKPKVNEQAEVTIRHADLMGVFCILSGSMNQK

>lcl|NZ\_FO834906.1\_prot\_WP\_002887794.1\_4428 [locus\_tag=BN49\_RS23920] [protein=YtjB family periplasmic protein] [protein\_id=WP\_002887794.1] [location=4635527..4636174] [gbkey=CDS]

MVRAKLKFRLHRAVIVLICLALLVALMQGASWFSQNSQKQRNPQLEELARTLAQQVVLNLAPLMRSETPD

EKRINQLLTQLTHNSRVLDAGVYDEQGDLVARSGESVEVRDRLALDGKKAGGYFNQQIVEPVPGKNGPLG

YLRLTLDTHTLATEAKQVDNTTNILRLMLLLSLAIGVVLTRTLLQGKRTRWQQSPFLLTANKPVEDEDDE

KKGNL

>lcl|NZ\_FO834906.1\_prot\_WP\_004146971.1\_4429 [gene=lplA] [locus\_tag=BN49\_RS23925] [protein=lipoate--protein ligase LplA] [protein\_id=WP\_004146971.1] [location=4636174..4637190] [gbkey=CDS]

MSTLRLLLSDSYDPWFNLAVEECIFRQMPATQRVLFLWRNADTVVIGRAQNPWKECNTRRMEEDHVRLAR

RSSGGGAVFHDLGNTCFTFMAGKPEYDKTVSTAIVLTALNSLGVTAEASGRNDLVVKTDSGDRKVSGSAY

RETMDRGFHHGTLLLNADLSRLANYLNPDQKKLQAKGITSVRGRVANLVELLPGITHQQVCEAIQEAFFS

HYGERVDAEVISPDNTPDLPNFAETFARQSSWEWNFGQAPAFSHLLDERFRWGGVELHFDVEKGHITRAQ

AFTDSLNPAPLEALAARLVGCQYRAEVLQQQCEALVGDFPEQEAELKELSAWIAGAVR

>lcl|NZ\_FO834906.1\_prot\_WP\_002887789.1\_4430 [gene=deoD] [locus\_tag=BN49\_RS23930] [protein=purine-nucleoside phosphorylase] [protein\_id=WP\_002887789.1] [location=complement(4637271..4637990)] [gbkey=CDS]

MATPHINAEMGDFADVVLMPGDPLRAKHIAETFLEDVREVNNVRGMLGFTGTYKGRKISVMGHGMGIPSC

SIYTKELITDFGVKKIIRVGSCGAVREDVKLRDVVIGMGACTDSKVNRLRFKDHDFAAIADFGMVRNAVD

AAKALGVDARVGNIFSADLFYTPDPSMFDVMEKYGILGVEMEAAGIYGVAAEFGAKALTICTVSDHIRTH

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151380.1\_4431 [gene=deoB] [locus\_tag=BN49\_RS23935] [protein=phosphopentomutase] [protein\_id=WP\_004151380.1] [location=complement(4638093..4639316)] [gbkey=CDS]

MKRAFIMVLDSFGIGATEDADRFGDVGADTLGHIAEACAKGEADHGRKGPLNLPNLTRLGLVKAHEGSTG

KIAAGMDGNAEVIGAYAWAHELSSGKDTPSGHWEIAGVPVLFDWGYFSDQENSFPQELLDKLVKRANLPG

YLGNCHSSGTVILDQLGEEHMKTGKPIFYTSADSVFQIACHEETFGLDKLYELCEIAREELTEGGYNIGR

VIARPFVGDKAGNFQRTGNRHDLAVEPPAPTVLQKLVDEKNGHVVSVGKIADIYANCGITKKVKATGLDA

LFDATIKEMKEAGDETIVFTNFVDFDSSWGHRRDVAGYAAGLELFDRRLPELMELVGEDDILILTADHGC

DPTWTGTDHTREHIPVLVYGPKVKPGSLGHRETFADIGQTIAKYFGTSDMEYGKAMF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530829.1\_4432 [gene=deoA] [locus\_tag=BN49\_RS23940] [protein=thymidine phosphorylase] [protein\_id=WP\_016530829.1] [location=complement(4639369..4640691)] [gbkey=CDS]

MFLAQEIIRKKRDGQALSDEEIRFFINGIRDNTISEGQIAALAMTIFFHDMSMPERVSLTMAMRDSGTVL

DWKSLNLNGPIVDKHSTGGVGDVTSLMLGPMVAACGGYVPMISGRGLGHTGGTLDKLEAIPGFDIFPDDN

RFREIIKDVGVAIIGQTSSLAPADKRFYATRDITATVDSIPLITASILAKKLAEGLDALVMDVKVGSGAF

MPTYELSEALAEAIVGVSNGAGVRTTALLTDMNQVLASSAGNAVEVREAVQFLTGEYRNPRLFDVTMALC

VEMLISGKLAADDAEAHAKLQAVLDNGKAAEVFGRMVAAQKGPSDFIENYANYLPTAMLSKAVYADTEGF

ISAMDTRALGMAVVSMGGGRRQASDTIDYSVGFTEMARLGDRVDGQRPLAVIHAKDENSWQEAAKAVKAA

IKLDDKAPEITPTVYRRITE

>lcl|NZ\_FO834906.1\_prot\_WP\_002887784.1\_4433 [gene=deoC] [locus\_tag=BN49\_RS23945] [protein=deoxyribose-phosphate aldolase] [protein\_id=WP\_002887784.1] [location=complement(4640805..4641584)] [gbkey=CDS]

MTDLKASSLRALKLMDLTTLNDDDTNEKVIALCHQAKTPVGNTAAVCIYPRFIPIARKTLNEQGTPDIRI

ATVTNFPHGNDDIDIALAETRAAIAYGADEVDVVFPYRALIAGNEQVGFELVKACKEACAAANVLLKVII

ETGELKEEALIRKASEISIKAGADFIKTSTGKVPVNATPESARIMMEVIRDMGVEKTVGFKPAGGVRSAE

DAQQFLAIADELFGADWADSRHYRFGASSLLASLLKALGHGDGKSASSY

>lcl|NZ\_FO834906.1\_prot\_WP\_004146034.1\_4434 [locus\_tag=BN49\_RS23950] [protein=NupC/NupG family nucleoside CNT transporter] [protein\_id=WP\_004146034.1] [location=complement(4642001..4643278)] [gbkey=CDS]

MQILMGLIGMVALLAIAVLLSNNRKAINLRTVLGAWIIQVGIGALILYVPAGRAALLAMSNGVASVIAYG

NEGISFIFGGLVSDKMFEVFGGGGFVFALRVLPVIVFFSSLIAVLYYLGIMQLVIRILGGALRAVLKTSR

TESLSATANIFVGQTEAPLVVRPYIATMTRSELFAVMCGGLASVAGSVLAGYAQMGVPLEYLIAASFMAA

PGGLLFAKIIVPETEKPDDNPAHDSQSADADKPANVLDAAASGAASGMQLALNVGAMLLAFIALIALLNG

ILSGVGGWFNHPELSLQMILGWIFSPLAWVIGVPWHEATVAGSFIGQKLIINEFVAYMNFGEYLKADAEV

AAAGLQVISDHTKAIISFALCGFANLSSIAILIGGLGGMAPNRRQDIAQLGLRAVAAGTLSNLMSATIAG

VFLAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004192101.1\_4435 [locus\_tag=BN49\_RS23955] [protein=metal-dependent hydrolase] [protein\_id=WP\_004192101.1] [location=complement(4643409..4644203)] [gbkey=CDS]

MTHRFIDTHCHFDFPPFAADEVASLARAAQAGVGRIIVPAISAERFSRVLALAAQHEALYAALGMHPIVI

EEHTDEGLAQLEALMAQRPPKLVAVGEIGLDLYRDDPQFDRQQALLEAQLRLAKRYDLPVILHSRRTHDK

LAMLLKKHALPRTGVIHGFAGSLQQAERFVQLGYKIGVGGTITYPRASKTREVMARLPLSALLLETDAPD

MPLNGFQGQPNRPEQAARVFEALCELRPESPAAIEEGIMHNTLALFSLPPVSVW

>lcl|NZ\_FO834906.1\_prot\_WP\_004146038.1\_4436 [locus\_tag=BN49\_RS23960] [protein=patatin family protein] [protein\_id=WP\_004146038.1] [location=complement(4644200..4645273)] [gbkey=CDS]

MGQRIPVTLGNIAPLAVKPFRPGKLALVCEGGGQRGIFTAGVLDEFMRAGFNPFDLMLGTSAGAQNLSAY

MCNQQGYARKVITRYTTSRQFFDPMRFVRGGNLIDLDWLVEATSQQMPLAMNYAEAQFALGKELWLCACR

GDDYSASYFSPTPQTWLDLIRASSAIPGFYRSGVLLDGVSYLDGGVSDAIPVQEAARRGAQTIVVIRTVP

SQMFYTPQWFKRMERWLGESSLQPLVNLVHHHETTYRAIQQFIEKPPGKLRIFEIYPQRPLRSMALGSRL

PALLEDYKTGRQCGRYFLATVGKLLADQPPLLRHAPRIARPAPVVVPPVPVANEAPQATIIPAPQANDPS

FDHEDLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887716.1\_4437 [locus\_tag=BN49\_RS23965] [protein=DUF1328 domain-containing protein] [protein\_id=WP\_002887716.1] [location=complement(4645427..4645588)] [gbkey=CDS]

MFRWGIIFLVIALIAAALGFGGLAGTAAGAAKIVFVVGIILFLVSLFTGRRRP

>lcl|NZ\_FO834906.1\_prot\_WP\_004146042.1\_4438 [gene=osmY] [locus\_tag=BN49\_RS23970] [protein=molecular chaperone OsmY] [protein\_id=WP\_004146042.1] [location=complement(4645718..4646338)] [gbkey=CDS]

MTRLKNANMLLALFLGLAALNASAETEKTTVDSAKSAASNAGEAVDNSINKVGDFMDDSTITARVKAALI

DHKDINSGDISVKTENKVVTLSGDVTSAEQKSQALSVAKEVKGVSHVNDKLTVHHKSSSETATLKGYAGD

TAITSEVKAKLLADDIVPSRNVKVETNAGAVHLTGTVASAAQAERAAEIAKAVSGVKSVRNDLSVK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043808.1\_4439 [gene=prfC] [locus\_tag=BN49\_RS23975] [protein=peptide chain release factor 3] [protein\_id=WP\_046043808.1] [location=complement(4646558..4648147)] [gbkey=CDS]

MTLSPYLQEVAKRRTFAIISHPDAGKTTITEKVLLFGQAIQTAGTVKGRGSSQHAKSDWMEMEKQRGISI

TTSVMQFPYHDCLVNLLDTPGHEDFSEDTYRTLTAVDCCLMVIDAAKGVEDRTRKLMEVTRLRDTPILTF

MNKLDRDIRDPMELLDEVENELKIGCAPITWPIGCGKLFKGVYHLYKDETYLYQTGKGHTIQEVRIVKGL

NNPDLDAAVGEDLAQQLRDELELVQGASNEFDKDLFLAGEITPVFFGTALGNFGVDHMLDGLVEWAPAPM

PRNTDTREVTATEEKFTGFVFKIQANMDPKHRDRVAFMRVVSGKYEKGMKLRQVRIGKDVVISDALTFMA

GDRSHVEEAYPGDIIGLHNHGTIQIGDTFTQGEMMKFTGIPNFAPELFRRIRLKDPLKQKQLLKGLVQLS

EEGAVQVFRPIANNDLIVGAVGVLQFDVVVARLKSEYNVEAIYESVNVATARWVESTDVKKLEEFKRKNE

VQLALDGGDNLTYIAPTMVNLNLTQERYPDVVFRKTREH

>lcl|NZ\_FO834906.1\_prot\_WP\_004146044.1\_4440 [gene=yjjG] [locus\_tag=BN49\_RS23980] [protein=pyrimidine 5'-nucleotidase] [protein\_id=WP\_004146044.1] [location=complement(4648238..4648915)] [gbkey=CDS]

MKWDWIFFDADETLFTFDSFSGLQRMFLDYSVTFTAEDFQDYQAVNKPLWVDYQNGAITSLQLQHQRFDS

WAERLNVPPGELNDAFMNAMAEICAPLPGAVSLLNALQGKVRMGIITNGFTSLQQTRLERTGLRDHFDLL

IISEQVGVAKPDARIFDYALAQAGNPPRSRVLMVGDTAESDIRGGVNAGLATCWLNAHQRELPADLEPDW

TVTSLSELEQLLCKH

>lcl|NZ\_FO834906.1\_prot\_WP\_002887706.1\_4441 [gene=rimI] [locus\_tag=BN49\_RS23985] [protein=ribosomal protein S18-alanine N-acetyltransferase] [protein\_id=WP\_002887706.1] [location=complement(4648930..4649376)] [gbkey=CDS]

MNTISTLSTADLTKAWHIEKRAHAFPWSEQTLASNQGERYRNYQLSVDGEMAAFAITQVVLDEATLFNIA

VDPAYQRRGLGRALLEHVIDEVEKLGVVTLWLEVRASNVAAIALYESVGFNEATIRRNYYPTADGREDAI

IMALPISM

>lcl|NZ\_FO834906.1\_prot\_WP\_004146046.1\_4442 [locus\_tag=BN49\_RS23990] [protein=DNA polymerase III subunit psi] [protein\_id=WP\_004146046.1] [location=complement(4649345..4649758)] [gbkey=CDS]

MTSRRDWQLQQLGITQWSLRRPGALQGEIAISLPEHIRLVMVAETPPSLTEPLIGDILRALAVTPDQVLQ

LTPERVAMLPQDSRCNSWRLGTEASLPLAGAQVSTPAFDELQTSAPARRALWQQICAHEHDFYPQHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177499.1\_4443 [gene=rsmC] [locus\_tag=BN49\_RS23995] [protein=16S rRNA (guanine(1207)-N(2))-methyltransferase RsmC] [protein\_id=WP\_004177499.1] [location=4649861..4650889] [gbkey=CDS]

MSAFTPASEVLLRHSDDFESARVLFAGDLQDDLPARLDTAASRAHTQQFHHWQVLNRQMGDTVRFSLVAE

AADVAECDTLIYYWPKNKPEAQFQLMNLLSLLPVGSDIFVVGENRSGVRSAEQMLAEYAPLNKVDSARRC

GLYHGRLEKQPTFDADAFWGEYTLDNLTIKTLPGVFSRDGLDVGSQLLLSTLEPHTKGKVLDVGCGAGVL

AAALASHSPKVRLTLCDVSAPAVEASRATLAANGLAGDVFASNVFSEVNGRFDMIISNPPFHDGLQTSLE

AAQALIRGAVRHLNSGGELRIVANAFLPYPQVLDETFGFHEVIAQTGRFKVYRTIMTRQAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002887654.1\_4444 [locus\_tag=BN49\_RS24015] [protein=DUF1435 domain-containing protein] [protein\_id=WP\_002887654.1] [location=complement(4651403..4651642)] [gbkey=CDS]

MLQRALGSGWGVMIPGALIVALGYAGVSADVWRVLVAVGMLMSAAMIWHRQLRHFILLPSCVALIGGIML

MIVDIKLRG

>lcl|NZ\_FO834906.1\_prot\_WP\_004221147.1\_4445 [locus\_tag=BN49\_RS31210] [protein=hypothetical protein] [protein\_id=WP\_004221147.1] [location=4651713..4651883] [gbkey=CDS]

MLCPFFFTFAVMTYIHEGDKLSGLSIYIKYFAYFANNLFLHIVIRLFIFGFHHFEI

>lcl|NZ\_FO834906.1\_prot\_WP\_046043811.1\_4446 [locus\_tag=BN49\_RS24025] [protein=sensor domain-containing diguanylate cyclase] [protein\_id=WP\_046043811.1] [location=4651907..4652953] [gbkey=CDS]

MTAQTWRAHYAQKYQYSLQLFLLLNFISSSLSLVTPLFTVVRFTLPCALIVVCSALLLLWHWKWPQSKIN

IPTISLLFGMLWAWHVVTKAMLLTPPHFNYLVIALLSILFIGTIAFSNNITAFTLHSLPTFLACLIMAEG

EQWLRMTYCFMLPIAGITLQNIIQKRSDAFTQGLMDKLMHERNTLNDLSMLAPLTGLYNRRGLQNRLDTL

LALDGDNHYVLLLDIDHFKAYNDHYGHMMGDQALIRVSTAIRNAVRSRDIVARFGGEEFMVLLTNSSEET

AWKTAERIRQRVYDLKIPHMFNESVATNVTISIGLTPLINDNIEQALARADGALYEAKNKGRNIILAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002887652.1\_4447 [gene=fhuF] [locus\_tag=BN49\_RS24030] [protein=siderophore-iron reductase FhuF] [protein\_id=WP\_002887652.1] [location=4653060..4653848] [gbkey=CDS]

MAWRSLPLSDELIWRAPLPTAEHALAESIREKIATLRPHLLDFLRLDEPAPRHALTLAEWSQPIALRSLL

ATWSDHIYRHQPTLPREQKPLLSLWAQWYIGLLVPPLMLALLNEPQGLSLAPEHFHVEFHESGRAACFWI

DVHSDADIERLSPQARMDALVTRTLQPVVEALAATGEINSKLIWSNTGYLINWYLGEMRALLGDERLAAL

RQHCFFEKQLADGQDNPLWRTVMLREGQLVRRTCCQRYRLPDVQQCGDCTLK

>lcl|NZ\_FO834906.1\_prot\_WP\_004146052.1\_4448 [locus\_tag=BN49\_RS24035] [protein=PTS cellobiose transporter subunit IIC] [protein\_id=WP\_004146052.1] [location=complement(4653898..4655241)] [gbkey=CDS]

MSANHAAFNLIFRFVENYISPIAGRISSQRHVMAIRDGFISAMPFMIVGSFLLVFAYPPFSPDTTWGFAR

AWLDLAKEFEGRILTPFDMTMGIMSIYICAAISYNLGKHYEKSNQLDPFMCAMLSIMAFLLIAAPKTNGT

LPVDSLGGTGIFTAILVAIYCVEMMRFLKAHNIGIRLPDQVPPMIKNSFDLLIPVLVVVLTLYPLSLFIQ

HHFDMLIPQAIMAIFKPLVSAADSLPAILLAVLIGHLLWFAGIHGAAIVSGMLQMFWLTNLGMNQQALAQ

GAPLPHIFMEAFWTFFIVVGGSGATMGLVFCYLRSRSAHLRSIGRLSVVPSLFNINEPVIFGTPIVMNPV

FFIPFLLAPMVNAVLAWAAMKLDLIGRVISVVPWTAPAPIGGAWALGWDFRAAILVIVLACVSAIIYFPF

FKVYEKQLLAQEAEEAERAEHESQQTA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151383.1\_4449 [locus\_tag=BN49\_RS24040] [protein=YbaK/EbsC family protein] [protein\_id=WP\_004151383.1] [location=4655580..4656038] [gbkey=CDS]

MSLQSVRQFFAEHAPDIEIIELNQSTATVALAAAAHNVEPGQIAKTLSLKIKDKIVLIVARGDARLDNKK

LKETFGAKARMLSSDEVVTWTGHPVGGVCPFGLENPLAVYCDVSLRHYQEVLPAAGAIHSAVRIEPERMA

QLTDATWVDVCL

>lcl|NZ\_FO834906.1\_prot\_WP\_002887647.1\_4450 [gene=bglJ] [locus\_tag=BN49\_RS24045] [protein=DNA-binding transcriptional activator BglJ] [protein\_id=WP\_002887647.1] [location=complement(4656044..4656718)] [gbkey=CDS]

MEKNSTTRHVAIVEKCVMTEMAWRYIFSREDNRRYHIHLFKNVSMLRAAEIPFPWSTIIFSLSGSRSSRA

ESLLFVHEMARCRPEVQTIILANNESEMHLIGHLMPACLHGILNKSAPRRGLQERLLQLLDNHHLSGSEQ

FCDREACNDPLSPTEHAILRYMSWGYSLSDIAIQLNRNIKTIRAHKFNAMTKLGVRSDIGLLNAADILLH

LPLNSTTSAVKQVA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887645.1\_4451 [locus\_tag=BN49\_RS24050] [protein=LuxR C-terminal-related transcriptional regulator] [protein\_id=WP\_002887645.1] [location=complement(4656679..4657401)] [gbkey=CDS]

MLPGQGKFGVVISKIPVMQSGLKVIFNENLPDYELSFCRSHDELTLLQLRRAVLVVADISGEIAHPRAVC

ERYYSLMTQYRDIHWVFMVSDSLYPLAVELLIRPESSLISESEPVNRLIEVICAGSRAAEQISRTLFAGD

EDSDFASYHSAAMLTLSERKVLRLLAKGWGINQIAALLKKSNKTISAQKNSAMRRLSLRSNAEMYAWINS

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>lcl|NZ\_FO834906.1\_prot\_WP\_009485342.1\_4452 [locus\_tag=BN49\_RS24055] [protein=helix-turn-helix domain-containing protein] [protein\_id=WP\_009485342.1] [location=complement(4657667..4658548)] [gbkey=CDS]

MPFVQTVPVFKLYGEECGWPTPDLLHCESILQRSSLYQWHIRVHQHAEMVQLLYLHQGRAEIEIEGATEV

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LREEYCEEHDAREMMLYSLLGTLLVWLNRQCHPASPAEDKAERKRSMMRHFARLIESHYRQHLPLAEYAK

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PKAFRETIKDNAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004146953.1\_4453 [gene=pobA] [locus\_tag=BN49\_RS24060] [protein=4-hydroxybenzoate 3-monooxygenase] [protein\_id=WP\_004146953.1] [location=complement(4658565..4659749)] [gbkey=CDS]

MKTQVAIIGAGPSGLLLGQLLHNAGIHTVILERQTPQYVLGRIRAGILESGTVDLLREAGVAQRMDAEGL

VHHGVEFLFDGQRVPVALSELTDGKSVMVYGQTEVTRDLMAARAASGAPIVYGVSEVAIHDAKSDRPTIT

YLSEGETCRLECDFIAGCDGFHGVSRQSIPAGILQTYESVWPFGWLGLLADTPPVNPELIYAHHQRGFVL

CSQRSLTRSRYYLQVPLSDKVEAWSDERFWQELKSRLPEELASRLVTGHSLEKSIAPLRSFVVEPMQYGR

LFLVGDAAHIVPPTGAKGLNLAASDVNYLWRILREYYHRGRSDLLAAYSQLALDRVWKGERFSWFMTRLL

HDFPDQNAFDAKMQAADRRYYLGSRAGLTTIAENYVGLPMERVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004146059.1\_4454 [locus\_tag=BN49\_RS24070] [protein=threonine/serine exporter ThrE family protein] [protein\_id=WP\_004146059.1] [location=4660029..4660805] [gbkey=CDS]

MQVDRTQQRAITRLCIQCGLFLLQHGAESALVEELSTRLGLALGMDSVESAISSNAIVLTTIKNGECLTS

TRKNVDRGINMHVVTEVQHIVILAEHKLLDYRDVEKRFAQIVPLRYPRWLLVLMVGLSCACFCKLNNGGW

DGALVSFCASTVAMYIRQVLTHRSMHPQINFCITAFVATTISGLLLRLPAFASTPTIAMAASVLLLVPGF

PLINAVADMFKGHINTGLARWAIASLLTLATCIGVVMAMTVWGLRGWA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887631.1\_4455 [locus\_tag=BN49\_RS24075] [protein=threonine/serine exporter] [protein\_id=WP\_002887631.1] [location=4660796..4661269] [gbkey=CDS]

MGIISFIFALAEDMLLAAIPAVGFAMVFNVPQRALRWCALLGAIGHGSRMIMMSAGFNIEWATFLAALLV

GSIGIQWSRWYLAHPKIFTVAAVIPMFPGISAYTAMISAVKISHFGYSEEMMILLLSNFLKASSIVGALS

IGLSIPGLWLYRKRPRV

>lcl|NZ\_FO834906.1\_prot\_WP\_002887624.1\_4456 [gene=dnaT] [locus\_tag=BN49\_RS24080] [protein=primosomal protein DnaT] [protein\_id=WP\_002887624.1] [location=4661372..4661911] [gbkey=CDS]

MSSRILTSHFSGLEEFLQQHAALLAKSTDGTVAVFANNAPAFYALTPARLAQLLELEARLARPGSDIALD

PQFFEEPAAAPVAVPMGKFAMYAGWQPDADFQRLAALWGIALSQPVTPEELAAFVAYWQAEGKVFHHVQW

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887623.1\_4457 [gene=dnaC] [locus\_tag=BN49\_RS24085] [protein=DNA replication protein DnaC] [protein\_id=WP\_002887623.1] [location=4661914..4662651] [gbkey=CDS]

MKNVGDLMKRLQKMMPAHIEPAFKTGEELLAWQKEQGRLRSEALERENRAMKMQRTFNRSGIRPLHQNCS

FDNYRVECEGQMNALARARQYVEEFDGNIASFIFSGKPGTGKNHLAAAICNELLLRGKSVLIITVADIMS

AMKDTFGNRETSEEQLLNDLSMVDLLVIDEIGMQTESRYEKVIINQIVDRRSSSKRPTGMLTNSNMEEMN

KLLGERVMDRMRLGNSLWVIFNWESYRHRVTGKEY

>lcl|NZ\_FO834906.1\_prot\_WP\_004177504.1\_4458 [locus\_tag=BN49\_RS24090] [protein=DUF2501 domain-containing protein] [protein\_id=WP\_004177504.1] [location=4662717..4663208] [gbkey=CDS]

MKSFKNSVVAALAVSAFTLSGAHAASWQDSLNSAASQLSGSNAQASGGMSVSSLTSLLNGSSQSLTASSM

NNAAGILSYCAKQKLASVTSADNVKNQVLDKLGLSTPEKQKQDTSYLDGLQGLLNSKNGQQLDLNTLGNS

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529368.1\_4459 [gene=opgB] [locus\_tag=BN49\_RS24095] [protein=phosphatidylglycerol--membrane-oligosaccharide glycerophosphotransferase] [protein\_id=WP\_016529368.1] [location=4663466..4665757] [gbkey=CDS]

MSELLSIALFLASVVLYAWKAGRNTWWFAATLTVLGLFVVLNITLYASDYFTGDGINDAVLYTLTNSLTG

AGIGKYILPGVGVAVALVAVFGALGWVLRRRRHHPHHVGYSLAALLLALASVDASPAFHQISELVKSQSR

EGDPDFAAYYKEPSKQIDNPQLNLVYIYGESLERTYFDNDAFPNLTPELGRIKDEAIDFSNTMQLPGTDY

TIAGMVASQCGIPLFAPFEGNASASVSSFFPQNICLGDILKNSGYENYFVQGANLRFAGKDVFLKSHGFD

HLYGAEELKTTVADPTYRNDWGFYDDTVLDETWKKFEELSQSGKRFSLFALTVDTHHPDGFISRTCERKR

YDVDGKKNLSFSAVSCSQEHIAALIEKIKASPYFKNTVIVVSSDHLAMKNSAWDYLNKHDRSNLFFVLRG

DKPQQETLAVKRNTMDNGATVLDILGGDNYIGLGRSSLSGQSLSGIFMNMKEKVLAWKPDVIRLWNFPKE

MKNFTIDSQKNMIAFSGSHFRLPLLLRVSDQRVEPLPESEYSAPLRFQLADFAPRDNFVWVDRCYKMGQL

WSPELALSTDWCVSQGQLGGEQKVQHVDKPQWHGKTAFRDTLIDMERYKGNVDTLKIVDNDIRYKADSFV

FNIAGAPEEVKQFSGISRPESWGRWSNAQLGSDVKIEYKEPLPEKFDLVITAKAYGPNANKPIPVRVGES

KQVLTLDNDVTTTTLHFDNPTRSNTLIITPPDPQTTNEGNILGHSPRQLGIGMVEIKVVKSEG

>lcl|NZ\_FO834906.1\_prot\_WP\_016831532.1\_4460 [locus\_tag=BN49\_RS24100] [protein=Rpn family recombination-promoting nuclease/putative transposase] [protein\_id=WP\_016831532.1] [location=complement(4665812..4666756)] [gbkey=CDS]

MAMKKRMTSTPHDAVFKRFLRHPETATDFLTLYLPEAIRQRCDFSTLRLQSASFIDEDLRAWYSDVLWSV

QTTCGTGYVYVVIEHQSSPDSHMAFRLMRYAIAAMQRHLDAGHKTLPLVVPMLFYHGATSPYPFSLNWLD

EFADPQLAKTLYGCPFPLIDVTVMPDDDIVQHRRVALLELMQKHIRQRDLSGITESLAAVVMLGYTNRRQ

LRMLFHYMLQYGNTAEPGVFLRRLARRLPQYEETLMSIAQKLKQEGRQQGRLEGREEGHLEGLQEGSRRE

ALRIAGSMLQNGLDKEMVQKITGLSADELQPLCG

>lcl|NZ\_FO834906.1\_prot\_4461 [locus\_tag=BN49\_RS24105] [protein=SIS domain-containing protein] [pseudo=true] [partial=3'] [location=complement(<4666858..4667721)] [gbkey=CDS]

MLGFNQDEYLTSAREIIAARKQAETVADDIYDSGCSALFFASVGGSLAPMMAINEFAKELTSVPVYLEQA

AELIHRGHKKLNKDAVVVTLSKSGDTKESVAIAEWCKAQGIRVVAITRHADSPLAAAASWHIPMCHKNGV

EYEYMLLYWLFFRVIFRHGEFADYARFASQLELLPENLLQAKRQFDPRADSIAAQYHDCDYMMWIGGAEM

WGEVYLFSMCILEEMQWKRTKSVSSAEFFHGTLELLEKEVPLFLVKGEGRCRALDERVERFAEKITDHLV

VIDPRDYP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529370.1\_4462 [locus\_tag=BN49\_RS24110] [protein=SIS domain-containing protein] [protein\_id=WP\_016529370.1] [location=complement(4667739..4668800)] [gbkey=CDS]

MRPTMMTYISEEPACLAQILRDYRQKLAPIETFVRQHPVRRILLLATGSSLNAALCARYFFEQRFGVLLD

IKEPYNFTHYDAIDPHADLVVAISQSGKSASTLEAMRKVQASGKSVFALTSDPQSPIGCASDGVLDINTG

IESVGFVTRGFSATVLNLLLIALIIARKQEKASEVEEQHYLAELQRLLAAIPEVIVRTSRFIDRHSETLR

SGERFVATGYGALVGVAKEFETKFTETVRVPSSGFELEAYMHGPYLEANARHVMLFIEDTPDARTRALRD

YLAPSIGRAFTLTLGDEEDAQTLALNCPCEHHLAPLLLIVPVQMLAWHTAGLKGIDLAKRIFDDFDRVLK

SKI

>lcl|NZ\_FO834906.1\_prot\_4463 [locus\_tag=BN49\_RS24115] [protein=PTS system mannose/fructose/sorbose family transporter subunit IID] [pseudo=true] [location=complement(4668813..4669665)] [gbkey=CDS]

MTTKMISEETLQPQAQEETRITPRDLRRVFWRSFQMEFSWNYERQMNLAFVYALIPVLKKLYPRREELAA

ALKRHLVFFNTTPHIVTLLLGITTAMEEKNSQQKNMDATAIDNVKAITDGTVSRAG\*LFLLGDAAPHRHR

DRHQPGAEGQHPRADPVSAGV\*RAAHSGALVFYPLGLRTGHRGPAADPEERNDGEPDLRGVDYRSDGSRG

DDRFNDRYHHSSLLRRRGGQNPGTGHYQRHSALHAAVGEFWHRLLATGTES\*TALNYWRHGAGGHSGFVD

RIVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002887608.1\_4464 [locus\_tag=BN49\_RS24120] [protein=PTS sugar transporter subunit IIC] [protein\_id=WP\_002887608.1] [location=complement(4669643..4670422)] [gbkey=CDS]

MVEALLLGLVAFIAQSEYALGTSLISRPIVTGLLTGLVLGDVQTGVIMGATLELAFIGSFSVGASIPPDV

VTGGILGVAFAITSGAGTETALLLGLPIATLTLILKNIYLGMFIPMLSQKADGYAERADLRGIERMHLIA

GFGLSLMLAAVVTVSFLVGSNAVKSLLDTIPEFIKHGLSVATGIIPALGFAMLARLLINKKVAPYFFLGF

VLMAYLKIPVTGIAILGAIVAVVMVNVTALNSPRITTEQGVSDDDEDDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004177515.1\_4465 [locus\_tag=BN49\_RS24125] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_004177515.1] [location=complement(4670439..4670909)] [gbkey=CDS]

MITLLRVDHRLLHGQVAFSWTQYVGADCILIANDSVPGDELRKTTIKLAKPPSVKLVIKNVNDSIEAIKS

GVTDKYNLFIVVESVNDAWRIASAIDEIKSINLGGIKAKEGSKNISKAINLLPTEIEQLQQLVGKGVEVE

IRQVPNDRKQLFAECV

>lcl|NZ\_FO834906.1\_prot\_WP\_004177518.1\_4466 [locus\_tag=BN49\_RS24130] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_004177518.1] [location=complement(4670924..4671346)] [gbkey=CDS]

MKRHYIFASHGSFANGLLNSVELILGKQPDIHTLCAYVEEEVDLTQQVEALVARFPAQDELIVITDIFAG

SVNNEFVRFLSRPHFHLLSGLNLPLIIDLLISAAEDDTEKLITEALTNAKESIQYCNQTIASAMTMDKDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004177521.1\_4467 [locus\_tag=BN49\_RS24135] [protein=sigma-54-dependent transcriptional regulator] [protein\_id=WP\_004177521.1] [location=complement(4671446..4674211)] [gbkey=CDS]

MRKTELLAFLQNQTDFFDPDNLSEVFTASWLARRFAMQRNTASHYLNQLVAQDVLVKINTRPVYFLHKKA

FCQQFYPLSRSEYASMAELLAESDRQPEQADHFSLLTGHDGSLRKPIEQMKTALFYPNGGLPLLITGDSG

TGKSYMAELMHEFAIAQGLLAPDAPFVSFNCAQYASNPELLAANLFGYVKGAFTGAQSDKAGAFEAANGG

MLFLDEVHRLDAQGQEKLFTWLDRKEIYRVGETAQGLPISLRLVFATTEDIHSTFLTTFLRRIPILVSLP

DLQHRSREEKEALTLQFFWQEARTLAARLQLTPRLLQVLTQYVYRGNVGELKNVVKYAVASAWARSPGRE

MLTVTLHDLPENVMAATPALSEAMGQQEPLLIEPQTSLVWLLRARDPVQGLIYDVQCRVLAQYEAVLNKK

TVWEEAQRSMGEEIETLFDRLIFDNHDSSSSQMLLLIAHQVREEYYRLEKRFNIQFNGNCLYALSHYLIH

RSRQPQSTINNEKARQLEDFLVQKFPLLYRFCEAILGALTLKLDIEPQRIDLLLLVLWFHKNGAISQQQV

TRAIILAHGYATASSIANVANRLLKSQLFESFDMPLDVTPEAIANQVMAYIESHALASGLIILVDMGSLN

AIHRHFNRRLSTPMAIINNVSTGMAMYVGERILQGVMLEDIVREIGDDLAVEHQLYYPQTDKPRAILTTC

ATGLGAAANLSALLKASIPEALGIDIVACDVETLADPARREPMLSRYEVLAIVGTLDPHLADLPWISLDS

LISGEGSRPLMRIFGELATAEQVSEINNLILKNFSLRRVIESVTILDTAKVINQVEQFLLRYEHLAGRDV

PNDRKVALYVHISCLIERLIRHASPAQYTGGQCPDRELATLREAFSVIESGYSVKIPVVELCYIHDILTR

ETEFIQEDQDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004214407.1\_4468 [locus\_tag=BN49\_RS24140] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_004214407.1] [location=complement(4674312..4675142)] [gbkey=CDS]

MELTAVPATQFSSVQLTDILNACFEAYLVPVTQSVEGFVQRFSAEGMSLVDSRVWLAGDEPAAIAIVARR

GSAARLAAFALRPAWRGKGLGRKLMQELLMLLQQQGIETVFLEVIRDNHAAVALYQSLGFTRRYGLCGYL

STELLPPVPGVLQLYPTLSLLRRAIEESNSQLPWLLDPLTFATLPCQVVTLEHRAFAVLTTAGSRPVLSF

LWVEPAARRQGLARELLMALAQQFPGIGTSVTVPETFTPLFAAAGYTPLSLQQYEMTMDLADAKSA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887560.1\_4469 [locus\_tag=BN49\_RS24145] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_002887560.1] [location=4675175..4675708] [gbkey=CDS]

MKTNTITAGAVLRLTQESDIALLPAIERSAAQAFRQIPSLAWLADSEVISVARHHDYLETEHSLLAVAAG

QPVGFILTEPLDDALFIVEVAVHQAWQQQGIGRMLLERVIESARQMGYPAVTLTTFREVPWNAPFYTRLG

FAMLDELTLPAGLAAKREQETRHGLPPESRCAMRLAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529366.1\_4470 [locus\_tag=BN49\_RS24150] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_016529366.1] [location=4675778..4676641] [gbkey=CDS]

MSWSIDIISCITDRFVELTATEKRIAQFILDDVAAAAELPIAEIARLTQTSQASVTRFARALGCKDVREL

KMKLAQSLAVGQRFILDVPDLEGVQGIYESIISVLETNRRALDIEALKRAVSWLSDARQILALGMGGGST

ICAQEIQYRLFRLGLPVVSQSDGLLVRMMSSAVTPQDVLIVLSLGGYTREIIESAAIASQYGAKVIAITP

AGTPLAEQADLVLPLLVRENDYIFKPSTSRYAMLAMVDVLATELAMANKTQAKGKLRRIKLALDSHRGGV

DRQPLGD

>lcl|NZ\_FO834906.1\_prot\_WP\_004146077.1\_4471 [locus\_tag=BN49\_RS24155] [protein=2-dehydro-3-deoxy-6-phosphogalactonate aldolase] [protein\_id=WP\_004146077.1] [location=complement(4676638..4677237)] [gbkey=CDS]

MDKIKLVAILRGIQPAEAADHIETLINAGFRYIEIPLNSPDWQQSIPAMVRQFGERAMIGAGTVLKVEQV

DFLAEAGAKLIVTPNTAPAVIRRAVDKGMLVCAGCATASEAFSALDAGAQWLKIFPSSAFGADYIRALKA

VLPPEVPVLAVGGVTPENLATWIQAGCAGAGLGSDLYRAGQAVERTREQAERFISASKS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043818.1\_4472 [locus\_tag=BN49\_RS24160] [protein=2-dehydro-3-deoxygalactonokinase] [protein\_id=WP\_046043818.1] [location=complement(4677224..4678096)] [gbkey=CDS]

MNEYIAVDWGSTQLRAWRMRDGECIDKLKLPCGVTRLNGQRAEAVFQQQLAPWRGDPALPVVMAGMIGSD

AGWQPVPYLACPLALEALNGQLYEVAEKVWIVPGLKVAQAADYDVMRGEETQLLGAWQLMPAECYVMPGT

HCKWVQVQNGVVRQFATAMTGELHHLLLNHSLLGQQLPAQLPDEAAFALGMEKGLNQPALLSGLFSARAA

RVLGALAATSVSDYLSGLLIGAEVATFSERYRARRVVLVGEHSLSALYQQAMAARGLAVSRCSGEAAFLS

GIARMIDGQD

>lcl|NZ\_FO834906.1\_prot\_WP\_004222484.1\_4473 [locus\_tag=BN49\_RS24165] [protein=sodium:solute symporter family protein] [protein\_id=WP\_004222484.1] [location=complement(4678106..4679593)] [gbkey=CDS]

MNNMSFMIWFSVYACAMITLGWYVSRKQKTGEDFLLGGRSLPMILTLGSTVGTMVGTGSSVGAVGFGYSN

GWAGMLYGLGGAVGILLVAWLFAPVRKLRFMTMSEEMSYYTGGSKIIKNLVAILIFIASIGWLGAHILGG

GLYLAWASGIDINVAKIIIALAFVVYVGIGGYSAVVWIDTIQSIVLFVGFILMAILAVHHVGGWSHIQQA

VDPAAQSLFAVDKLGVLPALSLAMVIGVGVLATPSYRQRIYSAKTVSSVRQSFTITGLLYLGFSFLPAII

GMAVWTMNPQLENSGFAFLFATQVLPPVLAMAILIAGMSANMSSGSSDAIAAVSIMLRDLYTLVTGHMPA

PEKAIRLSRIFLVLVIALALLFALTSNDIISYITKMISMIMSGMFICTMLGRFWTRFNWQGAVAALAGGA

GASVAVLVDSDWLAFWGNPCIPAVLTSLVASVVVTLLTPASSMSREQALEMITRERESRPTPPPLPIGKR

HTSRG

>lcl|NZ\_FO834906.1\_prot\_WP\_046043820.1\_4474 [locus\_tag=BN49\_RS24170] [protein=RidA family protein] [protein\_id=WP\_046043820.1] [location=complement(4679779..4680171)] [gbkey=CDS]

MSIKRYGVEGGTGTGGQHLPFARAVEAGGWLYVSGQTPMKNGEVVEGGIVDQSRLAIQNCVDIMTEACYT

LADVVHVKVILTDARYFQSFNKVFREFFGDNPPARICCVADLVVDCKVEVDVTCFNAARQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002887553.1\_4475 [locus\_tag=BN49\_RS24175] [protein=D-aminoacylase] [protein\_id=WP\_002887553.1] [location=complement(4680182..4681621)] [gbkey=CDS]

MKVDWLFKNVTVIDGSGGPQYRADVAVKGDRIMAIAPALDVAAEQVIDGQGRVLAPGFIDVHTHDDINVI

RMPEYLPKLSQGVTTVIVGNCGISAATATMRGEVPDPMNLLGEQQHFIYPTVEAYAHAVEAARPSLNVGT

LIGHTALRNNHMDDLFRPANETEIAGMRVQLRDALRQGALGLSTGLAYASAFQSTTEEVMALAEELAAGK

GVYTTHLRSEFEPILEALDEAFRIGRHGNVPVVVSHHKCAGAKNWGRTKETLAFFDEMRQQQDIACDCYP

YSASSSTLDMKQVTDEFDIVITWSEAQPEQAGKTLQQIADEWQVSLHDAAARLMPAGAIYHNMDEQDVRR

VMRYPVTMIGSDGLPNDPMPHPRLWGAFPRVLGHYSRDEQLFPLTTAVHKMTGLSAARFQLADRGLVKIG

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043822.1\_4476 [locus\_tag=BN49\_RS24180] [protein=hypothetical protein] [protein\_id=WP\_046043822.1] [location=4681599..4681778] [gbkey=CDS]

MKSQSTFIAITPFRHADKLTIYKRKKQWKTTQNSDQFAILLFKKNNIFILKIYLSNSYK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043823.1\_4477 [locus\_tag=BN49\_RS24185] [protein=amino acid deaminase] [protein\_id=WP\_046043823.1] [location=4681822..4683042] [gbkey=CDS]

MKYHSAPLIPHKSALMSAPANLLAEEVCLPAALLKKSALENNISWMQRYADARGVSLAPHGKTTMTPWIF

QAQQRAGAWGIGVGSVWQASAAMASGIQRVLMVNQLVGKANMQVVAQLKAHYRAVDFICCVDSEVNVRAL

STFFADQGQTLDVLIELGVPGGRCGCRSVNDALALAQRVSDLPGLRLRGLELYEGVLHGDDPQPQVEALL

QQAAALACRMEPLVDGEFILTGAGTVWYDVVCNIWLAAAKPRRCRIVIRPGCYITHDRGIYDLAQQALIA

RDPIACDLAGDLTSALELMAMVQSVPEADRAVVNFGKRDCAFDAGLPQPIAHYRNGQQLALRAESIVSTG

IMDQHCMLRLAPGSDVQVGDILLFGTSHPCLTFDKWKTLLLVDDDYNVLDELDTLF

>lcl|NZ\_FO834906.1\_prot\_WP\_046043825.1\_4478 [locus\_tag=BN49\_RS24190] [protein=Ldh family oxidoreductase] [protein\_id=WP\_046043825.1] [location=complement(4683073..4684089)] [gbkey=CDS]

MESVTLSLPEAYDLALEVLSANGFSADHAAAIARNVTAGERDGCASHGLWRLLGIVDTLRKGKVSPDAEP

QIHDQAPGIARADAGGAFSLLAYERALPLLLEKARHNGIAALAINRCVHFSALFADIEPLTEAGLVGLAC

TPSHAWVAPAGGTRPLFGTNPIAFGWPRQDKPPFIVDMATSAAARGEIQLHQRAGKALPEGWGIDSQGQP

TTDAAEVLNGAMLTFGGHKGSALAAMVELLAGPLIGDMTSAESLAWDNGAGGLPYGGELILALDPQRFLG

AQAPEQLARAETLFNAMQDQGARLPGERRFSCRQQSERQGVIISRSLHDEICALRQGG

>lcl|NZ\_FO834906.1\_prot\_4479 [locus\_tag=BN49\_RS31545] [protein=FAD/NAD(P)-binding oxidoreductase] [pseudo=true] [partial=5'] [location=<4684302..4684566] [gbkey=CDS]

RWQRFAAAINRTFRLAESLKNAATPESLLCRCEDVRCGDVAAADDWLQAKLTQRPLAVWLAAAAAERAAV

PRPRGNAYCPRQAERRAV

>lcl|NZ\_FO834906.1\_prot\_WP\_002887503.1\_4480 [gene=hpaR] [locus\_tag=BN49\_RS24205] [protein=homoprotocatechuate degradation operon regulator HpaR] [protein\_id=WP\_002887503.1] [location=complement(4684570..4685010)] [gbkey=CDS]

MHDSLTIALLQAREAAMAYFRPIVKRHNLTEQQWRIVRILAERPSMDFHDLAFRACILRPSLTGILTRME

RDGLVLRLKPVNDQRKLYVSLTPAGTALYESAQAEVEETYRLLEAQFTTEKLQQLTSLLEEFIALGVPAG

RGDEEE

>lcl|NZ\_FO834906.1\_prot\_WP\_020805208.1\_4481 [locus\_tag=BN49\_RS30635] [protein=hypothetical protein] [protein\_id=WP\_020805208.1] [location=4685075..4685239] [gbkey=CDS]

MYNRFLHLKSTSLFLKNIQIIDLQQISNCYVNIVLIRSQNIHFQLLNLSAKHKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004146085.1\_4482 [locus\_tag=BN49\_RS24215] [protein=fumarylacetoacetate hydrolase family protein] [protein\_id=WP\_004146085.1] [location=4685297..4685929] [gbkey=CDS]

MKGTIFAVALNHRSQLDAWREAFQQAPYKTPPKTAVWFIKPRNTVIGDGEAIPYPQGETVQSGATVALIV

GKTARKVAAEEAANYIAGYALANDVSLPEESFYRPAIKAKCRDGFCPIGTLSAVRNVDDLTIITEINGRE

ADSWHTGDLQRNAAQLLSALSEFATLNPGDAILIGTPHSRVTLRPGDRVRILADGFPALENPVVAEGELA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043829.1\_4483 [locus\_tag=BN49\_RS24220] [protein=fumarylacetoacetate hydrolase family protein] [protein\_id=WP\_046043829.1] [location=4685926..4686690] [gbkey=CDS]

MKQARIEWQGQVRDVLVNERDQVRLDDGTVLKEGEFRWLPPADGTLFALGLNYADHASELEFKPPTEPLV

FIKAPNTFTGHQQQSVRPDNVEYMHYEAELVVVIGKTARRVSEAEAMDYVAGYTVCNDYAIRDYLENYYR

PNLRVKSRDTLTPIGPWIVSKEAIPDPHNLALRTWVNGELRQQGTTADLIFSIPFLIAYLSEFMTLQPGD

MIATGTPKGLSDVVSGDEVIVEVEGVGRLVNHIISQQAYEETLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002887494.1\_4484 [gene=hpaE] [locus\_tag=BN49\_RS24225] [protein=5-carboxymethyl-2-hydroxymuconate semialdehyde dehydrogenase] [protein\_id=WP\_002887494.1] [location=4686687..4688153] [gbkey=CDS]

MKKINHWINGKNVAGADYFHTTNPATGEVLAEVASGGEAEINQAVAAAKEAFPKWANLPMKERARLMRRL

GDLIDQNVPEIAAMETADTGLPIHQTKNVLIPRASHNFEFFAEVCQQMNGKTYPVDDKMLNYTLVQPVGV

CALVSPWNVPFMTATWKVAPCLALGNTAVLKMSELSPLTADRLGELALEAGIPAGVLNVVQGYGATAGDA

LVRHHDVRAVSFTGGTATGRNIMKNAGLKKYSMELGGKSPVLIFEDADIERALDAALFTIFSINGERCTA

GSRIFIQQSIYPEFVKRFAERANRLRVGDPTDPNTQVGALISQQHWEKVSGYIRLGIEEGATLLAGGADK

PSDLPAHLKAGNFLRPTVLADVDNRMRVAQEEIFGPVACLLPFKDEAEGLRLANDVEYGLASYIWTQDVS

KVLRLARGIEAGMVFVNTQNVRDLRQPFGGVKASGTGREGGEYSFEVFAEMKNVCISMGDHPIPKWGV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529572.1\_4485 [gene=hpaD] [locus\_tag=BN49\_RS24230] [protein=3,4-dihydroxyphenylacetate 2,3-dioxygenase] [protein\_id=WP\_016529572.1] [location=4688155..4689012] [gbkey=CDS]

MGKLALAAKITHVPSMYLSELPGKNHGCRQGAIDGHKEIGKRCRERGVDTIIVFDTHWLVNSAYHINCAD

HFQGVYTSNELPHFIRDMTYDYDGNPELGQLIADEAVKLGVRAKAHNIPSLKLEYGTLVPMRYMNSDKHF

KVVSISAFCTVHDFADSRRLGEAILKAIEKYDGTVAVLASGSLSHRFIDDQRAEEGMNSYTREFDHQMDE

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LPAQA

>lcl|NZ\_FO834906.1\_prot\_WP\_004151392.1\_4486 [locus\_tag=BN49\_RS24235] [protein=5-carboxymethyl-2-hydroxymuconate Delta-isomerase] [protein\_id=WP\_004151392.1] [location=4689022..4689402] [gbkey=CDS]

MPHFIAECTDNIREQADLPGLFAKVNEALAATGIFPIGGIRSRAHWLDTWQMADGRQDYAFVHMTLKIGA

GRSLESRQDVGDMLFALIKSHFATLMESRYLALSFAMEELDPTLNYKQNNVHALFK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043831.1\_4487 [gene=hpaH] [locus\_tag=BN49\_RS24240] [protein=2-oxo-hepta-3-ene-1,7-dioic acid hydratase] [protein\_id=WP\_046043831.1] [location=4689511..4690314] [gbkey=CDS]

MLDKQTRTLIAQRLNQAEKQREQIRAISLDYPSITIEDAYAVQREWVEMKIAGGRVLKGHKIGLTSKAMQ

ASSQISEPDYGALLDDMFFHDGSDIPTDRFIVPRIEVELAFVLAKPLRDPNCTLFDVYNATDYVIPALEL

IDARCHNIDPETQRPRKVFDTISDNAANAGVILGGRPIKPDELDLRWISALLYRNGVIEETGVAAGVLNH

PANGVAWLANKLAPYDVQLEAGQIILGGSFTRPVPARKGDTFHVDYGNMGAISCRFV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043833.1\_4488 [gene=hpaI] [locus\_tag=BN49\_RS24245] [protein=4-hydroxy-2-oxoheptanedioate aldolase] [protein\_id=WP\_046043833.1] [location=4690325..4691122] [gbkey=CDS]

MNNAFKDALKAGRPQIGLWLGLCSSYSAELLAGAGFDWLLIDGEHAPNNVPTVLTQLQAIAPSPSQPVVR

PSWNDPVQIKQLLDVGAQTLLVPMVQNAEEARLAVRATRYPPAGIRGVGSALARASRWNRVPDYIHRAND

AMCVLVQIETREALKNLPQILDVDGVDGVFIGPADLSADMGHGGNPQHPEVQAAIEDAIQQIRQAGKAPG

ILMANEQLAKRYLELGALFVAVGVDTTLLARGAEALAARFTHNATTTTDNNKSVY

>lcl|NZ\_FO834906.1\_prot\_WP\_002887477.1\_4489 [gene=hpaX] [locus\_tag=BN49\_RS24250] [protein=4-hydroxyphenylacetate permease] [protein\_id=WP\_002887477.1] [location=4691144..4692502] [gbkey=CDS]

MTTSTLQHNDNKAVEVENRVIKKLFRRLITFLFVLFVFSFLDRINIGFAGLTMGKDLGLTSTMFGLAATL

FYVTYVLCGIPSNIMLAKVGARRWIAGIMVVWGIASTCTMFATSPHTLYILRMLVGIAEAGFLPGILVYL

TWWFPAYHRARANALFMIAMPVTMMLGSILSGYILALDGLWNLKGWQWLFLLEGLPSVVLGVVTWFFLND

TPDKANWLDNEEKQALKAMIDREREHAAIVPASPRSTLREVLTPAVLMYTLAYFCLTNTLSAINIWTPQI

LQSFNTGSSNIMIGLLAAIPQFCTIFGMIWWSRRSDRRKERKMHTILPYLFAAAGWLLASATHHSLIQLI

GIIMASVGSFTAMAIFWTTPDRVISLQSRAVALAVINAIGNVGSAVSPLLIGILRDTTGSFSSGLWFVAG

LLIVGALVLTRIPMSQREDAAAAPGLAAQKGH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530625.1\_4490 [gene=hpaA] [locus\_tag=BN49\_RS24255] [protein=4-hydroxyphenylacetate catabolism regulatory protein HpaA] [protein\_id=WP\_016530625.1] [location=4692512..4693402] [gbkey=CDS]

MCQHSIANIDINKDYDESLGTEEVHYQSFSRMAAFFGRDMQAHRHDRYFQMHYLDTGQIELQLDDHRYSV

QAPLFVITAPSVPHAFITESDSDGHVLTVHEELIWPLLEVLYPGTRETFGLPGICLSLADKPDELAALAH

YWQLIRRESTAQLPGREHTLALLAQAVFTLLLRNAKLDDHAASGMRGELKLFQRFNQMIDSHYHQHWTVP

DYARELHLTESRLTDICRRFANRSPKRLIFDRQLREAKRLLLFSDSAVNEIAWQLGFKDPAYFARFFSRQ

VGCSPSSYRAQKVPVS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530624.1\_4491 [gene=hpaB] [locus\_tag=BN49\_RS24260] [protein=4-hydroxyphenylacetate 3-monooxygenase, oxygenase component] [protein\_id=WP\_016530624.1] [location=4693628..4695190] [gbkey=CDS]

MKPEDFRADAKRPLTGEEYLKSLQDGREIYIYGERVKDVTTHPAFRNAAASVAQLYDALHKPEMQDSLCW

GTDTGSGGYTHKFFRVAKSADDLRQQRDAIAEWSRLSYGWMGRTPDYKAAFGCALGANPAFYGQFEQNAR

NWYTRIQETGLYFNHAIVNPPIDRHKPADEVKDVYIKLEKETDAGIIVSGAKVVATNSALTHYNMIGFGS

AQVMGENPDFALMFVAPMDAEGVKLISRASYEMVAGATGSPYDYPLSSRFDENDAILVMDKVLIPWENVL

IYRDFDRCRRWTMEGGFARMYPLQACVRLAVKLDFITALLKRSLECTGTLEFRGVQADLGEVVAWRNMFW

ALSDSMCSEATSWVNGAWLPDHAALQTYRVMAPMAYAKIKNIIERNVTSGLIYLPSSARDLNNPQIDQYL

AKYVRGSNGMDHVERIKILKLMWDAIGSEFGGRHELYEINYSGSQDEIRLQCLRQAQSSGNMDKMMAMVD

RCLSEYDQNGWTVPHLHNNADINMLDKLLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002887467.1\_4492 [locus\_tag=BN49\_RS24265] [protein=4-hydroxyphenylacetate 3-monooxygenase reductase subunit] [protein\_id=WP\_002887467.1] [location=4695210..4695722] [gbkey=CDS]

MQLDEQRLRFRDAMASLSAAVNVVTTAGEAGRCGITATAVCSVTDTPPSVMVCINANSAMNPVFQGNGKL

CINVLNHEQEIMARHFAGMTGVTMEERFALSGWQQGALGQPVLKGSLASLEGEISQVQTIGTHLVYLVEI

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>lcl|NZ\_FO834906.1\_prot\_WP\_004211335.1\_4493 [locus\_tag=BN49\_RS24270] [protein=carbon starvation protein A] [protein\_id=WP\_004211335.1] [location=4696023..4698173] [gbkey=CDS]

MDTKKLFKHIPWVVLGIIGAFCLSVVALRRGEHVSALWIVVASVSVYLVAYRYYSLYIAQKVMKLDPTRS

TPAVINNDGLNYVPTNRYVLFGHHFAAIAGAGPLVGPVLAAQMGYLPGTLWLLAGVVLAGAVQDFMVLFI

SSRRNGASLGEMIKQEMGPVPGSIALFGCFLIMIIILAVLALIVVKALAESPWGVFTVCSTVPIALFMGI

YMRFLRPGRVGEVSVIGIVLLVASIWFGGVIAHDPYWGPALTFKDTTITFTLIGYAFISALLPVWLILAP

RDYLATFLKIGVIVGLALGIVILNPDLKMPAVTQYIDGTGPLWKGALFPFLFITIACGAVSGFHALIASG

TTPKLLANETDARFIGYGAMLMESFVAVMALVAASIIEPGLYFAMNTPPAGLGIVMPNLHEMGGENAAMI

AAQLKEVTVHAAATVSSWGFVISPEQILQTAKDIGEPSVLNRAGGAPTLAVGIAHVFHKIIPMADMGFWY

HFGILFEALFILTALDAGTRAGRFMLQDLLGNFVPFLKKTDSLVAGIIGTAGCVGLWGYLLYQGVVDPLG

GVKSLWPLFGISNQMLAAVALVLGTVVLVKMQRTKYIWVTVIPAAWLLLCTTWALGLKLFSSNPQMEGFF

FMAQQYKEKIAAGGELTAQQIANMNHIVVNNYTNAGLSILFLVVVYSIIFYGIKTWLNVRNNKVRTDKET

PYVPVPEGGVKTSSHH

>lcl|NZ\_FO834906.1\_prot\_WP\_002887451.1\_4494 [locus\_tag=BN49\_RS24275] [protein=YbdD/YjiX family protein] [protein\_id=WP\_002887451.1] [location=4698283..4698486] [gbkey=CDS]

MFGNLGQAKKYLGQAAKMLIGIPDYDNYVTHMQTNHPDQPYMTYEEFFRERQQARYGGDGKGGVRCC

>lcl|NZ\_FO834906.1\_prot\_WP\_002887442.1\_4495 [gene=yjiA] [locus\_tag=BN49\_RS24280] [protein=GTPase] [protein\_id=WP\_002887442.1] [location=4698498..4699454] [gbkey=CDS]

MAPIAVTLLTGFLGAGKTTLLRHILNEQHGFKIAVIENEFGEVSVDDQLIGDRATQIKTLTNGCICCTRS

NELEDALLDLLDSRDRGEIEFDRLVIECTGMADPGPIIQTFFSHQVLCERYLLDGVIALVDAVHADQQMD

QFTIAQSQVGYADRILLTKTDVAGDTEKLRERLARINARAPIYTVIHGDIDLSQLFNTSGFMLEEKVVSA

TPRFHFVAEKQNDVSSIVVELDYPVDISEVSRVMENLLLSFAEQLMRYKGMLWIDGEPNRLLFQGVQRLY

SADWDRPWGDETPHSTLVFIGIQLPEEEIRAAFAGLRR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530623.1\_4496 [locus\_tag=BN49\_RS24285] [protein=YfaZ family outer membrane protein] [protein\_id=WP\_016530623.1] [location=4699846..4700391] [gbkey=CDS]

MRKLNILILAALAAVSGSAMAVGFTVEQGKNFTNLNMEMGKSSSGLYAESHWLKNTDDGSQTGGVGAGYN

LEVGPVMLNAGAKAIYIGPKKGDNGVAFPVGGGVNVALTDSIHVFGEGYVAPDGLNNSVKNYVEANGGVS

WSPIGPVTLKVGYRHVSVDGKEGRPNHTLIDGAYVGGGVTF

>lcl|NZ\_FO834906.1\_prot\_WP\_004146105.1\_4497 [locus\_tag=BN49\_RS24290] [protein=NAD-dependent succinate-semialdehyde dehydrogenase] [protein\_id=WP\_004146105.1] [location=complement(4700489..4701859)] [gbkey=CDS]

MAYQTVNPANNQLIKTYPAHSDADVEAALQQADALYHSAWAKGDIEPRLAVLHKLADLIDSRAEELAKIA

SQEMGKLIKQSRGEVKLCAQIARYYADNAKSFLAPVKYPSELGEAWVEHHPIGVLLAVEPWNFPYYQLMR

VLAPNLAAGNPVIAKHASIVPHCAETFAHLVREAGAPEGAWTNLFISQDQVAKIIADDRVQGAALTGSEK

AGSVVAAQAAKHIKKSTLELGGNDVFVVLDDADLERAVKIGVQARLNNAGQVCTAAKRFILHENIADAFL

TKFSEAFRQVKIGDPLDESTTLGPLSSKDALDTLSKQVDEAVKNGAKLHLGGKAVAREGNFFEPTILTGI

TRDNPAYFEEFFGPVAQIYVVKNDEEAIQLANDSHYGLGGAVFSQDIERAKRMASAIETGMVYINWLTDT

APELPFGGVKRSGYGRELSDLGIKEFVNQKLVVVRR

>lcl|NZ\_FO834906.1\_prot\_WP\_012737350.1\_4498 [locus\_tag=BN49\_RS24295] [protein=Rpn family recombination-promoting nuclease/putative transposase] [protein\_id=WP\_012737350.1] [location=complement(4702018..4702956)] [gbkey=CDS]

MAKGTTSTPHDAVFKQFLTQADTARDFLAIHLPPALRQRCDLDTLQLESASFIEESLRAWYSDVLWSLKT

ASGEGYIYVVIEHQSSPDAQMAFRLMRYAIAAMQRHLDGGHTKLPLVVPMLFYHGATTPYPWSLNWLDCF

ADPQLASELYISPFPLVDVTVIPDDEIVRHRRVALLELIQKHIRQRDLMGIVEQLTTILLSGDANDRQLK

TLFNYLLQTGNARRFGRFIHEVAQRVPQHRERLMTIAERLQEVGRRKGKREGRLEGRQEGRQEGQHAEAL

RIAQRMLADGIARETVVKITGLTADEIAALAH

>lcl|NZ\_FO834906.1\_prot\_WP\_004211325.1\_4499 [locus\_tag=BN49\_RS24300] [protein=AraC family transcriptional regulator] [protein\_id=WP\_004211325.1] [location=4703172..4703987] [gbkey=CDS]

MNHTRDIPQTFWRDDRLPWLELRSTWRSRQAYKRHSHPQLSVGAIIEGETRCLCAGQEYLLQPGDLIVIP

PHAPHSCNPLHDRPRSYHMLYLDATWCRAQRPDIPPGASITSPQPLLRDSPLFASFQQVVALMNRGSLEQ

LPARLAQLLHALPLCAAAPQAPHHASALLFQRLAMDLPASPSLDKLAHDSALRKETVIRAVKQDTGLTPA

SLINMARIEYAKTRLRAGDPIADVGYQAGFADQSHFHKTFVSYTAATPRQYAQSRSISDNK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177543.1\_4500 [locus\_tag=BN49\_RS24305] [protein=LysE family translocator] [protein\_id=WP\_004177543.1] [location=4704035..4704697] [gbkey=CDS]

MHTLSTLFPAAFPALALSHFVALLSPGPDFFLLVGYAVRYRIRGSIGLCLGIAAGNALYIVLAIVGWGLL

RQAPLLFLLIELLGAGYLLWIGSLLIRSRPATLAMESVRAARPGFGRQLLLGLGSSLLNPKNALFYLALM

TSLLGPAVTLLQQTVSGLWMVSVVFFWDLLLVSAIALPQIQRRLGAIVWRVERAAGAILMLFGLGIIWRF

LHDLAVRLYA

>lcl|NZ\_FO834906.1\_prot\_WP\_004146918.1\_4501 [locus\_tag=BN49\_RS24310] [protein=DUF445 domain-containing protein] [protein\_id=WP\_004146918.1] [location=4704690..4705982] [gbkey=CDS]

MLKHMEKLAELKRAKLLALSLLLIAAAIFITTLALPPSPWVGALKAISEAAMVGALADWFAVVALFRRIP

LPFVARHTAIIPRNKDRIADNLGRFVEEKFLDTPSLVALIRRYQPALMLGNWFSQPENARRVGQHLLQVM

SGFLELTDDARIQRLLRRAVHKAIDKVDLTQTSAMMLEGLTRDNRHQKLLDSLINQLIALLQRDSSRAFI

ARGIVHWLETEHPLKAKLLPTEWLGEHSAEMVTDAVNTLLDEVTHDRTHQIRQTFDRAVQKLIDNLKSDP

DMAQKADNIKAWLKNDETFNHYLGEVWGDLRGWVKNDISSDDSRIKQRIAEAGQWFGETLLRDDALRESL

NEHLEQAAHRVAPEFAAFLTRHISDTVKSWDARDMSRQIELNIGKDLQFIRINGTLVGGTIGLLLWLLSQ

IPSLLHLHIG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529770.1\_4502 [gene=mdtM] [locus\_tag=BN49\_RS24315] [protein=multidrug efflux MFS transporter MdtM] [protein\_id=WP\_016529770.1] [location=4706039..4707277] [gbkey=CDS]

MHRISHWLSRHAAALFFPAALILYDFSAYLTTDLIQPGILHVVRDFNADVALAPASVSLYMAGGMALQWL

LGPLSDRIGRRPVLLTGALIFTLACLATLFTTSMTQFLIARFVQGTSICFIATVGYVTVQEAFEEKRSIR

LMAVITSVVLVAPIVGPLSGAALMHFIHWKALFGIIAAMGLVAWLGLLLTMPETVRRGDVPFSPLGVLRD

FRNVFRNRIFLLGAATLSLSYIPLMSWVAVSPVILMDAGGLTTSEFAWSQVPVFSAVIIANLSVARWVKD

PTRPRFVLSAVPVQMLGLAILIVGNLVWHHVWLWSVLGTCFYAFGIGLIFPTLFRFTLFSNDLPKGTVSA

SLNIVILSVSALSIEGARWLWFHGGRLPFHLLAVAAGIVAACCLARLLRHQREQAVIEARQS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529771.1\_4503 [locus\_tag=BN49\_RS24320] [protein=DUF2164 domain-containing protein] [protein\_id=WP\_016529771.1] [location=4707303..4707542] [gbkey=CDS]

MNDIELGQAQRDLLRDRLSKYCAETFDLELEQFDAEFFVDFIAKELGPLFYNAGIEEAIRTHQAWSERIQ

EEMDLKKVY

>lcl|NZ\_FO834906.1\_prot\_WP\_016529772.1\_4504 [gene=yjiM] [locus\_tag=BN49\_RS24325] [protein=double-cubane-cluster-containing anaerobic reductase] [protein\_id=WP\_016529772.1] [location=4707640..4708791] [gbkey=CDS]

MSLITDLPAIFDQFSEARQKGFLTVMDLKEQNVPLVGTYCTFMPQEIAMAAGAVVVSLCSTSDETIEEAE

KDLPRNLCPLIKSSYGFGKTDKCPYFYFSDLVVGETTCDGKKKMYEYMAEFKAVHVMQLPNSASDAASRA

LWKTEILRLQQVIEARFGTPISEAALREAIVLKNRERRALAHFYRLGQLNPPALSGGDILKVVYGATFRF

DKTALIDELHAMAERIHQEWQQGKRLEPRQRILITGCPIGGAAEKVVRAIEENGGWVVGYENCTGAKATE

RCVAEEGDVYDALTDKYLAIGCSCISPNDQRLQLLSQMVEEYQADGVIDVILQACHTYAVESLAIKRHLR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887413.1\_4505 [gene=yjiL] [locus\_tag=BN49\_RS24330] [protein=putative 2-hydroxyacyl-CoA dehydratase activator YjiL] [protein\_id=WP\_002887413.1] [location=4708801..4709568] [gbkey=CDS]

MNYTVGIDSGSTATKGILLADGVIVRRFLCPTPFRPADAIHEAWETLRAGLTETPFLTLTGYGRQLVDFA

DKQVTEISCHGLGARLLAPDTRTVIDIGGQDSKVIQLDAGGNLSDFLMNDKCAAGTGRFLEVISRTLGAS

VEQLDAITDGVEPHAITSMCTVFAESEVISLRSAGVAPEAILAGVINAMARRSANFIGRLSAQGPLLFTG

GVSHCAAFARMLESHVGMAVTTHPDAQFAGAIGAALIGQRQRRRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887412.1\_4506 [locus\_tag=BN49\_RS24335] [protein=DUF3343 domain-containing protein] [protein\_id=WP\_002887412.1] [location=4709565..4709819] [gbkey=CDS]

MTTFLFLFHSTVGVVRMRKAMQAAGVAFEVKDIPRQLRSGCGLCILLEGTEADARGWIVPEQTAALYQQN

GEAWRCLATFPPAG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887411.1\_4507 [locus\_tag=BN49\_RS24340] [protein=DUF2955 domain-containing protein] [protein\_id=WP\_002887411.1] [location=complement(4709816..4710880)] [gbkey=CDS]

MSINTLAHVFTPHGNIVYTANDFRQTVRIAVAGTIALSISTFYDVQYGVFFVVYPLMLMSLVPMFNLHVA

RQFIFSAAVNCVEMVLIVGYLSQWPVIMTLVVFALYVMRFRFMSQGPLFLLGSMGVVCQSTMLNFMSYPT

SNWHTLMFSNMEACVMAVALSALLHYLIPDVEPRKPPPRIEKDAARIRHESLLSGTVATIIFVVFQICDL

SDSLSALMAGILILFPMHYRGAVISSIWRVVGVVLACLYILVVQLIIYDFSNHMILMMPLIGLGLAFSAR

LHVMEKVGAGVGFASITTIGIMFGQNLHPYQDLVFSDLYRITSVTVSLVVTLTLVFLMHRLLNCFAATRF

VVSD

>lcl|NZ\_FO834906.1\_prot\_WP\_002887394.1\_4508 [locus\_tag=BN49\_RS24345] [protein=HlyD family secretion protein] [protein\_id=WP\_002887394.1] [location=complement(4710870..4711937)] [gbkey=CDS]

MMTPEQKFARWVRVSIAAFLGIFAWFIVADIWIPLTPDSTVMRVVTPVSSRVSGYVSHVYVHNNSQVKKG

DLLYELDPTPFINKVEAAQIALEQAKLSNQQLDAQIAAARANLRTAQYTARNDKVTLDRYQRLSTMQNVS

QSDLDKVRTTWQTSEQSVSALNAQIQNLLIQRGERDDKRNVTLQKYRNALEEAQLNLAWTKVRAETDGMV

SNLQLNPGIYATAATAVLALVNNNTDIVADFREKSLRHTAVNTDAAVVFDALPGQVFPAHVTSSDAGILA

GQEAVNGQLSQPEQSTRWVRDAQRMRIHVALDQPLDKPLPTGARATVQLYNSEGPFARTFAGLQIHLVSW

LHYVY

>lcl|NZ\_FO834906.1\_prot\_WP\_004177547.1\_4509 [locus\_tag=BN49\_RS24350] [protein=MarR family transcriptional regulator] [protein\_id=WP\_004177547.1] [location=complement(4711944..4712408)] [gbkey=CDS]

MTEDELFARRPLGMRMAMVVRQWRAIIDSAITDTGLTQSSWTVLMQLHQLGDNVSVSELAEVQGIELPPL

MRTLSLLEKQGYLVRSTSPYDKRIRLLTLTAEGRAILEKLSCVIETYQERVTQTIPEADLATFSATLNQI

ACRLRNIREEDNKI

>lcl|NZ\_FO834906.1\_prot\_WP\_002887388.1\_4510 [locus\_tag=BN49\_RS24355] [protein=DUF1127 domain-containing protein] [protein\_id=WP\_002887388.1] [location=complement(4712573..4712737)] [gbkey=CDS]

MEFHENRARQPFIGFVLLVRFIKKWWLQEQTRRVLQQMSDEQLKDIGLRRDQIN

>lcl|NZ\_FO834906.1\_prot\_WP\_002887384.1\_4511 [locus\_tag=BN49\_RS24360] [protein=PLP-dependent aminotransferase family protein] [protein\_id=WP\_002887384.1] [location=4712915..4714327] [gbkey=CDS]

MTRYQHLATLLAERIEQGLYRHGEKLPSVRSLSQEHGVSISTVQQAYQLLEQQQMIVPQPRSGYFVAPRK

AQPPVPPMSRPVQRPVEITQWDQVLTMLDARYDKSIIPFGGGSPDVTQPSLKPIWRELSRAIQHNLTEVL

NYDELAGRRELREQIARLMLDGGSVVTADDLVLTSGCHSALSLALLSVCQPGDIIAVESPCYYGTMQMLR

GLGLKTIEIPTDPETGISIEALELALDQWPIKGVILVPNCNNPLGFIMPDARKRAVLNLAQRYDIVIFED

DIYGELATEYPRPRTIHSWDIDGRVMLCSSFTKTIAPGLRIGWIAPGRYYDKLLQMKYAASGTNVPSTQL

AACNFIREGHYHRHVRRMRQIYQRNIEIYTCWLREFFPCGICVTRPKGGFMLWVELPEQVDMVCVAKQLC

RLKIQVAPGSLFSAAGKYRNCVRINCALPPTEKHKAVMVKLGEAVKVAME

>lcl|NZ\_FO834906.1\_prot\_WP\_016531125.1\_4512 [gene=fosA] [locus\_tag=BN49\_RS24365] [protein=FosA5 family fosfomycin resistance glutathione transferase] [protein\_id=WP\_016531125.1] [location=complement(4714399..4714818)] [gbkey=CDS]

MLSGLNHLTLAVSQLAPSVAFYQQLLGMTLHARWDSGAYLSCGDLWLCLSLDPQRRITPPEESDYTHYAF

SISEADFASFAARLEAAGVAIWKLNRSEGASHYFLDPDGHKLELHVGSLAQRLAACREQPYKGMVFFDQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043839.1\_4513 [locus\_tag=BN49\_RS24370] [protein=LysR family transcriptional regulator] [protein\_id=WP\_046043839.1] [location=complement(4714812..4715720)] [gbkey=CDS]

MINLQRLDLNLLRTLDVLLSENNVTRAAQRLNLSQPSVSIQLARLREIFADPLLMPGPRGMQPTARADEL

RQPLRAALAALEQAVAPVSPFDPATAAETWRVAATDYMASAILLPMLAGLRQASPGSRLAVFELQPARLE

QQAANDTVDLFFHTREGAPPGLHQRLLFRERYVLAGRAEHSALRPGLSLETFCQLEHVIFSPDGGGFSAA

TDIALANLGLTRRVVLSVPHFLFMLETLRNSDLVAVLPERLVRGQSGLVVVEPPLAVAGFEMLMLWHERW

HRDPAHQWLRQFIVNSLEEQTC

>lcl|NZ\_FO834906.1\_prot\_WP\_016530660.1\_4514 [locus\_tag=BN49\_RS24375] [protein=NAD(P)H-dependent oxidoreductase] [protein\_id=WP\_016530660.1] [location=4715807..4716589] [gbkey=CDS]

MKVLLIYAHPEPRSLNGALKNFAIRHLQQAGHEVQVSDLYAMRWKAGYDADDSGAPPVGEFWRPTLDSKQ

AFAQGTQSADIVAEQEKLLWADTVIFQFPLWWFSMPAIMKGWIDRVYAWGFAYGVGEHSDRHWGDRYGEG

TFIGKRAMLIVTAGGWAEHYSPRGINGPIDDILFPIQHGMLFYPGFEVLPPLVFYRTDKTDAGQFADQCA

ALAERLDTLWQIEPIPFRRQNHGDYLIPSLTLRPELAPGQSGLAVHLRSE

>lcl|NZ\_FO834906.1\_prot\_WP\_002887352.1\_4515 [locus\_tag=BN49\_RS24380] [protein=ABC transporter permease] [protein\_id=WP\_002887352.1] [location=complement(4716626..4717582)] [gbkey=CDS]

MKKSWRNNVEFYLIGLLLLMVIAFSIAMPNIFWSVSNFQSIASQMPVLGILALAMAMTMLCGGINLSIIA

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TGGSAIANYPQWVLWLNHAQWFGIPLPMWLFAVVAAGLWVLLEKSPLGRAIMLIGSNERATHYSGINTRR

VLMWVYVISALLCAVAAFLMMSKLNSAKASYGESYLLVSILAAVLGGVNPDGGSGRIVGMVLALFLLQII

ESGFNILGISPYLTMALWGVLLLCFIQARGMLGLERAG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530659.1\_4516 [locus\_tag=BN49\_RS24385] [protein=ABC transporter permease] [protein\_id=WP\_016530659.1] [location=complement(4717579..4718550)] [gbkey=CDS]

MANLLKRHEFWLGMFIIALCLLLGWRSEEFFTFGNLYDLANNYAMLTILACGLFVVLIAGGIDISFPAMT

IIAQYGMVVMLQKVGGNFAVAFVLAGGIGVLLGLVNALLVNRLRVPSIIITISTLNIFYGLLLWLSKGVW

LYDFPPWFEKGVMLFKYTDADGYDYGLGLPLLTMIAVVLLTAFIMNFTTVGRKIYAMGGNRESASRVGFS

VLRLQLFVYGYMGLMSGAAGVVQAWTVMTVAPDSLLGYELTVLAAVVLGGTSLIGGRGTLTGTLLGVILL

AVMQNGLNLLGVSSYWQILITGAIIVVSISVTAWSQHQNRSLL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530658.1\_4517 [locus\_tag=BN49\_RS24390] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_016530658.1] [location=complement(4718543..4720027)] [gbkey=CDS]

MEPFLSLRHVSKTFHANRALNDISIDFMPGEVHCLAGQNGCGKSTLIKIISGVYRPDEGAAMTLGGKTWP

KLTPAASVAHGIQVIYQDLSLFPNLSVWENIAINHYHRGVLVRRSELRRSAEQAMRSINVSLPLDAAVES

LSIARCQLVAICRALAQDARLIIMDEPTASLTHQEVEGLLHVVRQLRERGICIVFVSHRLEEVMAVSDRI

SVLKDGNLVGTMPAAEVTTRRLGFLMTGQEFDYQVRDLWQGQGSTPVLEVRNLTRKGEYHNVSLKVEAGE

VVSIVGLLGAGRTELCLSLFGMTRPDSGEILINGQPVRLRSNQDAIRHGIGYVSEDRMSRGLVMSQSIEN

NIISTVFHKVKGACGLLSDSKAQQLVARMVNALTIKAPDTHLPVNTLSGGNAQRVSIAKWLAISPKLLIL

DSPTVGVDIANKAGIYHIISDLAAHGIAVLMICDEIEEAWYQSHRILVMKQGELTHSFLPDSSTQQQIAE

VVNG

>lcl|NZ\_FO834906.1\_prot\_WP\_002887349.1\_4518 [locus\_tag=BN49\_RS24395] [protein=autoinducer 2 ABC transporter substrate-binding protein] [protein\_id=WP\_002887349.1] [location=complement(4720078..4721061)] [gbkey=CDS]

MHKRLVVNIFSSLLLGAALISAPVYAAEKTVVNISKVDGMPWFNRMGEGVVQAGKEFNLNASQVGPSSTD

APQQVKIIEDLIARKVDAITIVPNDANVLEPVFKKARDAGIVVLTNESPGQPSANWDVEIIDNEKFAAEY

VEHMAKRMGGKGGYVIYVGSLTVPQHNLWADLLVKYQKEHYPDMHEVTRRMPVAESVDDSRRTTLDLMKT

YPDLKAVVSFGSNGPIGAGRAVKEKRAKNKVAVYGMMIPSQAASLIKSGDITEGITYDPATAGYALAAVA

STLLNGKTIEPGFELKELGKAEVDSDKHIIRFHKVLLVNKDNIDSLY

>lcl|NZ\_FO834906.1\_prot\_WP\_004178473.1\_4519 [gene=trpS] [locus\_tag=BN49\_RS24400] [protein=tryptophan--tRNA ligase] [protein\_id=WP\_004178473.1] [location=4721566..4722573] [gbkey=CDS]

MNHPQTILTGDRPTGQLHLGHYVGSLRQRVALQHNHQQFILIADLQGLTDNGSNPQKISHHILEVMADYL

AVGIDPRLTTICLQSALPALAELSALYMNIVTVARVERNPTVKNEIAQKGFARSLPVGFLAYPISQAADI

TAFKAELVPVGDDQLPMIEQTNEIVHKMNSLTGEPVLRHCKALLSEVSRLPGVDGNAKMSKSLGNTLTLS

ATEEEIHHAVSAMYTDPTHLRVSDPGHVEGNVVFTYLDAFHSDKARVAEMKAHYQRGGLGDRQCKNELET

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043842.1\_4520 [locus\_tag=BN49\_RS24405] [protein=HlyD family efflux transporter periplasmic adaptor subunit] [protein\_id=WP\_046043842.1] [location=4722880..4723947] [gbkey=CDS]

MDKIKKRWAGYFVGLLVVLAAAAWWLLRPPGLPAGFASSNGRIEATEVDIASKIAGRIDTILVKEGQSVH

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TLSQRGAVSAQQLDDDRAAAESARAALESAKAQVSAARAAIEAARTSIIQAQTRVEAAQATERRILADID

DSELKAPRDGRIQYRVAEPGEVLAAGGRVLNMVDLADVYMTFFLPTEQAGLLALGSEARLVLDAAPDLVI

PANISFVASVAQFTPKTVETSDERLKLMFRVKARIPPELLAQHLEYVKTGLPGMAYVRLDKQQPWPEALA

VRLPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043844.1\_4521 [gene=rbbA] [locus\_tag=BN49\_RS24410] [protein=ribosome-associated ATPase/putative transporter RbbA] [protein\_id=WP\_046043844.1] [location=4723944..4726688] [gbkey=CDS]

MKLTPQDTSPPVALLEHVGQQFGATIALRDISLAIPARRMVGLIGPDGVGKSSLLSLIAGARTIEQGNVM

VLGGDMRDVHHRREVCPKIAWMPQGLGKNLYHTLSVYENVDFFARLFGHDKAERELRINELLQSTGLAPF

RDRPAGKLSGGMKQKLGLCCALIHDPQLLILDEPTTGVDPLSRAQFWELIDSIRQRQPAMSVLVATAYME

EAERFDWLVAMNAGEVLATGSAAELKAQTGSQTLEQAFIALLPEAKRQAHRAVVIPPRDSREEEIAIEAR

GLTMRFGNFVAVDHVNFRIARGEIFGFLGSNGCGKSTTMKMLTGLLPASEGEAWLFGQPVDPKDIATRQR

VGYMSQAFSLYSELTVRQNLELHARLFHIPDGEIPGRVAEMCERFMLTEVEDALPVDLPLGIRQRLSLAV

AVIHRPEMLILDEPTSGVDPVARDMFWQLMVDLARQDQVTIFISTHFMNEAERCDRISLMHAGKVLASDT

PQALVEQRGSNSLEEAFIAWLKEAQPSSPVPEEPTSAVASHSGHTAPRQAFSLRRLFSYSRREALELRRD

PVRSTLALLGTVILMFIMGYGISMDVEDLRFAVLDRDQTLSSQGWSQNIAGSRYFIEQAPLHSYDELDRR

MRDGELAVAIEIPPNFGRDIARGTPVQIGVWVDGAMPNRAETVRGYVQAMHLAWLQEMAGRQSSPQRDTS

LISIETRYRYNPDVKSLPAIVPAVIPLLLMMIPAMLSALSVVREKELGSIINLYVTPTTRSEFLLGKQLP

YIVLGMFNFFLLCALSVFVFGVAHKGSFLTLTLAALLYVTIATGLGLLISTFMKSQIAAIFGTAIITLIP

ATQFSGMIDPVASLEGPGRWIGQIYPTSHFLTIARGTFSKALNISDLWGSFIPLLIAVPLVLGLSVLLLK

KQEG

>lcl|NZ\_FO834906.1\_prot\_WP\_016529729.1\_4522 [locus\_tag=BN49\_RS24415] [protein=ABC transporter permease] [protein\_id=WP\_016529729.1] [location=4726688..4727812] [gbkey=CDS]

MRGLRNIYNLGVKELRSLLGDKAMLALIVFAFTVSVYSSATVMPGSLHLAPIAVADMDKSQLSSRIINAF

YRPWFLEPELITADEMDAGLDAGRYTFAINIPPNFQRDVLAGRQPEIQVNVDATRMSQAFTGNGYIQNII

TGEVNSFVARYRDNSVLPVELAVRMRFNPNLEQERFGAVMAIINNITMLAIVLTGSALIREREHGTIEHL

LVMPVTPFEIMLAKIWSMGLVVLVVSGLSLVLMVQGILQVPIEGSVPLFMLGVALSLFATTSIGIFMGTL

ARSMPQLGLLMILVLLPLQMLSGGSTPRESMPQLVQDIMLTMPTTHFVSLAQAILYRGASFAIVWPQFLT

LLAIGGVFFTIALLRFRKTIGEMA

>lcl|NZ\_FO834906.1\_prot\_WP\_002887322.1\_4523 [locus\_tag=BN49\_RS24420] [protein=hypothetical protein] [protein\_id=WP\_002887322.1] [location=complement(4727853..4728170)] [gbkey=CDS]

MKILLNWSPLRQLFTYIQERFTFLVLLCWPAIIWLFCRVGVWLTDNVYELLGKSPAQSFTVYLQPFMTPG

TLLRISISWVVLLFILFSMAMAFTWGLRRFMNRHK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531877.1\_4524 [gene=purH] [locus\_tag=BN49\_RS24460] [protein=bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase] [protein\_id=WP\_016531877.1] [location=4734453..4736042] [gbkey=CDS]

MQQRRPVRRALLSVSDKAGIVEFAQALSARGVGLLSTGGTARLLADKGLPVTEVSDYTGFPEMMDGRVKT

LHPKVHGGILGRRGQDDGIMQQHGIAPIDMVVVNLYPFAQTVAREGCSLEDAVENIDIGGPTMVRSAAKN

HKDVAIVVKSSDYDAIINEMDANEGSLTLATRFDLAIKAFEHTAAYDSMIANYFGSMVPAYHGESKEAAG

RFPRTLNLNFIKKQDMRYGENSHQQAAFYIEENVEEASVATATQLQGKALSYNNIADTDAALECVKEFNE

PACVIVKHANPCGVAVSDSILDAYDRAYKTDPTSAFGGIIAFNRELDAETAQAIISRQFVEVIIAPSASE

EALKITAAKQNVRVLTCGQWDTRVAGLDFKRVNGGLLVQDRDLGMVTAGELRVVSKRQPTEQELRDALFC

WKVAKFVKSNAIVYAKDNMTIGIGAGQMSRVYSAKIAGIKAGDEGLEVKGSAMASDAFFPFRDGIDAAAA

VGITCVIQPGGSIRDDEVIAAADEHGIAMIFTDMRHFRH

>lcl|NZ\_FO834906.1\_prot\_WP\_020804630.1\_4525 [gene=purD] [locus\_tag=BN49\_RS24465] [protein=phosphoribosylamine--glycine ligase] [protein\_id=WP\_020804630.1] [location=4736058..4737353] [gbkey=CDS]

MKVLVIGNGGREHALAWKAAQSPLVDTVYVAPGNAGTALEPSLQNVAIGVTDIPALLRFAQDEKIDLTIV

GPEAPLVIGVVDAFRAAGLAIFGPTEGAAQLEGSKAFTKDFLARHHIPTAEYQNFTEVEPALAYLREKGA

PIVIKADGLAAGKGVIVAMTLEEAEAAVKDMLAGNAFGDAGHRIVIEEFLDGEEASFIVMVDGEHVLPMA

TSQDHKRVGNGDTGPNTGGMGAYSPAPVVTDEVHQRTMERIIWPTVKGMAAEGNTYTGFLYAGLMIDKQG

NPKVIEFNCRFGDPETQPIMLRMKSDLVELCLAACAGKLDEKTSEWDDRASLGVVVAAGGYPGSYNTGDE

IYGLPQQEVADGKVFHAGTKLSDDQRVVTNGGRVLCVTALGDSVAQAQQRAYQLLTDIRWDGSFSRSDIG

WRAIEREKANG

>lcl|NZ\_FO834906.1\_prot\_WP\_004895015.1\_4526 [gene=zraR] [locus\_tag=BN49\_RS24470] [protein=sigma-54-dependent response regulator transcription factor ZraR] [protein\_id=WP\_004895015.1] [location=complement(4737343..4738674)] [gbkey=CDS]

MSSDKVQILVVDDDISHCTILQALLRGWGYQVGLAHNGLQALEQIHQQVFDLVLCDIRMAEMDGIATLKE

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MIGDSPAMQALLNDITLVAPSDATVLIYGESGTGKELVAHAIHACSERRDKPLVTLNCAALNESLLESEL

FGHEKGAFTGADRRREGRFVEADGGTLFLDEIGDISPVMQVRLLRAIQEREVQRVGSNQTLAVDVRLIAA

THRNLAEEVSAGRFRQDLYYRLNVVTIEIPPLRRRREDIPQLAQHFLKRYTERNRKTVKGFTPQAMDLLI

HYPWPGNIRELENAVERAVVLLTGNYISERELPLAIAGTPLPSGGSEEGGIQPLVEVEKEVILAALEKTG

GNKTEAARQLGITRKTLLAKLSR

>lcl|NZ\_FO834906.1\_prot\_WP\_002884349.1\_4527 [gene=zraS] [locus\_tag=BN49\_RS24475] [protein=two-component system sensor histidine kinase ZraS] [protein\_id=WP\_002884349.1] [location=complement(4738661..4740055)] [gbkey=CDS]

MKIKSLSRDAAAGALSWLLTGTVVLLVMLFSAMIVRDYGRETTAARQTIEEKGSVLIRALESGTRVGMGM

RMHHAQLQALLEEMAWQPGVLWFAVTDENGKIIAHSDPQQVGKTLYSPAQMRALAVGEQARWRRLSEPQP

ALEIYRHFRPLNPARGHHMGMMNRGNSALAQATVPQVIFIAFDSRELDAAQARGQRNMAIMLGAAALVIA

ATILAQFWFRRYRRSRKQLLEAMARKEKLVALGHLAAGVAHEIRNPLSSIKGLAKYFAERTSPGGESHQL

AQVMAKEADRLNRVVSELLELVRPAHLNYQTVDINALIRHSLQLVSQDAQSRGIALQFTPRPELTTISAD

PDRLNQVLLNLYLNAMQAIGRDGVIRVTASEADRQRVKIVVTDSGKGMSDEELQAIFTPYFTTKADGTGL

GLAVVQNIIEQHGGTIRAESQPGAGAIFTLWLPVDAQRREDEQR

>lcl|NZ\_FO834906.1\_prot\_WP\_002884346.1\_4528 [gene=zraP] [locus\_tag=BN49\_RS24485] [protein=zinc resistance sensor/chaperone ZraP] [protein\_id=WP\_002884346.1] [location=4740315..4740752] [gbkey=CDS]

MKRNRTLPLALVTFAALTFASNAAWANHHWGNNNGMGNQGYSQLTQEQQATVQKLHNDYYAQTSALRQQL

QSKRYEYNALLTAQKPDSGKIEAVAQEMEGLRQKLDQQRVKFDIALAEAGVPRGAGMGYGGCRGSAGGHM

GMNHW

>lcl|NZ\_FO834906.1\_prot\_WP\_016530968.1\_4529 [locus\_tag=BN49\_RS24490] [protein=DUF1481 domain-containing protein] [protein\_id=WP\_016530968.1] [location=complement(4740756..4741451)] [gbkey=CDS]

MNSFIEGAIKPLLSVWRRPLALAGILLLTACSHDTSLPPFTASGYADNQGAMRIWRKDSGDEVHLLAAFS

PWRHGDTSTSEYRWQGDQLALIELNVYGKPPEHIRARFDAQGDLSFMQREVDGQKQQLSSDQVALYRYRA

EQIRQTSDALRQGRVVLRQGRWNAATHTVLTCEGQTVTPDLDSRALAHIERRQSHASAAVSIAWLEAPEG

SQLLLVANENFCTWQPTEKSF

>lcl|NZ\_FO834906.1\_prot\_WP\_002884342.1\_4530 [gene=hupA] [locus\_tag=BN49\_RS24495] [protein=DNA-binding protein HU-alpha] [protein\_id=WP\_002884342.1] [location=complement(4741464..4741736)] [gbkey=CDS]

MNKTQLIDVIADKADLSKAQAKAALESTLAAITESLKEGDAVQLVGFGTFKVNHRAERTGRNPQTGKEIK

IAAANVPAFVSGKALKDAVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002884331.1\_4531 [locus\_tag=BN49\_RS24500] [protein=YjaG family protein] [protein\_id=WP\_002884331.1] [location=complement(4741923..4742513)] [gbkey=CDS]

MLQNPIHLRLEKLESWQHVTFMACLCERMYPNYAMFCKQTEFGDGLLYRRILDLIWETLTVKDAKVNFDS

QLEKLEEAIPAADDFDMYGVYPAIDACVALSELIHSRLSGETLEHAIEVSKTSITTVAMLEMTQEGREMT

DEELKANPAVEQEWDIQWEIFRLLADCEERDLELIKGLRADLREAGESNIGINFQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004152311.1\_4532 [gene=nfi] [locus\_tag=BN49\_RS24505] [protein=deoxyribonuclease V] [protein\_id=WP\_004152311.1] [location=complement(4742556..4743227)] [gbkey=CDS]

MDLAALRTQQQQLAASVERADRLDRDPPALIGGADVGFEQEGEITRAAMVLLTWPELELVEYQVARVATS

MPYIPGFLSFRETPALLAAWEQLSQKPDLLFVDGHGISHPRRLGVASHFGLMIDVPTIGVAKKRLCGKIG

DLGDEPGALAPLMDKNEQLAWVWRSKVRCNPLFISTGHRVGMDSALMWVERCMRGYRLPEPTRWADAVAS

RRPSFVRWQANHS

>lcl|NZ\_FO834906.1\_prot\_WP\_002884329.1\_4533 [gene=hemE] [locus\_tag=BN49\_RS24510] [protein=uroporphyrinogen decarboxylase] [protein\_id=WP\_002884329.1] [location=complement(4743240..4744304)] [gbkey=CDS]

MTELKNDRYLRALLRQPVDVTPVWMMRQAGRYLPEYKATRAQAGDFMSLCKNAELACEVTLQPLRRYPLD

AAILFSDILTIPDAMGLGLYFEAGEGPRFTSPVKSKADVDKLPIPDPEQELGYVMNAVRTIRRELKGEVP

LIGFSGSPWTLATYMVEGGSSKAFTVIKKMMYAEPQALHALLDKLAKSVTLYLNAQIKAGAQSVMIFDTW

GGVLTGRDYQQFSLYYMHKIVDGLLRENEGRRVPVTLFTKGGGQWLEAMAETGCDALGLDWTTDIADARR

RVGNKVALQGNMDPSMLYASAPRIEEEVATILAGFGQGEGHVFNLGHGIHQDVDPEHAGVFVEAVHRLSA

PYHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002884327.1\_4534 [gene=nudC] [locus\_tag=BN49\_RS24515] [protein=NAD(+) diphosphatase] [protein\_id=WP\_002884327.1] [location=complement(4744345..4745118)] [gbkey=CDS]

MDRIIEKLDRGWWVVSHEQKLWLPGGELPHGEAVNFDLVGQHALHIGEWQGESVWMVRQDRRHDMGSLRQ

VLDQDPGLFQLAGRGIQLAEFYRSHKFCGYCGHPMHASKSEWAMLCSHCRERYYPQIAPCIIVAIRRDDA

ILLAQHTRHRNGVHTVLAGFVEVGETLEQAVAREVMEESGIRVKNLRYVTSQPWPFPQSLMTAFMADYAD

GEIVVDKKELLTADWYRYDDLPLLPPPGTVARRLIEDTVAMCRAEFE

>lcl|NZ\_FO834906.1\_prot\_WP\_002884324.1\_4535 [locus\_tag=BN49\_RS24520] [protein=Rsd/AlgQ family anti-sigma factor] [protein\_id=WP\_002884324.1] [location=4745212..4745709] [gbkey=CDS]

MLNQLENLTERVGGSNELVDRWLQVRKHLLVAYYNLVGLKPGKESFMRLNEKALDDFCQSLVDYLSSGHF

SIYERIIGEMEGDTPLLAATRLYPQLEANTQQMMDYYDTCLENAIDHDNYLEFQQALSDIGESLEARFAL

EDKLIALAVAHNLSNDVRDNIAPTA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043856.1\_4536 [gene=thiC] [locus\_tag=BN49\_RS24525] [protein=phosphomethylpyrimidine synthase ThiC] [protein\_id=WP\_046043856.1] [location=4745972..4747867] [gbkey=CDS]

MSTTKLTRREQREHAQQFIDTLAGTAFPNSRRIYVHGSQADIRVPMREIQLSPTLVGGDKDNPRYETNEP

IPVYDTSGPYGDPDISIDVRQGLAKLRQPWIDARNDCAPLSERSSAYTKARLADDGLDELRFSGLLTPKR

AVVGKCVTQLHYARQGIVTPEMEFIAIRENMGRERIRSEVLRQQHAGEGFGAHLPENITPEFVRDEVAAG

RAIIPANINHPESEPMIIGRNFLVKVNANIGNSAVTSSIEEEVEKLVWSTRWGADTVMDLSTGRYIHETR

EWILRNSPVPIGTVPIYQALEKVNGIAENLTWQVFRDTLLEQAEQGVDYFSIHAGVLLRYVPMTAKRLTG

IVSRGGSIMAKWCLSHHQENFLYQHFREICEICAAYDVSLSLGDGLRPGSIQDANDEAQFSELRTLGELT

KIAWEYDVQVMIEGPGHVPMQMIRRNMTEQLEHCHEAPFYTLGPLTTDIAPGYDHFTSGIGAAMIGWFGC

AMLCYVTPKEHLGLPNKEDVKQGLITYKIAAHAADLAKGHPGAQIRDNAMSKARFEFRWEDQFNLALDPF

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A

>lcl|NZ\_FO834906.1\_prot\_WP\_004152310.1\_4537 [gene=thiE] [locus\_tag=BN49\_RS24530] [protein=thiamine phosphate synthase] [protein\_id=WP\_004152310.1] [location=4747867..4748502] [gbkey=CDS]

MYQPDFPPVPFRLGLYPVVDSVAWIERLLEAGVRTLQLRIKDRRDSEVEDDVIAAIALGRRYHARLFIND

YWQLAIKHQAYGVHLGQEDLETTDLSAIRQAGLRLGVSTHDDMEIDVALAARPSYIALGHVFPTQTKQMP

SAPQGLEQLARHIQRLADYPTVAIGGISLEKAPGVLATGVGSIAVVSAITQAADWRAATDQLLALAGAGD

E

>lcl|NZ\_FO834906.1\_prot\_WP\_004177871.1\_4538 [gene=thiF] [locus\_tag=BN49\_RS24535] [protein=thiazole biosynthesis adenylyltransferase ThiF] [protein\_id=WP\_004177871.1] [location=4748495..4749250] [gbkey=CDS]

MNDHDFMRYSRQLLLEDIAIEGQQKLLASRVLIIGLGGLGSPAALYLAGAGVGTLTLADDDAVHLSNLQR

QILFTSADIDRPKAAAAQTRLSQLNPQIKLVALQQRLSGEALRAEVAKADVVLDCTDNMVTRQAINAACV

ALDTPLVTASAVGFGGQLMVLTPPWTQGCYRCLWPESDEPQRNCRTAGIVGPVVGMMGTLQALETIKLLS

GMATPRNTLRLFDARTSNWRALALQRSRSCPVCGGRHADLV

>lcl|NZ\_FO834906.1\_prot\_WP\_002884183.1\_4539 [gene=thiS] [locus\_tag=BN49\_RS24540] [protein=sulfur carrier protein ThiS] [protein\_id=WP\_002884183.1] [location=4749234..4749434] [gbkey=CDS]

MQIWFNDEPLACADNLSVSALLTQLEQQQPGVALALNQHILPRDRWEDHLLQEGDRVLLFQVIAGG

>lcl|NZ\_FO834906.1\_prot\_WP\_004146302.1\_4540 [gene=thiG] [locus\_tag=BN49\_RS24545] [protein=thiazole synthase] [protein\_id=WP\_004146302.1] [location=4749436..4750206] [gbkey=CDS]

MLRIADKTFESHLFTGTGKFAAPEVMVEAIRASGSQLVTLAMKRVDLRQRNDAILAPLLAAGVSLLPNTS

GAKTAEEAVFAARLAREALGTHWLKLEIHPDARWLLPDPIETLKAAELLVREGFVVLPYCGADPVLCKRL

EEVGCAAVMPLGAPIGSNQGLETKAMLEIIIEQATVPVVVDAGIGVPSHAAQALEMGADAVLVNTAIAVA

DDPVAMARAFRMAIDAGLLARQAGPGARSTQAQATSPLTGFLEALA

>lcl|NZ\_FO834906.1\_prot\_WP\_004212852.1\_4541 [gene=thiH] [locus\_tag=BN49\_RS24550] [protein=2-iminoacetate synthase ThiH] [protein\_id=WP\_004212852.1] [location=4750203..4751336] [gbkey=CDS]

MKTFSDRWRQLEWDDIRLRINSKTAADVERALAAKQLTRDDMMALLSPAAANYLEPLAQRAQRLTRQRFG

NTVSFYVPLYLSNLCANDCTYCGFSMSNRIKRKTLDAAEIARECAAIRNLGFEHLLLVTGEHQGKVGMDY

FRRHLPAIRSQFASLHMEVQPLATEEYAELKTLGLDGVMVYQETYHESMYAQHHLKGKKQDFFWRLDTPD

RLGAAGIDKIGLGALIGLSDSWRVDCFIVAEHLLWLQQRYWRSRYSVSFPRLRPCAGGIEPASLMDERQL

VQTICAFRLLAPEVELSLSTRESPWFRDRVIPLAINNVSAFSKTQPGGYADDHPELEQFAPHDDRRPEEV

ASALAARGLQPVWKDWDSWLGRASQTS

>lcl|NZ\_FO834906.1\_prot\_WP\_016530055.1\_4542 [locus\_tag=BN49\_RS24560] [protein=sensor domain-containing diguanylate cyclase] [protein\_id=WP\_016530055.1] [location=4751653..4753185] [gbkey=CDS]

MALHNRKLSFTTPIVVGFAGILLSFMLIAIFVTLAQQKDFLEDYHDINRNFTHNLAINYTETLLRENDFI

LGRAAAFFARNDELNRAVNVEPEKGLTTLMQLQNMMPSVSSISLADTKGHYLRAPEVLENEDSRAFDPKT

RPWFIKQAEASTFSHYTSPYMDYFTHHPTITIFKPIITPEGKLKGSLAFHLDLTSMGFALRQMVAPVQGE

FFVVQRDGKVVLHSDPGALFKPFVRDELMDKMTSGEGQLYDPGSDTWYYHYSFTNPDWFVIFRVDNATLV

NLTRHETNLVIGGFTLAAIIIILFGLYLRHASRTVLMNIINAIKTGDVKRAPRLEAMLSKAIETNKQREL

SYVRQATIDALTGCKNRRAFDSDIAALMNDHQPFALALVDIDNFKSINDTWGHLNGDIVLRNVAREGLQV

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SVDEALYKAKQQGKNRILRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002884150.1\_4543 [locus\_tag=BN49\_RS24565] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_002884150.1] [location=4753358..4753663] [gbkey=CDS]

MKNIVLCCAAGMSTSMLVQRMQDAAQKKGVEVSIKAVPVAEFKDNLAAADIILLGPQVKYEQAKLQALAD

PFGKKVAVIDMMDYGMMKGDAVLDKALKMLE

>lcl|NZ\_FO834906.1\_prot\_WP\_004212847.1\_4544 [locus\_tag=BN49\_RS24570] [protein=PTS lactose/cellobiose transporter subunit IIA] [protein\_id=WP\_004212847.1] [location=4753667..4753984] [gbkey=CDS]

MEDLETIIMELLVNAGSARSAALTALQLARKGDFAAAEQAMAESHEFVKHAHKIQTQLIGMDEGSGKLPV

NLITVHSQDHLMNAMVIQDLATDMIELYRRLPLAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530058.1\_4545 [locus\_tag=BN49\_RS24575] [protein=anaerobic C4-dicarboxylate transporter] [protein\_id=WP\_016530058.1] [location=complement(4754027..4755367)] [gbkey=CDS]

MEFAIQLIIILICLFYGARKGGIALGLLGGIGLVILVFVFHLQPGKPPVDVMLVIIAVVAASATLQASGG

LDVMLQIAEKLLRRNPKYVSIVAPFVTCTLTILCGTGHVVYTILPIIYDVAIKNNIRPERPMAASSIGAQ

MGIIASPVSVAVVSLVAMLGNFTFNGKHLEFLDLLAITIPSTLLGILAIGIFSWFRGKDLDQDEAFQAFI

ALPENRHYVYGDTATLLDKNLPTSNWIAMWIFLASIAVVALLGAFSELRPAFDGKPLSMVLVIQMFMLLS

GALIIIITKTNPASISKNEVFRSGMIAIVAVYGIAWMAETMFGAHMTEIKGVLGEMVKEYPWAYAIVLLL

VSKFVNSQAAALAAIVPVALAIGVDPAYIVASAPACYGYYILPTYPSDLAAIQFDRSGTTHIGRFVINHS

FILPGLIGVGVSCVFGWVFAAMYGFL

>lcl|NZ\_FO834906.1\_prot\_WP\_002884146.1\_4546 [gene=rpoC] [locus\_tag=BN49\_RS24580] [protein=DNA-directed RNA polymerase subunit beta'] [protein\_id=WP\_002884146.1] [location=complement(4755768..4759991)] [gbkey=CDS]

MKDLLKFLKAQTKTEEFDAIKIALASPDMIRSWSFGEVKKPETINYRTFKPERDGLFCARIFGPVKDYEC

LCGKYKRLKHRGVICEKCGVEVTQTKVRRERMGHIELACPTAHIWFLKSLPSRIGLLLDMPLRDIERVLY

FESYVVIEGGMTNLERNQILTEEQYLDALEEFGDEFDAKMGAEAIQALLRNMDLEQECEQLREELNETNS

ETKRKKLTKRIKLLEAFVQSGNKPEWMILTVLPVLPPDLRPLVPLDGGRFATSDLNDLYRRVINRNNRLK

RLLDLAAPDIIVRNEKRMLQEAVDALLDNGRRGRAITGSNKRPLKSLADMIKGKQGRFRQNLLGKRVDYS

GRSVITVGPYLRLHQCGLPKKMALELFKPFIYGKLELRGLATTIKAAKKMVEREEAVVWDILDEVIREHP

VLLNRAPTLHRLGIQAFEPVLIEGKAIQLHPLVCAAYNADFDGDQMAVHVPLTLEAQLEARALMMSTNNI

LSPANGEPIIVPSQDVVLGLYYMTRDSVNAKGEGMVLTGPKEAERIYRAGLASLHARVKVRITEYEKDDN

GEFVAKTSLKDTTVGRAILWMIVPKGLPFSIVNQALGKKAISKMLNTCYRILGLKPTVIFADQTMYTGFA

YAARSGASVGIDDMVIPEKKYEIISEAEAEVAEIQEQFQSGLVTAGERYNKVIDIWAAANDRVSKAMMDN

LQTETVINRDGQEEQQVSFNSIYMMADSGARGSAAQIRQLAGMRGLMAKPDGSIIETPITANFREGLNVL

QYFISTHGARKGLADTALKTANSGYLTRRLVDVAQDLVVTEDDCGTLEGITMTPVIEGGDVKEPLRDRVL

GRVTAEDVLKPGTADILVPRNTLLHEHWCDLLEANSVDSVKVRSVVSCDTDFGVCAHCYGRDLARGHLIN

KGEAIGVIAAQSIGEPGTQLTMRTFHIGGAASRAAAESSIQVKNKGSIKLSNAKSVVNSSGKLVITSRNT

ELKLIDEFGRTKESYKVPYGAVMAKGDGEQVAGGETVANWDPHTMPVITEVSGFIRFTDMIDGQTITRQT

DELTGLSSLVVLDSAERTAGGKDLRPALKIVDAQGNDVLIPGTDMPAQYFLPGKAIVQLEDGVQISSGDT

LARIPQESGGTKDITGGLPRVADLFEARRPKEPAILAEISGIISFGKETKGKRRLVITPVDGSEPYEEMI

PKWRQLNVFEGERVERGDVVSDGPEAPHDILRLRGVHAVTRYIVNEVQDVYRLQGVKINDKHIEVIVRQM

LRKATIESAGSSDFLEGEQVEYSRVKIANRELEANGKVGATFSRDLLGITKASLATESFISAASFQETTR

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LGGSDND

>lcl|NZ\_FO834906.1\_prot\_WP\_046043859.1\_4547 [gene=rpoB] [locus\_tag=BN49\_RS24585] [protein=DNA-directed RNA polymerase subunit beta] [protein\_id=WP\_046043859.1] [location=complement(4760068..4764096)] [gbkey=CDS]

MVYSYTEKKRIRKDFGKRPQVLDVPYLLSIQLDSFQKFIEQDPEGQYGLEAAFRSVFPIQSYSGNSELQY

VSYRLGEPVFDVKECQIRGVTYSAPLRVKLRLVIYEREAPEGTVKDIKEQEVYMGEIPLMTDNGTFVING

TERVIVSQLHRSPGVFFDSDKGKTHSSGKVLYNARIIPYRGSWLDFEFDPKDNLFVRIDRRRKLPATIIL

RALNYTTEQILDLFFEKVVFEIRDNKLQMELIPERLRGETASFDIEANGKVYVEKGRRITARHIRQLEKD

DIKHIEVPVEYIAGKVAAKDYIDEATGELICPANMELSLDLLAKLSQSGHKRIETLFTNDLDHGPYISET

VRVDPTNDRLSALVEIYRMMRPGEPPTREAAESLFENLFFSEDRYDLSAVGRMKFNRSLLRDEIEGSGIL

SKDDIIEVMKKLIDIRNGKGEVDDIDHLGNRRIRSVGEMAENQFRVGLVRVERAVKERLSLGDLDTLMPQ

DMINAKPISAAVKEFFGSSQLSQFMDQNNPLSEITHKRRISALGPGGLTRERAGFEVRDVHPTHYGRVCP

IETPEGPNIGLINSLSVYAQTNEYGFLETPYRKVTNGVVTDEIHYLSAIEEGNYVIAQANSNLDENGHFV

EDLVTCRSKGESSLFSRDQVDYMDVSTQQVVSVGASLIPFLEHDDANRALMGANMQRQAVPTLRADKPLV

GTGMERAVAVDSGVTAVAKRGGTVQYVDASRIVIKVNEDEMYPGEAGIDIYNLTKYTRSNQNTCINQMPC

VSLGEPIERGDVLADGPSTDLGELALGQNMRVAFMPWNGYNFEDSILVSERVVQEDRFTTIHIQELACVS

RDTKLGPEEITADIPNVGEAALSKLDESGIVYIGAEVTGGDILVGKVTPKGETQLTPEEKLLRAIFGEKA

SDVKDSSLRVPNGVSGTVIDVQVFTRDGVEKDKRALEIEEMQLKQAKKDLSEELQILEAGLFSRIYAVLV

SGGVEAEKLDKLPRDRWLELGLTDEEKQNQLEQLAEQYDELKHEFEKKLEAKRRKITQGDDLAPGVLKIV

KVYLAVKRRIQPGDKMAGRHGNKGVISKINPIEDMPHDANGTPVDIVLNPLGVPSRMNIGQILETHLGMA

AKGIGDKINAMLKQQQEVAKLREFIQRAYDLGADVRQKVDLNTFSDEEVLRLAENLRKGMPIATPVFDGA

KESEIKELLQLGDLPTSGQITLFDGRTGEQFERPVTVGYMYMLKLNHLVDDKMHARSTGSYSLVTQQPLG

GKAQFGGQRFGEMEVWALEAYGAAYTLQEMLTVKSDDVNGRTKMYKNIVDGNHQMEPGMPESFNVLLKEI

RSLGINIELEDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002884142.1\_4548 [gene=rplL] [locus\_tag=BN49\_RS24590] [protein=50S ribosomal protein L7/L12] [protein\_id=WP\_002884142.1] [location=complement(4764421..4764786)] [gbkey=CDS]

MSITKDQIIEAVSAMSVMDVVELISAMEEKFGVSAAAAVAVAAGPVEAAEEKTEFDVILKAAGANKVAVI

KAVRGATGLGLKEAKDLVESAPAALKEGISKDDAEALKKSLEEAGAEVEVK

>lcl|NZ\_FO834906.1\_prot\_WP\_001207203.1\_4549 [gene=rplJ] [locus\_tag=BN49\_RS24595] [protein=50S ribosomal protein L10] [protein\_id=WP\_001207203.1] [location=complement(4764853..4765350)] [gbkey=CDS]

MALNLQDKQAIVAEVSEVAKGALSAVVADSRGVTVDKMTELRKAGREAGVYMRVVRNTLLRRVVEGTQFE

CLKDTFVGPTLIAYSMEHPGAAARLFKEFAKANAKFEVKAAAFEGELIPASQIDRLATLPTYEEAIARLM

ATMKEASAGKLVRTLAAVRDAKEAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002884036.1\_4550 [gene=rplA] [locus\_tag=BN49\_RS24600] [protein=50S ribosomal protein L1] [protein\_id=WP\_002884036.1] [location=complement(4765764..4766468)] [gbkey=CDS]

MAKLTKRMRVIREKVDATKQYDINEAIALLKELATAKFTESVDVAVNLGIDARKSDQNVRGATVLPHGTG

RSVRVAVFTQGANAEAAKAAGAELVGMEDLAEQIKKGEMNFDVVIASPDAMRVVGQLGQVLGPRGLMPNP

KVGTVTPNVAEAVKNAKAGQVRYRNDKNGIIHTTIGKVDFDADKLKENLEALLVALKKAKPTQAKGVYIK

KVSISTTMGAGVAVDQAGLNASAN

>lcl|NZ\_FO834906.1\_prot\_WP\_002884034.1\_4551 [gene=rplK] [locus\_tag=BN49\_RS24605] [protein=50S ribosomal protein L11] [protein\_id=WP\_002884034.1] [location=complement(4766472..4766900)] [gbkey=CDS]

MAKKVQAYVKLQVAAGMANPSPPVGPALGQQGVNIMEFCKAFNAKTDSLEKGLPIPVVITVYADRSFTFV

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ED

>lcl|NZ\_FO834906.1\_prot\_WP\_016529936.1\_4552 [gene=nusG] [locus\_tag=BN49\_RS24610] [protein=transcription termination/antitermination protein NusG] [protein\_id=WP\_016529936.1] [location=complement(4767057..4767602)] [gbkey=CDS]

MSEAPKKRWYVVQAFSGFEGRVATSLREHIKLHNMEELFGEVMVPTEEVVEIRGGQRRKSERKFFPGYVL

VQMVMNDASWHLVRSLPRVMGFIGGTSDRPAPISDKEVDAIMNRLQQVGDKPRPKTLFEPGEMVRVNDGP

FADFNGVVEEVDYEKSRLKVSVSIFGRATPVELDFSQVEKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883772.1\_4553 [gene=secE] [locus\_tag=BN49\_RS24615] [protein=preprotein translocase subunit SecE] [protein\_id=WP\_002883772.1] [location=complement(4767604..4767987)] [gbkey=CDS]

MSANTEAQGSGRGLEAMKWIIVAVLLIVAIVGNFLYRDIMLAVRALAVVILIAAAGGVALLTTKGKATVA

FAREARTEVRKVIWPTRQETLHTTLIVAAVTAVMSLILWGLDGILVRLVSFITGLRF

>lcl|NZ\_FO834906.1\_prot\_WP\_004174069.1\_4554 [gene=tuf] [locus\_tag=BN49\_RS24620] [protein=elongation factor Tu] [protein\_id=WP\_004174069.1] [location=complement(4768324..4769508)] [gbkey=CDS]

MSKEKFERTKPHVNVGTIGHVDHGKTTLTAAITTVLAKTYGGSARAFDQIDNAPEEKARGITINTSHVEY

DTPTRHYAHVDCPGHADYVKNMITGAAQMDGAILVVAATDGPMPQTREHILLGRQVGVPYIIVFLNKCDM

VDDEELLELVEMEVRELLSQYDFPGDDTPIVRGSALKALEGDAEWEAKIIELAGHLDTYIPEPERAIDKP

FLLPIEDVFSISGRGTVVTGRVERGIIKVGEEVEIVGIKETAKTTCTGVEMFRKLLDEGRAGENVGVLLR

GIKREEIERGQVLAKPGTINPHTKFESEVYILSKDEGGRHTPFFKGYRPQFYFRTTDVTGTIELPEGVEM

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>lcl|NZ\_FO834906.1\_prot\_WP\_002883524.1\_4555 [gene=coaA] [locus\_tag=BN49\_RS24645] [protein=type I pantothenate kinase] [protein\_id=WP\_002883524.1] [location=4770494..4771444] [gbkey=CDS]

MSQKEQTLMTPYLQFNRHQWAALRDSVPMTLTEEEITRLKGINEDLSLEEVAEIYLPLSRLLNFYISSNL

RRQAVLEQFLGTNGQRIPYIISIAGSVAVGKSTTARVLQALLSRWPEHRHVELITTDGFLHPNSVLKERG

LMKKKGFPQSYDMHRLVKFVSDLKSGVPQATAPVYSHLIYDVIPNGDKTVAQPDILILEGLNVLQSGMDY

PHDPHHVFVSDFVDFSIYVDAPEELLKSWYINRFLKFREGAFTDPDSYFHNYAKLSKEEAVDIATSLWNE

INLMNLKENILPTRERASLIMTKSANHSVNQVRLRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883521.1\_4556 [gene=birA] [locus\_tag=BN49\_RS24650] [protein=bifunctional biotin--[acetyl-CoA-carboxylase] ligase/biotin operon repressor BirA] [protein\_id=WP\_002883521.1] [location=complement(4771470..4772432)] [gbkey=CDS]

MKDHTIPLTLISILADGEFHSGEQLGEQLGMSRAAINKHIQTLRDWGVDVFTVPGKGYSLPEPIHLLDEK

KISQEIDHGRVTVLPVIDSTNQYLLDRLDELTSGDACVAEYQQAGRGRRGRKWFSPFGANLYLSMYWRLE

QGPAAAIGLSLVIGIVIAEVLQQLGAEQVRVKWPNDIYLQDRKLSGILVELTGKTGDAAQIVSGAGINLV

MRRVESDVVNQGWISLQEAGVVIDRNLLAARLIKELRLGLELFEQEGLAPYLPRWEKLDNFIHRPVKLII

GDKEIYGISRGIDAQGALLLEQDGVIKAWVGGEISLRSAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004177874.1\_4557 [gene=murB] [locus\_tag=BN49\_RS24655] [protein=UDP-N-acetylmuramate dehydrogenase] [protein\_id=WP\_004177874.1] [location=complement(4772429..4773457)] [gbkey=CDS]

MNHSLKPWNTFGIERFAKTIVRAETEQQLLSAWQTAAAAGEPTLILGEGSNVLFLNDYAGTVILNRIMGI

EVSETPEAWRLHVGAGENWHQLVQFTLQHAMPGLENLALIPGCAGSSPIQNIGAYGVELQRVCEYVDCIE

LETGRKQRLSAAECRFGYRDSIFKHEYQDRYAIVAIGLSLAKTWQPVLSYGDLTRLDPQTVTPQQVFDAV

CHMRMTKLPDPKINGNAGSFFKNPIVSAQVAKALLAQFPHAPHYPQANGSVKLAAGWLIDQCELKGQRIG

GAAVHRQQALVLINEDRATSEDVVKLAHYVRQRVGAKFDVWLQPEVRFIGTHGEVNAEESIA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883453.1\_4558 [gene=hemG] [locus\_tag=BN49\_RS24685] [protein=menaquinone-dependent protoporphyrinogen IX dehydrogenase] [protein\_id=WP\_002883453.1] [location=complement(4779275..4779808)] [gbkey=CDS]

MKTLILFSTRDGQTREIASFLASELKELGIDADTLNLNRTDVVEWHHYDRVVIGASIRYGHFHPAVDRFV

KKHLAALQALPGAFFSVNLVARKPEKRTPQTNSYTRKFLLNSPWQPQSCAVFAGALRYPRYSWYDRFMIR

LIMKMTGGETDTRKEVVYTDWQQVSRFAREIAQMARK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883450.1\_4559 [gene=trkH] [locus\_tag=BN49\_RS24690] [protein=Trk system potassium transporter TrkH] [protein\_id=WP\_002883450.1] [location=complement(4779820..4781271)] [gbkey=CDS]

MHFRAITRIVGLLVILFSGTMIVPGLVALIYRDGAGRAFTQTFFVALAIGSMLWWPNRKQKGELKSREGF

LIVVLFWTVLGSVGALPFIFSEQPNLTVTDAFFESFSGLTTTGATTLVGLDSLPHAILFYRQMLQWFGGM

GIIVLAVAILPILGVGGMQLYRAEMPGPLKDNKMRPRIAETAKTLWLIYVLLTIACALALWFAGMPAFDA

IGHSFATIAIGGFSTHDASVGYFNSPMINSIIAIFLLISGCNYGLHFSLLSGRSLKVYWRDPEFRMFIGV

QLTLVIVCTLVLWLHNVYGSVLTTLNQAFFQVVSMATTAGFTTDSIARWPLFLPVLLLCSAFIGGCAGST

GGGLKVIRILLLFKQGNRELKRLVHPNAVYSIKLGNRALPERILEAVWGFFSAYALVFIISMLAIIATGV

DDFSAFASVVATLNNLGPGLGVVADNFATMNPVAKWILIANMLFGRLEVFTLLVLFTPTFWRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002883449.1\_4560 [locus\_tag=BN49\_RS24695] [protein=IMPACT family protein] [protein\_id=WP\_002883449.1] [location=complement(4781310..4781924)] [gbkey=CDS]

MESWLIPAAPVTVVEEIKKSRFITLLAHTDGVAAAKAFVESVRADHPDARHHCVAWVAGPPDDSQQLGFS

DDGEPAGTAGKPMLAQLMGSGVGEITAVVVRYYGGILLGTGGLVKAYGGGVHQALAQLTTLRKTPLTAYT

LQCEYGQLAGVEALLAQFSGNVVESEYLASVRLRVALPQAEVAAFSARLADFSRGSLQLLKINE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150459.1\_4561 [gene=pepQ] [locus\_tag=BN49\_RS24700] [protein=Xaa-Pro dipeptidase] [protein\_id=WP\_004150459.1] [location=complement(4781924..4783255)] [gbkey=CDS]

MESLAALYKNHIVTLQERTRDVLARFQMDALLIHSGELVNVFLDDHPYPFKVNPQFKAWVPVTQVPNCWL

LVDGVNKPKLWFYLPVDYWHNVEPLPTSFWTEEIDVIALPKADGIGSQLPAARGNIGYIGPVPERALGLG

IAADKINPKGVIDYLHYYRAYKTDYELACMREAQKSAVNGHRAAYEAFQSGMSEFDINQAYLTATGHRDT

DVPYSNIVALNEHASVLHYTKLDHRAPAEMRSFLLDAGAEYNGYAADLTRTWAAHGDNDFAHLIKDVNDE

QLALISTMKAGTSYIDYHIQFHQRIAKLLRKHQLVTDMSEEAMVENDLTGPFMPHGIGHPLGLQVHDVAG

FMQDDTGTHLAAPSKYPYLRCTRIIEPRMVLTIEPGIYFIESLLAPWREGPFSKHFNWQKIDAMKPFGGI

RIEDNVVVHENSIENMTRDLKLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004213300.1\_4562 [gene=fadB] [locus\_tag=BN49\_RS24705] [protein=fatty acid oxidation complex subunit alpha FadB] [protein\_id=WP\_004213300.1] [location=4783447..4785636] [gbkey=CDS]

MLYKGDTLYLDWLEDGIAELVFDAPGSVNKLDTATVASLGHALDVLEKQSDLKGLLLRSEKAAFIVGADI

TEFLSLFLVPEEQLSQWLHFANSVFNRLEDLPVPTISAVNGYALGGGCECVLATDYRLATPDLRIGLPET

KLGIMPGFGGSVRLPRLLGADSALEIIAAGKDVGADQALKIGLVDGVVAAEKLRDGALAILRQAMNGDLD

WKAKRQPKLEPLKLSKIEAAMSFTIAKGMVAQTAGKHYPAPITAVKTIEAAARLGREEALVLENKSFVPL

AHTNEARALVGIFLNDQYVKAKAKKLTKDVETPKHAAVLGAGIMGGGIAYQSAWKGVPVVMKDISDKSLT

LGMTEAAKLLNKQLERGKIDGLKLAGVISTIQPTLEYSGFDRVDVVVEAVVENPKVKKAVLAETETKVRP

DTVLASNTSTIPISELASVLQRPENFCGMHFFNPVHRMPLVEVIRGEKTSDNTIAKVVAWASKMGKTPIV

VNDCPGFFVNRVLFPYFAGFSQLLRDGADFRKVDKVMEKQFGWPMGPAYLLDVVGIDTAHHAQAVMAAGF

PQRMQKDYRDAIDALFDANRFGQKNGLGFWRYKDDSKGKPKKEEDAAVDSLLADVSQSKRDFSDEEIIAR

MMIPMVNEVVRCLEEGIIASPAEADMALVYGLGFPPFHGGAFRWLDTIGSAKYLDMAQQYQHLGPLYEVP

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043864.1\_4563 [gene=fadA] [locus\_tag=BN49\_RS24710] [protein=acetyl-CoA C-acyltransferase FadA] [protein\_id=WP\_046043864.1] [location=4785646..4786809] [gbkey=CDS]

MEQVVIVDAIRTPMGRSKGGAFRHVRAEDLSAHLMRSLLSRNPSLEASAIDDIYWGCVQQTLEQGFNIAR

NAALLAEIPHSVPANTVNRLCGSSMQALHDAARMIMTGDASVCLIGGVEHMGHVPMSHGVDFHPGLSRNV

AKAAGMMGLTAEMLARLHDISREMQDQFAARSHARAWAATQSGAFKAEIIPTGGHDADGVLKSFNYDEVI

RPETTVETLSTLKPAFDPVTGTVTAGTSSALSDGAAAMLLMSESRARELGLKPRARVRSMAVVGCDPSIM

GYGPVPASKLALKKAGLSTSDIDVFEMNEAFAAQILPCIKDLGLMEQIDEKINLNGGAIALGHPLGCSGA

RISTTLINQMERKDAQFGLATMCIGLGQGIATVFERV

>lcl|NZ\_FO834906.1\_prot\_WP\_002883448.1\_4564 [gene=fre] [locus\_tag=BN49\_RS24715] [protein=NAD(P)H-flavin reductase] [protein\_id=WP\_002883448.1] [location=complement(4786916..4787617)] [gbkey=CDS]

MTTLSCKVTSVEAITDTVYRVRLVPEAAFSFRAGQYLMVVMDERDKRPFSMASTPAEQEFIELHIGASEL

NLYAMAVMDRILKEREIEVDIPHGEAWLRDDEDRPLILIAGGTGFSYVRSILLSALARNPDRDIAIYWGG

REAKHLYDLAELEALSIKHPNLRIEPVVEQPEEGWRGRSGTVLTAVLQDYGTLAEHDIYIAGRFEMAKIA

RDLFCNERGAREDRLFGDAFAFI

>lcl|NZ\_FO834906.1\_prot\_WP\_009309755.1\_4565 [gene=ubiD] [locus\_tag=BN49\_RS24720] [protein=4-hydroxy-3-polyprenylbenzoate decarboxylase] [protein\_id=WP\_009309755.1] [location=complement(4787667..4789142)] [gbkey=CDS]

MKYHDLRDFLTLLEQQGELKRITLPVDPHLEITEIADRTLRAGGPALLFENPKGYTMPVLCNLFGTPRRV

ALGMGQEDVSSLREVGKLLAFLKEPEPPKGFRDLFDKLPQFKQVLNMPTKRLRGAPCQQKIIQGDDVDLN

KIPIMTCWPEDAAPLITWGLTVTRGPHKERQNLGIYRQQLIGKNKLIMRWLSHRGGALDFQEWCAARPGE

RFPVSVALGADPATILGAVTPVPDTLSEYAFAGLLRGTKTEVVKCVSNDLEVPASAEIVLEGYIEAGEMA

PEGPYGDHTGYYNEVDQFPVFTVTHITQREDAIYHSTYTGRPPDEPAVLGVALNEVFVPILQKQFPEIVD

FYLPPEGCSYRLAVVTMKKQYAGHAKRVMMGVWSFLRQFMYTKFVIVCDDDVNARDWNDVIWAITTRMDP

ARDTVLVENTPIDYLDFASPVSGLGSKMGLDATNKWPGETQREWGRPIKKDPAVTARIDAIWDELAIFKQ

Q

>lcl|NZ\_FO834906.1\_prot\_WP\_002883430.1\_4566 [gene=rfaH] [locus\_tag=BN49\_RS24730] [protein=transcription/translation regulatory transformer protein RfaH] [protein\_id=WP\_002883430.1] [location=4789321..4789809] [gbkey=CDS]

MQAWYLLYCKRGQLQRAQEHLERQSVNCLMPTIALEKIIRGKRTMVSEPLFPNYLFIEFDPEVIHTTTIS

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LLLNLLNKQVLQSVKNTDFQKI

>lcl|NZ\_FO834906.1\_prot\_WP\_004146458.1\_4567 [gene=tatD] [locus\_tag=BN49\_RS24735] [protein=3'-5' ssDNA/RNA exonuclease TatD] [protein\_id=WP\_004146458.1] [location=complement(4789806..4790609)] [gbkey=CDS]

MGAIMFDIGVNLTSSQFSRDHDEVVARALAAGVNGMLLTGTNLAESQQAQKLASRYSGCWSTAGVHPHDG

SSWTPAVAEAIYTLAGEPQVVAIGECGLDFNRNFSTPHEQEVAFSAQLALAAELSMPVFLHCRDAHDRFL

TLLKPWLEKIPGAVLHCFTGSRSEVQECLDLGLFIGITGWVCDERRGLELRELLPAIPAERLLLETDAPY

LLPRDLKPKPASRRNEPAYLPHILASVAAWRGEEAQWLEAQTDANVRALFGVDINGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002883427.1\_4568 [gene=tatC] [locus\_tag=BN49\_RS24740] [protein=Sec-independent protein translocase subunit TatC] [protein\_id=WP\_002883427.1] [location=complement(4790642..4791421)] [gbkey=CDS]

MGVDDTQPLISHLIELRKRLLNSIIAILVIFLALVYFANDIYQLVSAPLISKMPVGATMIATDVASPFFT

PIKLTFMVSVILSVPIILYQVWAFVAPALYKHERRLVVPLLVSSTLLFYIGMAFAYFVVFPLAFGFLTHA

APEGVLVSTDIRSYLDFVMALFMAFGVSFEVPVAIVLLCWMGVTTPEDLRKKRPYVLVGAFVVGMLLTPP

DVFSQTLLAIPMYCLFEVGVFFARFYTGKRLTRDDDAAAEAEAAEHREE

>lcl|NZ\_FO834906.1\_prot\_WP\_016532478.1\_4569 [gene=tatB] [locus\_tag=BN49\_RS24745] [protein=Sec-independent protein translocase protein TatB] [protein\_id=WP\_016532478.1] [location=complement(4791424..4791960)] [gbkey=CDS]

MFDIGFSELLLVFVIGLIVLGPQRLPVAVKTVVGWIRTLRSLATTVQNELAQELKLQEFQESLKKVEKAS

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APEPVADEQSASPADLQAEKTSATAAVPHSSPASSDKP

>lcl|NZ\_FO834906.1\_prot\_WP\_002883425.1\_4570 [gene=tatA] [locus\_tag=BN49\_RS24750] [protein=Sec-independent protein translocase subunit TatA] [protein\_id=WP\_002883425.1] [location=complement(4791964..4792215)] [gbkey=CDS]

MGGISIWQLLIVVVIVVLLFGTKKLSSLGSDLGASIKGFKKAMSDDDKPEKSAPDADFTAKTIADKQDDA

KKDETKRHDKEQV

>lcl|NZ\_FO834906.1\_prot\_WP\_002883424.1\_4571 [gene=ubiB] [locus\_tag=BN49\_RS24755] [protein=ubiquinone biosynthesis regulatory protein kinase UbiB] [protein\_id=WP\_002883424.1] [location=complement(4792345..4793985)] [gbkey=CDS]

MTPGELRRLYFIIHTFLSYGLDELIPKMRITLPLRIWRRMLFWMPNRHQDQPLGARLRLALQELGPVWIK

FGQMLSTRRDLFPPHIADQLALLQDRVAPFEGKLAQQQIEKAMGGLPVETWFDDFSVEPLASASIAQVHT

ARLKENGKEVVIKVIRPDILPIIKADMKLIYRLARWVPRLLPDGRRLRPQEVVREYEKTLLDELNLLRES

ANAIQLRRNFEDSPMLYVPEVYPDYCSESMMVMERIYGIPVSDVEALEAQGTNMQLLAERGVQVFFTQVF

RDSFFHADMHPGNIFVSYEHPEDPQYIGIDCGIVGSLNKEDKRYLAENFIAFFNRDYRKVAELHVDSGWV

PPDTNVEEFEFAIRTVCEPIFEKPLAEISFGHVLLNLFNTARRFNMEVQPQLVLLQKTLLYVEGVGRQLY

PQLDLWKTAKPFLESWIKDQVGIPALVRAFKDKAPFWIERMPEIPELVYQSLQQSKQLQTSVDTIVRDMR

VRHVRQGQSRYLFGIGAVLLLSGTLLFIHRPEWGMMPGWLMAGGVVTWLIGWRKTH

>lcl|NZ\_FO834906.1\_prot\_WP\_016532477.1\_4572 [locus\_tag=BN49\_RS24760] [protein=SCP2 domain-containing protein] [protein\_id=WP\_016532477.1] [location=complement(4793982..4794587)] [gbkey=CDS]

MPFTPLVTAGIETALNTFLWRDKALKPARQRLLGKVLRVQLQDFATPVVLVFSERQVDVLSSWDGEADCT

VITRLSVLPKLRNRQQLTALIRSGDLEVQGDLQVVQNMVSLCDLAEFDPAELLAPYTGDIVAEGVGKVLR

GGAQFLLKGAERQQRYVTEAITEEWRLAPGPLELAWFAEETTAIERALAALEKRLETLEGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883421.1\_4573 [gene=ubiE] [locus\_tag=BN49\_RS24765] [protein=bifunctional demethylmenaquinone methyltransferase/2-methoxy-6-polyprenyl-1,4-benzoquinol methylase UbiE] [protein\_id=WP\_002883421.1] [location=complement(4794601..4795356)] [gbkey=CDS]

MVEDSQETTHFGFQTVAKEQKADMVAHVFHSVAAKYDVMNDLMSFGIHRLWKRFTIDCSGVRRGQTVLDL

AGGTGDLTAKFSRLVGETGRVMLADINDSMLKMGREKLRNIGIVGNVEYVQANAEALPFADNTFDCITIS

FGLRNVTDKEKALRSMYRVLKPGGRLLVLEFSKPIIEPLSKAYDAYSFHILPKVGELVAKDGDSYRYLAE

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MDLSIIISAVIALAAGLMVGWLATKARADQIRADLIEERRELDIELSAARQQLAQEAHWREECELLNNEL

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GLLTPLREQLDGFRRQVQESFGQEARERHTLAHEIRNLQQLNAQMAQEALNLTKALKGDNKTQGNWGEVV

LTRVLEASGLREGYEYQTQVSIETDNRSRMQPDVIVRLPQGKDVVIDAKMTLVAYERYFNAEDDYTREVA

LQEHLASVRNHIRLLGRKDYQQLPGLRSLDYVLMFIPVEPAFLLAIDRQPELISEALQNNIMLVSPTTLL

VALRTIANLWRYEHQSRNAQKIAERAGRLYDKMRLFVDDMSAIGQSLDKAQESYRQAMKKLASGRGNLLA

QAEAFRGLGVEVKRGINPDLVEQATAQDEQYRLEDEDNLPENDAFSPDSAETVRSREAAPPC

>lcl|NZ\_FO834906.1\_prot\_WP\_002883419.1\_4575 [gene=udp] [locus\_tag=BN49\_RS24775] [protein=uridine phosphorylase] [protein\_id=WP\_002883419.1] [location=complement(4797011..4797772)] [gbkey=CDS]

MSKSDVFHLGLTKNDLQGATLAIVPGDPERVEKIAALMDKPVKLASHREFTSWRAELDGKPVIVCSTGIG

GPSTSIAVEELAQLGVRTFLRIGTTGAIQPHINVGDVLVTTASVRLDGASLHFAPMEFPAVADFACTTAL

VEAAKSIGATTHIGVTASSDTFYPGQERYDTFSGRVVSRFKGSMEEWQAMGVMNYEMESATLLTMCASQG

LRAGMVAGVIVNRTQQEIPNAETMKQTESHAVKIVVEAARRLL

>lcl|NZ\_FO834906.1\_prot\_WP\_016532476.1\_4576 [locus\_tag=BN49\_RS24780] [protein=dienelactone hydrolase family protein] [protein\_id=WP\_016532476.1] [location=4798045..4798857] [gbkey=CDS]

MTTTKQPGFAPAASPHAATAVHTPEEHIIAGETSIPSQGENMPAYHARPKNADGPLPIVIVVQEIFGVHE

HIRDLCRRLAQEGYLAIAPELYFRQGDPNEYHDIPTLFKELVSKVPDAQVLADLDHVASWAARHGGDAHR

LLITGFCWGGRITWLYAAHNPQLKAAVAWYGKLVGEKSLNSPKHPVDIAVDLNAPVLGLYGAKDASIPQD

TVETMRQALRAANATAEIVVYPEADHAFNADYRASYHEESAKDGWQRMLAWFAQYGGKRG

>lcl|NZ\_FO834906.1\_prot\_WP\_016532475.1\_4577 [locus\_tag=BN49\_RS24785] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_016532475.1] [location=complement(4798964..4799638)] [gbkey=CDS]

MASSSALRFAINLGNALLAKQLTDGSLQGLTVELARKIAEFCQQPERLLPYPAAKGIVDDASNNQWDIAF

LAVDPARENELRFTSPYLTIDCTLLVRSCSGIHSVLEMDREGVTINVGKGSAYSLPLIRTLKHARLCEYP

TTQQALNAFLAGKGDMVANIRQLLEAAALGQDSVCVLPDNYSQIQQAICVPRAVPHYYERMEALVRQWQQ

DGTLAALVARHIYA

>lcl|NZ\_FO834906.1\_prot\_WP\_032105227.1\_4578 [locus\_tag=BN49\_RS24790] [protein=LysR family transcriptional regulator] [protein\_id=WP\_032105227.1] [location=complement(4799675..4800610)] [gbkey=CDS]

MKSELLGTKAFVTIADFGCFTRAADELNLSQPALTRRVKKLEEHLKVSLFERTTRKVTLTYAGKALLPHA

RALLDYMDNAILSVQELAAHQKGVIKLSCIPTATFYFLPLVLEKFNSLYPNIRVHIHEQATMDSLDSLMS

GETDFGINMNRVTHPQISFTPLVDEPYILVCRRDHPLATKKLVEWNELASHRLIGIRRTSGNRILIEQEI

AQTAGTLEWFYEVRHYSTAIGLVEAGLGIAALPCMAMSHHQHESLVSIPLVEPVIRRSIGLIRRNDVPLS

PIAERLVNLFLEMWFERKPEKWTAPFDLFSR

>lcl|NZ\_FO834906.1\_prot\_WP\_016528912.1\_4579 [locus\_tag=BN49\_RS24795] [protein=lactonase family protein] [protein\_id=WP\_016528912.1] [location=4801103..4802161] [gbkey=CDS]

MSVSYVGSRTTALRNARGKGLSVWSIDDDTGNWTKIQTLKEQENPSYLTFDNTKNFLYSVHGDYTEVTSY

AINPEDGKLTYINKITLDDGKNPVFITADKTNRYLLVATLQGGAVYVVRREENGALGEVVSVWRFPGKTN

ESISHAHQCIWDQEKNYLFVPQQGRVIGYAGVSVLKFNPEDGSLIETDYFRAREYSEPRHMAIHPNNQYC

YLVNEKDNTVTWFFFEQNSGKIEPQQIIPVLPETYTGEGQSSAVLVDKSGKWVIESTRIHESLSIFRINP

LTGYLTRVETMKVPGLTPRFITFNDAGDRLFVANEDSDTIIQYAFDNITGSLTQLQPVVATESPVCILFK

SL

>lcl|NZ\_FO834906.1\_prot\_WP\_016528913.1\_4580 [locus\_tag=BN49\_RS24800] [protein=SLC13 family permease] [protein\_id=WP\_016528913.1] [location=4802174..4803493] [gbkey=CDS]

MPNLAIISLLAIFIAIIVGFYKKTNVGIIMVAFAFILSLAYHIPTAKLFKGFSVSLFLTMLGVTYLFSIL

HNNKTLEILSKKIVGAVHKRNLLPIAIYIVGFVLCAVGPGAIPVLAIVPVIAIPIAFQARLNPIMMAIIG

QCGVFGGRITQITPEGVLVMELMDKQQLTPSLFPVWLCLFITSVLMAILCYVWYRGWRLDDLDINAAGST

INATPKFTTVHWCSLAGLLALIICAVVFSLNVGLTAFVIGAILSALGAGLTAFVIGAILSALGAGDENAA

IKSIPWSVLILVCGVGLLMNVVMESGGISLLAKTLTTVMNETTASSVMVTTAAIMSFFSSGLGVVFPTLI

PTCQGIVEHLGANISAIELVAMVVVGGTVSGVSPVSTTGALIMSGVATNKEAEQKYTPSKMFIELFGWAF

AAMILSFVMAIIGIYALFC

>lcl|NZ\_FO834906.1\_prot\_WP\_016528914.1\_4581 [locus\_tag=BN49\_RS24805] [protein=aconitate hydratase] [protein\_id=WP\_016528914.1] [location=4803505..4805442] [gbkey=CDS]

MKQNITQKIIAQHLLSGNMVAGEEISIRIDHTLTHDVTGTPAYLAFETLGIPQVKTERSVSYIDHNMLYT

DNKNPDDHIYLQTVAKKHGIYLSKAGNGICHTVHFERFSRPGITLLGSDSHTPTGGAVGAMALGAGGLDV

ALAMAGEPTWLKMPRVINVRLHGRMQPGVSAKDIILEMLRRETVKGGLGKVYEYTGEGVEHISIRDRSTI

TNMGAEMGATTSIFPSDEVTREFFIKENREQDWISLHPDEGCEYDDYIDIDLNTLEPLVAMPDMPDNVTE

ARNCRDVKINQVFLGSCTNASYTDFAKAAAIMEGRFTHPEVSFVVAPGSRQLYQMLLRDGIIGKLIAAGA

RVIDCGCGACCGIGQAPSTDGVSLRTSNRNFKGRGGHLNARLYLSSPEIAAASAITGYISDPRDVVDVAV

LNDIVEPHDYIIDDRLILAPAENGEEVEVIRGPNIKPMPINEPLPDTLTIQVSAVRGDNITTDDITPANA

QFSALRSNIPEISKYCYGRIDPEFHDRCKELGKSIIIGGENYGQGSSREHAAIAPMYLGVKAVIAKSMAR

IHKNNLVNHGVVPLIFANPEDYACFETFDELRIENLHEGLRQRCVLLKNVTKNREVSLNVDLTPREIEIV

IDGGQLRHVASKNAK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528915.1\_4582 [locus\_tag=BN49\_RS24810] [protein=hypothetical protein] [protein\_id=WP\_016528915.1] [location=4805556..4806689] [gbkey=CDS]

MRKFRTVFMRGGTSKGCMFLKDDLPADRGQWDHIFLQAMGDPDPKQIDGMGGTVSSNNKIVIVWKSELPD

VDVEYLVGQVIVGKSQVDYKSNCGNMTAAVGPYAIEEGLIPAVEPIATVRMLNHNTGKRIDITVPCENNT

FALDGDCQIAGVDGTCAELKVNFLNPACSKTGTLLPTGNTLDVLSIPGHGDIEATILDISNPMVLVRAED

IGLTGSELPDDINQNQAVSDLLEKIRGTAACLMGFAKDLDDARDNSPAVPKVGMVTTPKSYADISGQPTQ

QQEMDLCARVISVFKCHKACPLTSASAISVAAFLPGSLVQRIVTVGDWNQGVRIGHPSGVMKMYPSLVQN

GDSTDVPGVAVQRTARRIMDGMVYIRD

>lcl|NZ\_FO834906.1\_prot\_WP\_016528916.1\_4583 [locus\_tag=BN49\_RS24815] [protein=hydratase] [protein\_id=WP\_016528916.1] [location=4806738..4809002] [gbkey=CDS]

MIKLSDGGVYLLNGTEVVEEKNAPASLNKAEAQKGTISWSILNAHNTSGDMSRLKLKFDALTSHDITFVG

IVQTAKASGMTYFPIPYVLTNCHNSLCAVGGTINSDDHMFGLSAAKKYGGTYVPPHLAVIHQYMREMMAG

GGKMILGSDSHTRYGALGTMAIGEGGGELVKQLLNDTYDVAYPGVIAIHLTGKPQPGIGPHDVALAIIGA

VFEKGYVKNKVMEFVGPGVSTMDTDYRNGIDVMTTETTCLSSIWRTDADTHCFLAKHGRPEAYQRLDPAD

VAYYDGCVHVDLSAIKPMIALPFHPSNVYTIDALNDNLTDILHSVDQEAKQIAGEQIPFSLLKHVENGKL

RVQQGIIAGCAGGNYSNVYAAAQMLRGKSCGNDAFSLAVYPSSQPVFMDLVKKGAIADLMAAGAIIRTAF

CGPCFGAGDTPCHDGLSIRHTTRNFPNREGSKPGVGQMSAVALMDARSIAATAANGGLLTPSTDLPPVEV

PEYDFDPTPYHSRVYIGTHQKLNDAELVYGPNIKDWPEMEQLHDNILLKVVSRIMDPVTTTDELIPSGET

SSYRSNPLGLAEFTLSRRDPQYVSRSKAVHALEKARAQGEIAEELQPVFAQIQSIPGFAEIKPLDVEIGS

MIYAVKPGDGSAREQAASCQRVLGGLANIAEEYATKRYRSNVINWGMLPFQMVGEPTFDVGDSIFVPGIR

AALDADSRTFQAFVIRQDGRVQEIELTMAPVTKDEREIIKAGCLINYNKARNNK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528917.1\_4584 [locus\_tag=BN49\_RS24820] [protein=isocitrate/isopropylmalate family dehydrogenase] [protein\_id=WP\_016528917.1] [location=4809018..4810181] [gbkey=CDS]

MTFIEEAQAKFAELITSELARIEAMKQAGEAKDFSQLERIVVGILPGDGIGPIIMKQALRVLEFLAKDEI

AAGKLELRPVSGMTIEDRARLGQSLPDNVLEQVKQCDVLLKGPMVTPRPGEEWPNMVSANSLLRRSLDLF

AAVRPVSIPEKNIDWTFFRENIEGEYIWGNKGIQVTDDLAVDFKVQTAPGTERIARQAFEFARKNGKTNV

TVITKSNIVKLADGNFLQGVRKVGAEHYPDIEVQDRLVDAMCARMGDETFCKGLQVFVLPNLYGDIVTDI

AAELQGGLGTASSANIGSRYAMFEAIHGTAPGLVSEGRGEYADPCSLIRAVGMLLAHIGYGEKSRQLSKA

LIQCTVTERKKVVTTYTKDASAAEFTDYLLETLARQA

>lcl|NZ\_FO834906.1\_prot\_WP\_016528918.1\_4585 [gene=acnB] [locus\_tag=BN49\_RS24825] [protein=bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase] [protein\_id=WP\_016528918.1] [location=4810248..4812836] [gbkey=CDS]

MLEAYRQHQAARAAKGLVAKPLDAGQVQKLTELLQHPPAGEEAFLYDLFVNRVPPGVDDAAKVKAAFLTA

LAEGKAVSPLIGKEQAITLLGTMLGGYNIPPLIAALDSPELASAAVAALSHTLLIFDNFQLVETKAAAGN

RHAQQVMRAWADAEWFLKRPAVAEKITVSVFKVPGETNTDDLSPAQDVWSRPDIPLHALTMLKNPHEGIE

PDQPGVIGPLQKIAQLKEKGFPLVYVGDTVGTGSSRKSAANSVLWFMGEDIPFVPNKRGGGMVIGGKIAP

IFFNTMEDSGALPIEADVSQLNMGDVIDVYPWQGEIRRHDDNVLLANFTLKTDVLLDEARAGGRIPLIIG

RALTAKARQALNLPQSDVFGQAHAAQESSRGFSLAQKIVGRACGVAGIRPGTYCEPKITSIGSPDTSGPM

TRDELKDLACLRFSADLVMQSFCHTAAYPKQVDVQTHQTLADFMRERGGVSLRPGDGVIHSWLNRMVLPD

TVGTGGDSHTRFPIGLSLPAGSGLVAFAAATGVMPLDMPESVRVRFHGNMRPGITLRDLVHAIPYYASKQ

GLLTVEKKDKKNIFSGRILEIEGLEDLAVEQAFELTAATAERSAAGCTIKLNSMPIIDSIKGNIVLLKWL

IAEGYGDRETLERRILAMENWLDDPQLLAADADAEYAATIDIDLNDIHEPLLCAPNDPDDVRPLSAVAGH

SIDEVFIGSCMTNIGHFRAVGEVFSAHKGQLPVRLWITPPTKMDANKLKDEGWFSVFGQRGARIETPGCS

LCMGNQARVADGATVVSTSTRNFPNRLGAGANVYLASAELAAVTARLGKLPQPEEYFALTEKIDKHIYHY

LQFDRLDSYVQKVAEVIFQTHS

>lcl|NZ\_FO834906.1\_prot\_WP\_016528919.1\_4586 [locus\_tag=BN49\_RS29575] [protein=GntR family transcriptional regulator] [protein\_id=WP\_016528919.1] [location=complement(4812999..4813148)] [gbkey=CDS]

MAKFLDIKRSRPAMVRQHTCLAGDDKLILWGETWYREEYEFQYSTYRDK

>lcl|NZ\_FO834906.1\_prot\_WP\_016528920.1\_4587 [gene=citC] [locus\_tag=BN49\_RS24830] [protein=[citrate (pro-3S)-lyase] ligase] [protein\_id=WP\_016528920.1] [location=4813272..4814330] [gbkey=CDS]

MDATTMISRVTSKNTAKIIQIARFLQANNLDIDPHITDFVVLHQHGEMVACGGISGDIIKCVAISPQLRG

QGVLLKLVTELINLAMESGNSTLFVYTRSHNENLFHHCGFTTLVSIPGCMVLMENSGSRLTRYLQQLAQW

RKPGKRIAAIVMNANPFTNGHLHLIRYASSHFDWLHLFLVNEDAAQFPFADRLALVREATQGIVKLTVHP

GSQYMISRATFPAYFLKEQALVERCYTQIDITLFRQYIAPVLGITHRVVGNEPFCPITARYNLDMRHWLS

TPELPFASVELVEISRLQWHGTPVSASRVRRLLQQNRFTEVAPLVPDTTLRYLKRHQKTVLANMTQTPTG

AL

>lcl|NZ\_FO834906.1\_prot\_WP\_016528921.1\_4588 [gene=citD] [locus\_tag=BN49\_RS24835] [protein=citrate lyase acyl carrier protein] [protein\_id=WP\_016528921.1] [location=4814327..4814608] [gbkey=CDS]

MKQIVPAVAGTLESSDALIRIEPLAPELPPEIEITSSVQKQFGDAIRATLIAVLQQHAIRGVSIIVDDKG

ALDCVLRARLETALMRAGALTLC

>lcl|NZ\_FO834906.1\_prot\_WP\_016528922.1\_4589 [gene=citE] [locus\_tag=BN49\_RS24840] [protein=citrate (pro-3S)-lyase subunit beta] [protein\_id=WP\_016528922.1] [location=4814620..4815516] [gbkey=CDS]

MTPKRKNRLRRSMLFVPGANAAMLSNAFIYPADALMFDLEDAVAVREKDAARHLVYHALQHPLYRDVETI

VRVNALDSQWGIDDLEAVVRAGVDIVRLPKTDTADDVIAMEKEIARIERDCGRKPGSTGMLAAIESAKGI

LQAPAIALASPRLIGIALGAEDYVRDIRTERSADGIELLFARCTILQAARAAGIQAFDTVYSDANNEEGF

LREAAHIKQLGFDGKSLVNPRQITLLHNLYAPTQKDVDHAKRVVEAAEAAEQEGLGVVSLNGKMIDSPII

ARAHLVLSRAELSGVREE

>lcl|NZ\_FO834906.1\_prot\_WP\_032439089.1\_4590 [gene=citF] [locus\_tag=BN49\_RS24845] [protein=citrate lyase subunit alpha] [protein\_id=WP\_032439089.1] [location=4815523..4817019] [gbkey=CDS]

MNHTQDLSRIIGELTPFADTDKQTQRQQRRAKTCASLTEAIRRSGLRDGMTISFHHAFRGGDLTLNLVMD

QLATMGFKNLTLASSSLSACHAPLVDHIRNGVVNRIYTSGLRGPLAEEISRGLMAHPVQIHSHGGRAHLV

KSGELNIDVAFLGVPSCDDMGNANGYTGSATCGSLGYAMVDAQYANQVILLTEDILPYPHHPASIRQDQV

DLVVLVECVGDAEKIGADATRMTTNPRELQIAQNAALVIEASGYFREGFSLQTGTGGAALAVTRFLGEKM

RRKNIRADFALGGITATIVGLHEEGYIRRLLDVQGFDSVAARSLARNPNHIEISANEYANFSSKGASVNK

LDVVVLSALEIDTDFNVNVLTGSDGVLRGASGGHCDTAFGSALSIIVAPLVRGRIPTVVGKVLTRITPGS

SVDVLVTDHGVAVNPARPELAQRLEAAGLKTVTIEWLCDRARQLTDEPQPIAFTDKPVAIVRYRDGSVID

VVYQVRDE

>lcl|NZ\_FO834906.1\_prot\_4591 [locus\_tag=BN49\_RS24850] [protein=triphosphoribosyl-dephospho-CoA synthase] [pseudo=true] [partial=3'] [location=4817016..>4817789] [gbkey=CDS]

MMRPVPTESWGAPVARQEKLPQAYRSRYYARLACRAMQTEARLTPKPGLVDGRNTGAHKDMALPDFLRSA

SEIALIFPLFFEEGAASAVCDPDCVLARLKPIGLRCETEMLQATGGVNTHKGAIFTLGLFCAALGRHEAL

GQPLTPNALAATVSTFCHGIVERELVELRGRMPLTAGQRLFISAGLTGARGEAQAGYPLVIDHALPRYRQ

LRREGLSEELALLNTLLLIMSRNDDTCVASRGGINGLRWLQRQAQQLL

>lcl|NZ\_FO834906.1\_prot\_4592 [locus\_tag=BN49\_RS29580] [protein=arginine:ornithine antiporter] [pseudo=true] [partial=3'] [location=4817846..>4818034] [gbkey=CDS]

MKIQRKSLFLFWAWMDLFFVLQFLWWNIAHRRLPFYDDLLAYLQLLHTWGSAAVWLYPLNVLL

>lcl|NZ\_FO834906.1\_prot\_4593 [locus\_tag=BN49\_RS24855] [protein=sodium ion-translocating decarboxylase subunit beta] [pseudo=true] [partial=5'] [location=<4818024..4818461] [gbkey=CDS]

MFCFGNLMRESGVVERLSDTVQNALINIVTIFLGLSVGAKLVADKFLQPQTLGILVLGVIAFCVGTAAGV

LMAKLMNVFSRHKINPLIGSAGVSAVPMAARVSNKVGLEADGQNFLLMHAMGPNVAGVIGSAIAAGVMLK

YVLAM

>lcl|NZ\_FO834906.1\_prot\_WP\_016531184.1\_4594 [locus\_tag=BN49\_RS24860] [protein=hypothetical protein] [protein\_id=WP\_016531184.1] [location=4818521..4819129] [gbkey=CDS]

MSETIIAEHTAVRINRTMLAGYLHQSLQQVCKLASGLKILRLPASDTTRRATILTEPVYAAARLRLAQQQ

PLAQNPLCDDVLRRFRHAPGLTADLPDLIDTMRSVTLPVWSRLRRDGHSDDVALRQTLLHILAWKSESSW

LQDQAQRVLWQGGVLGEKGGRVLVSLDDEAALRGAGFCGLSELLITTGFLVHFPVGPQFSEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531183.1\_4595 [locus\_tag=BN49\_RS24865] [protein=fumarylacetoacetate hydrolase family protein] [protein\_id=WP\_016531183.1] [location=4819144..4819992] [gbkey=CDS]

MKLLSFCVSNIPSYGLLREDGVVDLTRHFLQYPSLKSFLAAMDNIPAEMLAHMPVDYTLDEIAFLPLIPD

PQKILCVGMNYQAKRLEFNEQDPDPTLFIRFPDSQCGHLGEIIKPAASHEFDYEGELALVIGKRGRNIPV

GRALEHVSGYSCYMDGSARDWQHAWFTAGKNWPSTGGFGPWLVTRDEIADPNALDIKTRLNGMEVQNDNT

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SE

>lcl|NZ\_FO834906.1\_prot\_WP\_032104629.1\_4596 [locus\_tag=BN49\_RS24870] [protein=anaerobic sulfatase maturase] [protein\_id=WP\_032104629.1] [location=complement(4820071..4821369)] [gbkey=CDS]

MELAGCQVMAKPTGSVCNIDCTYCFYLEKEALYPERNKNWRMSDETLECYIRQHIEAQMGETVTFAWQGG

EPTMMGLPFFRRVVALSNQYARGKKIEHALQTNGMLVDEEWARFFAEEHFLVGISIDGPAHLHNQYRVNR

AGKGTHDKVMAAIALLKKHRVEFNTLTVVGKHNVGHPREVYDFLLATGSRHIQFIPLVERVSSDESSLLQ

LVMPGESAARLASWTVPSWQFGDFLNQIFDIWIRRDVERVIVQMFEVALAAWMGQPPVLCVHSPTCGHAF

ALESNGDLYNCDHYVYPEHKLGNIHHSDIKTLNNSEQAIAFGQAKREMLTAECRSCEFRFVCHGGCPKHR

FAVSPSGHPGHNYLCAGYKHFFQHITRYMNVCQQLLEAGYPLAAIMPWLADEERKPSKTRSRNEPCPCGS

GKKYKKCCGAQH

>lcl|NZ\_FO834906.1\_prot\_WP\_016530522.1\_4597 [locus\_tag=BN49\_RS24875] [protein=DUF202 domain-containing protein] [protein\_id=WP\_016530522.1] [location=complement(4821370..4821717)] [gbkey=CDS]

MTLSLRTRDPGLQPERTALAWQRTLFSVFVLALASTRFGFARGDLVSGGIAGIALGLTVILAIVVRNQQR

QVGGNTALTTFASVMIKRLLSVVLGLEAISLVLSAVLSLLREGVV

>lcl|NZ\_FO834906.1\_prot\_WP\_016530523.1\_4598 [locus\_tag=BN49\_RS24880] [protein=DUF202 domain-containing protein] [protein\_id=WP\_016530523.1] [location=complement(4821714..4822058)] [gbkey=CDS]

MSWLTQGKDPDYRFSLANERTFLAWIRTALAFMAAAIGIDQLAENLAPSMVKELLVCALGITAAILAWYA

YLRWSGNERAMRDDAALTYPRLLIWLSAGLAAVMMMTLGVMLLL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530524.1\_4599 [locus\_tag=BN49\_RS24885] [protein=GntR family transcriptional regulator] [protein\_id=WP\_016530524.1] [location=complement(4822055..4822783)] [gbkey=CDS]

MKEELDYSPGAKPLYAQLHDILLGKLKAGEYKKNDVLPTEAEFEEIFGVSRITARRALAELAAKGLVKRQ

AGIGTMVISTSEKQEVKARIRLVDGQQQHPIERNNLKLEQLVPPGGVAQAFELNDDKTPLWLLTRTIYRQ

NEQPAQVNYIWLTTRLQHLTLDALKNGLYSMLENNNENIESFQDVITAEMPTEDDCRILHIDTREPLLVK

TRKGYNDRGELVEFSIAKHIASCYQYIVENSR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530525.1\_4600 [locus\_tag=BN49\_RS24890] [protein=sulfatase] [protein\_id=WP\_016530525.1] [location=complement(4822827..4824572)] [gbkey=CDS]

MKAIMLMFDSLNKRLLSAYGSDRAITPNFQRLKERTVRFDNFYVGSMPCMPARRELHTGRYNFLHRGWSP

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EEIKQRRITSRVQHQINVQFMQNEEDHHLARTINKGLEFIDTNHASDNWFLQLECFDPHEPFFVPEKYLR

MYGIDDPSQFDGWPPYYFVTESPERKSVIQKYYMALLTMVDAYVGKVLDYMDHYDLWQDTMLIVNTDHGF

LLGEHEWWGKNIMPLYNEVANIPCFIWHPQHGCAGESRQALAQTIDIPATLLDSFGLPKPQDMQGVSLLP

VLRDDTPVRNYALFGYHGCHINITDGRYVYMRAPVTQGVSGLYEYTLMPTRINRRFTPSELQGMTLHPPF

GFTKGCKVLKIPAESVMTRGADRFGHRLYDLHDDPLQQTQSRDTAAAERLCSSMKAMMAQSDAPSELYPR

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EVPQEQHQSVYYKMALEMRLD

>lcl|NZ\_FO834906.1\_prot\_WP\_023302341.1\_4601 [locus\_tag=BN49\_RS24895] [protein=PTS transporter subunit EIIC] [protein\_id=WP\_023302341.1] [location=complement(4824588..4826003)] [gbkey=CDS]

MNYNMVGDAIVKHCGGLANFIHVTNCMTRVRMTIADTSLVDMTALKAIEGVLGVVEDDTLQVIVGPGKST

KVAGVINARLKGQPDSGEALSAVEQKAKTAREKAKKQTRTKVILKHIANIFVPILPALIAAGILMGLNNV

IFNSAASWALTHHVASVGDLSPTQVVLDQRHLLGLSQFLDIVSKALFGFLAIYAGVTSAREFEGNLILGG

LLGAITIMPQVTTFGLIPGQGGLIGVIFAVWLMCLLEKPVRRFVPDIVDVVVTPTLVLLVMAAALLFIIM

PAAGIVSNGILSGLNGLLEHGGIVAGFVLSALFPFLISLGLHHGLFPIHLEMINATGHAPLFAIQIMSNA

GMVGAATAVLLLTRDPVMKKIARGAIPTSILAVGEPTIFGVNIPAGFAFITGSIGAGFGGVMVVLLGVST

NGVGAAGLSALPLIADGKYLQYILAWLVGCAAAFALTYIVGKVRGYDKETV

>lcl|NZ\_FO834906.1\_prot\_WP\_032104628.1\_4602 [gene=metE] [locus\_tag=BN49\_RS24900] [protein=5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase] [protein\_id=WP\_032104628.1] [location=complement(4826505..4828766)] [gbkey=CDS]

MTIINHTLGFPRVGLRRELKKAQESYWAGNATREELLAVGRELRARHWEQQKQAGVDLLPVGDFAWYDHV

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TQLLDEVDEALALGHKIKPVLLGPVTYLWLGKVKGEPFDRLTLLNAILPVYQQVLAELAKRGIDWVQIDE

PALVLELPPAWLEAFQPAYDALQGQVKLLLTTYFEGVSDNLATIAALPVQGLHVDLVHGKDDVAELHNRL

PAGWLLSAGLINGRNVWRADLTEKYAQIKDLVGKRELWVASSCSLLHSPIDLSVETRLDAEVKSWFAFAL

QKCGELALLRDALNSGDTAAITEWSAPIQARRHSTRVHNAEVEKRLAAITAQDSQRASPYEVRAQAQRQR

FNLPKWPTTTIGSFPQTTEIRGLRLDFKKGNLDASHYRTGIAEHIKQAIVEQERLGLDVLVHGEAERNDM

VEYFGEHLDGFIFTQNGWVQSYGSRCVKPPVVIGDVSRPQAITVDWAKYAQSLTDKPVKGMLTGPVTILC

WSFPREDVSRETIAKQIALALRDEVADLEAAGIGIIQIDEPALREGLPLKRSDWDAYLQWGVEAFRLNAA

VAKDDTQIHTHMCYCEFNDIMDSIAALDADVITIETSRSDMELLESFEAFEYPNEIGPGVYDIHSPNVPS

VEWIEALLKKAAQRIPVERLWVNPDCGLKTRGWPETRAALANMVQAAQNLRQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883415.1\_4603 [gene=metR] [locus\_tag=BN49\_RS24905] [protein=HTH-type transcriptional regulator MetR] [protein\_id=WP\_002883415.1] [location=4829014..4829967] [gbkey=CDS]

MIEIKHLKTLQALRNSGSLAGAAAALHQTQSALSHQFSDLEQRLGFRLFVRKSQPLRFTPQGEILLQLAN

QVLPQIARALQDCNEPQQTRLRLAIECHSCIQWLTPALENFRARWPHVEVDFHSGVTFDPQPALQQGELD

LVMTSDILPRSGLHYSPMFDFEVRLVLAPEHPLAMKTLVTPEDLAAETLLIYPVQRGRLDIWRHFLQPAG

ISPQLKSVDNTLLLIQMVAARMGIAALPHWVVESFERQGLVVTKTLGEGLWSRLYAAVRDGEQRQPVTEA

FIRSARNHACDHLPFVRSAERPSGDGPTARPGSPTLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002883414.1\_4604 [locus\_tag=BN49\_RS24910] [protein=carboxylate/amino acid/amine transporter] [protein\_id=WP\_002883414.1] [location=complement(4829855..4830754)] [gbkey=CDS]

MALLIITTILWAFSFSLIGEYLAGSVDSYFSVLMRVGLAALVFLPFLRTRGQSPRTIVLYMLVGAMQLGI

MYLLAFRAYLYLTVSEFLLFTVFTPLYITLIYDLLSGRKLRWGYLLSAALAVLGAAIIRYDKVSDHFWTG

LLLVQLSNLCFAIGMVGYKRLMEVRPMPQHNAFAWFYVGAFIVAVAAWFMLGNAQKLPTTTLQWSVLVWL

GVVASGLGYFMWNYGATQVDAGTLGIMNNVHVPAGLLVNLAIWQEQPHWPSFISGALVILASLWVHRRWV

APHSGQTADDRRRGSAQSE

>lcl|NZ\_FO834906.1\_prot\_WP\_004146466.1\_4605 [gene=yigL] [locus\_tag=BN49\_RS24915] [protein=sugar/pyridoxal phosphate phosphatase YigL] [protein\_id=WP\_004146466.1] [location=complement(4830843..4831643)] [gbkey=CDS]

MYQVVASDLDGTLLSPDHFLTPYAKETLKLLTARGINFVFATGRHYIDVGQIRDNLGIRSYMITSNGARV

HDSDGQQIFAHNLDRDIAADLFEIVRNDPKIVTNVYREDEWYMNRHRPEEMRFFKEAVFNYKLYEPGELD

PQGISKVFFTCEDHEHLLPLEQAMNARWGDRVNVSFSTLTCLEVMAGGVSKGHALEAVAKMLGYTLSDCI

AFGDGMNDAEMLSMAGKGCIMANAHQRLKDLHPELEVIGSNADDAVPHYLRKLYLD

>lcl|NZ\_FO834906.1\_prot\_WP\_002883412.1\_4606 [gene=pldB] [locus\_tag=BN49\_RS24920] [protein=lysophospholipase L2] [protein\_id=WP\_002883412.1] [location=complement(4831688..4832680)] [gbkey=CDS]

MFGQKKDWETRENAFAAFSMGPLTDFWRQREEAEFKGVDDVPVRFVRFCAQHNDRLVLICPGRIESYVKY

AEVAYDLFHCGFDVMIIDHRGQGRSGRLLSDTHRGHVVNFSDYVDDLAALWQQQVVPGHWRKRFILAHSM

GGAIATLFLQRYRAHCDAIALCAPMFGIIIRLPDWMVRHILDWAEGHQRIREEYAIGTGRWRALPFAVNV

LTHSRQRYRRNLRFYADEPRLQVGGPTWHWVREGMLAGDEVLANVEKDTAPTLLLQAEEERVVDNLMHDR

YCELRAAAGHPCEGGKPLVIEGAYHEILFEKDAMRSVALNAIVEFFNRHT

>lcl|NZ\_FO834906.1\_prot\_WP\_002883411.1\_4607 [gene=rhtB] [locus\_tag=BN49\_RS24925] [protein=homoserine/homoserine lactone efflux protein] [protein\_id=WP\_002883411.1] [location=4832790..4833410] [gbkey=CDS]

MTIEWWFAYLLTSIILSLSPGSGAINTMTTSINHGYRGAAASIAGLQTGLAIHIVLVGVGLGTLFSRSVL

AFEVLKWAGAAYLIWLGIQQWRAAGAIDLNTLAKAQTRGKLFQRAVFVNLTNPKSIVFLAALFPQFILPH

QPQVMQYLVLGVTTIVVDIIVMIGYATLAQRISAWIKGPKQMKALNKVFGSLFMLVGALLASARHA

>lcl|NZ\_FO834906.1\_prot\_WP\_016532000.1\_4608 [locus\_tag=BN49\_RS24930] [protein=Rpn family recombination-promoting nuclease/putative transposase] [protein\_id=WP\_016532000.1] [location=4833573..4834481] [gbkey=CDS]

MAETATPHDAVFKTFLSRVETARDFIELHLPPSLTQICKLDTLRLESGSFLEDDLRPYYSDILYSLETTR

GAGYVHVLIEHQSAPDKLMAFRLMRYAIAAMQRHLESGHKTLPLVIPILFYQGRRSPYPWSMRWLDNFAD

PETASQLYSGAFPLVDITVIPDDDIMQHRSMAALTLVQKHIRQRDMAQLLDKLTHLLVLEQMSGQQITVL

VNYMAQAGDAEDTRTLLYGLAQRVPQHGGLLMTLAETWLAEGMEKGVQQGIKEGKHQALVQVAEAMRSRG

IDDQAIMEMTGLSEDELQRLRH

>lcl|NZ\_FO834906.1\_prot\_WP\_004177928.1\_4609 [gene=rhtC] [locus\_tag=BN49\_RS24935] [protein=threonine export protein RhtC] [protein\_id=WP\_004177928.1] [location=complement(4834526..4835146)] [gbkey=CDS]

MLMLFLTVALVHIIALMSPGPDFFFVSQTAISRSRREAMMGVLGITCGVMVWAGVALLGLNLILARMAWL

HNIIMVGGGLYLCWMGYQMLRGALKKETVASAEPQVELARSGRSFVKGLLTNLANPKAIIYFGSVFSLFV

GDSVGAGARWGIFLLIIVETLAWFMVVASLFALPGMRRGYQRMAKWIDGIAGTLFAGFGIHLIISR

>lcl|NZ\_FO834906.1\_prot\_WP\_004152055.1\_4610 [gene=recQ] [locus\_tag=BN49\_RS24940] [protein=ATP-dependent DNA helicase RecQ] [protein\_id=WP\_004152055.1] [location=complement(4835208..4837034)] [gbkey=CDS]

MAQAEVLNQESLAKQVLQETFGYQQFRPGQETIIETALEGRDCLVVMPTGGGKSLCYQVPALVMGGLTVV

VSPLISLMKDQVDQLLANGVAAACLNSTQSREQQQEVMAGCRSGQVRLLYIAPERLMLDNFLEHLANWNL

AMLAVDEAHCISQWGHDFRPEYAALGQLRQRMPQIPFMALTATADDTTRRDIVRLLGLNDPLIQVSSFDR

PNIRYMLMEKFKPLDQLMRYVQDQRGKSGIIYCNSRSKVEDTAARLQSRGISAAAYHAGLENDVRAEVQE

KFQRDDLQIVVATVAFGMGINKPNVRFVVHFDIPRNIESYYQETGRAGRDGLPAEAMLFYDPADMAWLRR

CLEEKPAGPLQDIERHKLNAMGAFAEAQTCRRLVLLNYFGEGRQEPCGNCDICLDPPKQYDGLMDARKAL

STIYRVNQRFGMGYVVEVLRGANNQRIREMGHDKLPVYGIGREQSHEHWVSVIRQLIHLGLVTQNIAQHS

ALQLTEAARPVLRGEVPLQLAVPRIVALKPKAMQKSFGGNYDRKLFAKLRKLRKAIADEENIPPYVVFND

ATLIEMAEQSPLTAGEMLSVNGVGTRKLERFGKPFMALIRAHVDGDDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002883408.1\_4611 [gene=pldA] [locus\_tag=BN49\_RS24945] [protein=phospholipase A] [protein\_id=WP\_002883408.1] [location=complement(4837102..4837962)] [gbkey=CDS]

MRISLACLVALCALPAGVMAQDASVHDKPAVRGSIIANLLQDHDNPFLLYPYESNYLLYTWTSDLNKEAI

RSYDWAENARKDEVKFQLSLAFPLWRGILGDNSLLGASYTQKSWWQLSNSKESAPFRETNYEPQLFLGFA

TDYQFAGWTLRDIEMGYNHDSNGRSDPTSRSWNRLYARLMAQNGNWLVEVKPWYVVGNTDDNPDITKYMG

YYRLKVGYQLGEAILSAQGQYNWNTGYGGAELGVSYPITKHVRAYTQIYSGYGESLIDYNFNQTRVGVGL

MLNDLF

>lcl|NZ\_FO834906.1\_prot\_WP\_016531996.1\_4612 [locus\_tag=BN49\_RS24950] [protein=thioesterase family protein] [protein\_id=WP\_016531996.1] [location=4838115..4838579] [gbkey=CDS]

MSELTAEAALKLVGEIFVYLMPFNRALGLELERYEKAFAQLSFNNQPMMVGNWAQSILHGGVIASALDVA

AGLVCVGSTLTRHDTINEEELRQRLSRMGTIDLRVDYLRPGRGERFTATSTLLRAGNKVAVARVELHNEA

QVYIASATATYMVG

>lcl|NZ\_FO834906.1\_prot\_WP\_002883402.1\_4613 [gene=rarD] [locus\_tag=BN49\_RS24955] [protein=EamA family transporter RarD] [protein\_id=WP\_002883402.1] [location=4838628..4839521] [gbkey=CDS]

MDAKQTRLGIILALAAYFIWGIAPAYFKLIYYVPADEILTHRVIWSFFFMVALISVSRQWPQVKKLLKTP

RKIFLLALSAVLVGGNWLLFIWAVNNHHMLEASLGYFINPLVNILLGMIFLGERFRRLQWLAVILAFCGV

LVQLWTFGSLPIIGLGLAFSFAFYGLVRKKIAVDAQTGMLVETLWLLPVAAIWLFGITDSPTSHMGENPW

SLNLLLMAAGVVTTIPLLCFTGAATRLRLSTLGFFQYIGPTLMFLLAVTFYGEVPGKDKMVTFGFIWVAL

AVFIVDALYTQRRLRRG

>lcl|NZ\_FO834906.1\_prot\_WP\_002883400.1\_4614 [gene=corA] [locus\_tag=BN49\_RS24960] [protein=magnesium/cobalt transporter CorA] [protein\_id=WP\_002883400.1] [location=complement(4839565..4840515)] [gbkey=CDS]

MLSAFQLENNRLTRLEADEIKHLASSVWVDLVEPDDDERSRVQTELGQNLATRPELEDIEASARFFEDED

GLHIHSFFFFEDADDHAGNSTVAFTIREGRLFTLRERELPAFRLYRMRVRNQTLVDGNAYELLLDLFETK

IEQLADEIENIYSDLEKLSRVIMEGHQGDEYDEALSTLAELEDIGWKVRLCLMDTQRALNFLVRKARLPA

GQLEQAREILRDIESLLPHNESLFQKVNFLMQAAMGFINIEQNRIIKIFSVVSVVFLPPTLVASSYGMNF

EFMPELHWSFGYPGAIVFMMLAGLAPYLYFKRKNWL

>lcl|NZ\_FO834906.1\_prot\_WP\_002883398.1\_4615 [gene=uvrD] [locus\_tag=BN49\_RS24970] [protein=DNA helicase II] [protein\_id=WP\_002883398.1] [location=complement(4840871..4843033)] [gbkey=CDS]

MDVSYLLDSLNDKQREAVAASRTNMLVLAGAGSGKTRVLVHRIAWLLSVENCSPYSIMAVTFTNKAAAEM

RHRIGQLMGTTQGGMWVGTFHGLAHRLLRAHHLDANLPQDFQILDSEDQLRLLKRLIKAMNLDEKQWPPR

QAMWYINSQKDEGLRPHHIQSYGNPVEQTWQKVYQAYQEACDRAGLVDFAELLLRAHELWLNKPHILQHY

RERFTNILVDEFQDTNNIQYAWIRLLAGDTGKVMIVGDDDQSIYGWRGAQVENIQRFLNDFPGAETIRLE

QNYRSTSNILSAANALIENNNGRLGKKLWTDGADGEPISLYCAFNDLDEARFVVNRIKTWQENGGALEQC

AILYRSNAQSRVLEEALLQASMPYRIYGGMRFFERQEIKDALSYLRLIANRNDDAAFERVVNTPTRGIGD

RTLDVVRQTSRDRQLTLWQASRELLKEKALAGRAASALQRFMELIDALAQETTDMPLHVQTDRVIKDSGL

RAMYEQEKGEKGQTRIENLEELVTATRQFSYNEEDEDLMPLQAFLSHAALEAGEGQADTWQDAVQLMTLH

SAKGLEFPQVFIVGVEEGMFPSQMALDEGGRLEEERRLAYVGVTRAMQKLTLTYAETRRLYGKEVYHRPS

RFIGELPQECVEEVRLRATVSRPVNHQRLGAPIAESDTGYKLGQRVRHPKFGEGTIVNLEGSGEHSRLQV

AFQGQGIKWLVAAYARLEAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004146477.1\_4616 [gene=yigB] [locus\_tag=BN49\_RS24975] [protein=5-amino-6-(5-phospho-D-ribitylamino)uracil phosphatase YigB] [protein\_id=WP\_004146477.1] [location=complement(4843097..4843813)] [gbkey=CDS]

MRFYRPLGQISALTFDLDDTLYDNRPVIDRTMHESLAFVRSYHPSLSQFDAHELNQLRQTLLAAEPEIYH

DVTVWRHRALELGMRNAGLSAEAAKAGADAAMEHFAHWRSRVDVPQETHDTLAKLAEKWPLVAITNGNAR

PELFGLSDYFRFVLRAGPDGRSKPFADMYHLAAERLNVPLGQILHVGDDLTTDVAGAIRCGMQACWIKPQ

GADLMHTADSRLLPHIEISRLASLTSLI

>lcl|NZ\_FO834906.1\_prot\_WP\_002883396.1\_4617 [gene=xerC] [locus\_tag=BN49\_RS24980] [protein=tyrosine recombinase XerC] [protein\_id=WP\_002883396.1] [location=complement(4843813..4844715)] [gbkey=CDS]

MTDSPLFSAVARFLRHLGVERQLSPITLLNYQRQLDALIALADEAGLKSWSQCDAAQVRSFAVRSRRAGL

GPASLALRLSALRSFFDWLVGQGELSANPAKGIAAPKIPRHLPKNIDVDDVNRLLDIDLNDPLAVRDRAM

LEVMYGAGLRLSELVNLDIKHLDLESGEVWVMGKGSKERRLPIGRNAVAWIEHWLDLRGLFGTDDDALFL

SKLGKRISARNVQKRFAEWGIKQGLNSHVHPHKLRHSFATHMLESSGDLRGVQELLGHANLSTTQIYTHL

DFQHLASVYDAAHPRAKRGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883395.1\_4618 [locus\_tag=BN49\_RS24985] [protein=DUF484 domain-containing protein] [protein\_id=WP\_002883395.1] [location=complement(4844712..4845419)] [gbkey=CDS]

MKPIGEEQQEVASALNDRAVVDYLLQHPEFFIRNAAQVEHLRVPHPVRGTISLVEWHMMRARNHIHVLEE

NMSLLMEQAVANESLFQRLLQLQTRLAAAESLDDMLNRLHRWARELGLAGATVRLFPDCWRLGAPSKFTH

LALNRQAFEPIRIQRLGQARHYLGPLNGPELLVVLPEAKAIGSVAISLLGGDNAPGVMLFSSRDAQHYQP

GQGTQLLQEIAQMLPGLLERWIERA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883394.1\_4619 [gene=dapF] [locus\_tag=BN49\_RS24990] [protein=diaminopimelate epimerase] [protein\_id=WP\_002883394.1] [location=complement(4845416..4846240)] [gbkey=CDS]

MQFSKMHGLGNDFMVVDAVTQNVFFSPELIRRLADRHLGVGFDQLLVVEPPYDPDLDFHYRIFNADGSEV

SQCGNGARCFARFVRLKGLTNKRDIRVSTANGRMVLSVTEDDLVRVNMGEPNFEPSQVPFRANKAEKTYI

MRAAEQTVLCGVVSMGNPHCVIQVDDVDTAAVETLGPVMESHERFPERANIGFMQVVGRSHIRLRVYERG

AGETQACGSGACAAVAVGIQQGLLAETVRVELPGGRLDIAWKGPGQPLFMTGPAAHVYDGFIHL

>lcl|NZ\_FO834906.1\_prot\_WP\_004901868.1\_4620 [locus\_tag=BN49\_RS24995] [protein=lipoprotein] [protein\_id=WP\_004901868.1] [location=complement(4846276..4846479)] [gbkey=CDS]

MKNVFPTLAVLFAIFSLTGCGLKGPLYFPPADKTAPPPTKPVNPGIQSATPDRNDRGDIGGPSQVNY

>lcl|NZ\_FO834906.1\_prot\_WP\_002883389.1\_4621 [gene=cyaY] [locus\_tag=BN49\_RS25000] [protein=iron donor protein CyaY] [protein\_id=WP\_002883389.1] [location=4846626..4846946] [gbkey=CDS]

MNDSEFHRLADSLWMTIEERLDDWDGDSDIDCEINGGVLTISFENGSKIIINRQEPLHQVWLATKQGGYH

FDLKGDEWICDRSGETFWDLLEQAASQQAGETVKFR

>lcl|NZ\_FO834906.1\_prot\_WP\_002883383.1\_4622 [gene=cyaA] [locus\_tag=BN49\_RS25005] [protein=class I adenylate cyclase] [protein\_id=WP\_002883383.1] [location=complement(4846995..4849547)] [gbkey=CDS]

MYLYIETLKQRLDAINQLRVDRALAAMGPAFQQVYSLLPTLLHYHHPLMPGYLDGNVPRGICLYTPDETQ

RHYLEELELHRGMQTQEPPKGELPITGVYSMGSTSSVGQSCSSDLDIWVCHQAWLDSEERQLLQRKCSLL

ESWAASLGVEVSFFLIDENRFRHNESGSLGGEDCGSTQHILLLDEFYRTAVRLAGKRILWNMVPCDEEEH

YDDYVMGLYAQGVLTPNEWLDLGGLSSLSAEEYFGASLWQLYKSIDSPYKAVLKTLLLEAYSWEYPNNRL

LAKDIKQRLHDGEIVSFGLDPYCMMLERVTTYLQAIEDETRLDLVRRCFYLKVCEKLSRERACVGWRREV

VSQLVNAWGWDEKRLMMLDNRANWKIDEVRKAHNELLDAMMQSYRNLIRFARRNNLSVSASPQDIGVLTR

KLYAAFEALPGKVTLVNPQISPDLSEPNLTFIHVPPGRANRTGWYLYNRAPDMESIISHQPLEYNRYLNK

LVAWAWFNGLLTSRTRLFIKGNGIVDLAKLQEMVADVSHHFPLRLPAPTPKALYSPCEIRHLAIIVNLEY

DPTAAFRNQVVHFDFRKLDVFSFGEEQKCLIGSVDLLYRNSWNEVRTLHFNGEQAMIEALKTILGKMHQD

AAPPDSVEVFCYSQHLRGLIRTRVQQMISECIELRLSSTRQDTGRFKALRVSGQTWGLFFERLNVSVQKL

ENAIEFYGAISHNKLHGLSVQVETNHVKLPAVVDGFASEGIIQFFFEDADNNDSGFNIYILDESNRAEVY

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ASPVLQQRYS

>lcl|NZ\_FO834906.1\_prot\_WP\_002883381.1\_4623 [gene=hemC] [locus\_tag=BN49\_RS25015] [protein=hydroxymethylbilane synthase] [protein\_id=WP\_002883381.1] [location=4849905..4850846] [gbkey=CDS]

MLDKVLKIATRQSPLALWQAQYVKARLEQAHPGLKVELVPMVTRGDVILDTPLAKVGGKGLFVKELELAM

LEGRADIAVHSMKDVPVEFPEGLGLVTICERDDPRDAFVSNRYASIDELPAGSVVGTSSLRRQCQLAATR

PDLAIRSLRGNVGTRLSKLDNGEYDAIILAAAGLKRLQLEARIRQPLSPEQSLPAVGQGAVGIECRLDDA

WTRGLLAPLNHTETAVRVRAERAMNTRLEGGCQVPIGSYAELKDGELWLRALVGAPDGSQLVRGERRGPA

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>lcl|NZ\_FO834906.1\_prot\_WP\_016531671.1\_4624 [gene=hemD] [locus\_tag=BN49\_RS25020] [protein=uroporphyrinogen-III synthase] [protein\_id=WP\_016531671.1] [location=4850843..4851583] [gbkey=CDS]

MSILVTRPLPQGEALVSRLRAMGRVAWSFPLIEFTPGRELPALGDALARLGPDDLLFALSQHAVEFAHAR

LQLQGLPWPTSPRYFAIGRTTALALHTVSGQHIHYPLDREISEILLQLPELQNIAGKNALILRGNGGREL

LGATLTERGARVTFCECYQRSAKHYDGAEEAMRWQSRGVTTLVVTSGEMLQQLWSLIPQWYREQWLLHCR

VVVVSERLALQARELGWQEIQVADSADNDALLRALQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004150429.1\_4625 [gene=hemX] [locus\_tag=BN49\_RS25025] [protein=uroporphyrinogen-III C-methyltransferase] [protein\_id=WP\_004150429.1] [location=4851605..4852786] [gbkey=CDS]

MTEQQNQSAVVEETREAVETTPQPENTEKKKAGNKTSLALSAIAIAIAIAAGIGLYGLNKQQATRQNATT

SELASQVAALQKAQENQKSELEGVIKQQADQLNEAKHQQETLAKQLDELQQKVAVISGSDAKTWLLAQAD

FLVKLAGRKLWSDQDVTTAAALLKSADASLADMNDPSLIGARRAITDDIATLSAVSQVDYDGMILKVNQL

ANQIDNLRLADNNDDDSPMDADSDELSSSISEWRVNLQKSWQNFMDSFITVRRRDETAVPLLAPNQDIYL

RENIRSRLLVAAQAVPRHQEETWKQSLDNVSTWVRAYYDTDDATTKAFLDEVDKLSQQSITMTVPETLQS

QALLEKLMQTRVRNLMAQPAVTAGGAPSPAPAAPAAPAAPQGE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043873.1\_4626 [gene=hemY] [locus\_tag=BN49\_RS25030] [protein=protoheme IX biogenesis protein HemY] [protein\_id=WP\_046043873.1] [location=4852790..4853986] [gbkey=CDS]

MLKILLLFALLIAGIVLGPMIAGHQGYVLIQTDNYNIETSVTGLVIILILAMVVLFAIEWLLRRIFRTGA

HTRGWFVGRKRRRARKQTEQALLKLAEGDYQQVEKLMAKNADHAEQPVVNYLLAAEAAQQRGDEARANQH

LERATELAGDDLIPVEITRVRLQLARNENHAARHGIDKLLEITPRHPEVLRLAEQAYTRTGAWQSLLDII

PSMAKANVGDEAHRAALEQLAWVGLMDKALADGGSEGLREWWRNQSRKTRALVPLQVATAERLIESDDHD

TAQQIIIDGLKKQYDDRLVMPIPRLKTNNPEQLEKVLRQQIKAVGDRPLLWSTLGQSLMRHGEWQEASIA

FRAALKQRPDAFDYAWLADALDRLHQPEEAAAMRRDGLLLTLQNNPQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002883322.1\_4627 [locus\_tag=BN49\_RS25060] [protein=amino acid permease] [protein\_id=WP\_002883322.1] [location=complement(4854987..4856372)] [gbkey=CDS]

MTEKKAELQRGLEARHIELIALGGTIGVGLFMGAASTLKWAGPSVLLAYIIAGLFVFFIMRSMGEMLFLE

PVTGSFAVYAHRYMSPFFGYLTAWSYWFMWMAVGISEITAIGVYVQFWFPEMAQWIPALIAVGLVALANL

AAVRLYGEIEFWFAMIKVTTIIVMIVVGLGVIFFGFGNGGHSIGFGNLTEHGGFFAGGWKGFLTALCIVV

ASYQGVELIGITAGEAKNPQVTLRSAVGKVLWRILIFYVGAIFVIVTIFPWDQIGSNGSPFVLTFAKIGI

TAAAGIINFVVLTAALSGCNSGMYSCGRMLYALAKNRQLPAAIGKVSRNGVPSVGVALSILILLVGSCLN

YIIPNPQRVFVYVYSASVLPGMVPWFVILISQLRFRRVHQAAIASHPFRSLLFPWANYFTMAFLICVLVG

MGLNDETRMSLFVGIIFLAAVTLIYKVFGLGRQGQVNNTAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004186366.1\_4628 [gene=rffM] [locus\_tag=BN49\_RS25065] [protein=lipopolysaccharide N-acetylmannosaminouronosyltransferase] [protein\_id=WP\_004186366.1] [location=complement(4856578..4857318)] [gbkey=CDS]

MTGTISAPLYLLRGLQLIGWRDMPHALDYLFADGVLREGTLVAINAEKMLAVEDNPEVRALIEAAEFKYA

DGISVVRSLRKKYPQAQVSRVAGADLWEALMQRAGAEGTPVFLVGGKPEVLAQTESRLRQRWQVNIVGSQ

DGYFTPEQRQALFERIRDSGAKIVTVAMGSPRQEIFMRDCRRLYPHALYMGVGGTYDVFTGHVHRAPKFW

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>lcl|NZ\_FO834906.1\_prot\_WP\_004146500.1\_4629 [gene=wzyE] [locus\_tag=BN49\_RS25070] [protein=ECA oligosaccharide polymerase] [protein\_id=WP\_004146500.1] [location=complement(4857330..4858676)] [gbkey=CDS]

MTLMQFSGLLVVWLLSTLFIATATWFEFRRVRFNFNVFFSLLFLLTFFFGFPLTSILVFRFDVSVAPPEI

LLQTLLIAVCFYAVYYVTYKTRLRSASREVAHRPLFTMNRVETHLAWGILMGLALLCVGIFFAHNGFLLF

KLNSYSQIFSAEVSGVALKRFFYFFIPAMLVVYFLRQDYKAWIFFLVSTVAFGLLTYAIVGGTRANIIIA

FAIFLFIGIIRGWISLWMLAAAGVLGIVGMFWLALKRYGMNVSGDEAFYTFLYLTRDTFSPWENLALLLQ

NYDKIDFQGLAPMIRDFYVFIPSWMWHGRPTMVLNTANYFTWEVLNNHSGLAISPTLIGSLVVMGGVWFV

PLGAVAVGLIIKWFDWLYELGNRESNRYKAAILHSFCFGAIFNMIVLAREGLDSFGSRVVFFLVIFGICL

LAAKLLYWFLDSVGLIHKRVKPLSQPQV

>lcl|NZ\_FO834906.1\_prot\_WP\_015959223.1\_4630 [locus\_tag=BN49\_RS25075] [protein=TDP-N-acetylfucosamine:lipid II N-acetylfucosaminyltransferase] [protein\_id=WP\_015959223.1] [location=complement(4858673..4859749)] [gbkey=CDS]

MTALIHVLGSDIPHHNQTVLRFFNDELAADPQARRFMIVGDEASVRDGYPALDITCYPGKKALAQAVIAT

AKANRQQRFFFHGQFNTGLWLALLSGGIRPSQFNWHIWGADLYENSASLKFRLFYPLRRMAQGRVGRVFA

TRGDLSWFANRHPRVPGELLYFPTRMDPALNTLADNDPRGDTLTILVGNSGDRSNEHIAALKAIHQQFGD

TVNVIVPMGYPAKNDAYINEVREAGAALFSGEHLQILSEKLEFHDYLALLRRCDLGYFLFARQQGIGTLC

LLIQAGIPCVLNRENPFWQDMAEQHVPVLFTSDALDVSVVREAQRQLASVDKSAIAFFRPNYLTGWQRAL

RLAAEGQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883312.1\_4631 [gene=wzxE] [locus\_tag=BN49\_RS25080] [protein=lipid III flippase WzxE] [protein\_id=WP\_002883312.1] [location=complement(4859746..4860996)] [gbkey=CDS]

MSLAKASLWTAASTLVKIGAGLLVVKLLAVSFGPAGVGQAGNFRQLVTVLGVLAGAGIFNGVTKLVAQHH

DDPPRLKQVVGTSSAMVLGFSTLLALVFLLAAAPISQGLFGHTHYQGLVRLVALVQMGIAWANFLLALMK

GFRDAAGNAFSLIAGSLIGVAAYYACYVLGGYQGALLGLALVPALVVVPAGIMLWRRGNIPLSALRPRWD

NGLAGQLSKFTLMALITSVTLPVAYVMMRNLLAAHYGWEAVGIWQGVSSISDAYLQFITASFSVYLLPTL

SRLSAKTDITREIVKSLKFVLPAVAAASLTVWLLRDFAIWLLFSDRFTAMRDLFAWQLVGDVLKVGAYVY

GYLVIAKASLRFYILTEISQFALLTAFSHWLIPAHGAVGAAQAYMATYIVYFALCSGVFLLWRKRA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883310.1\_4632 [gene=rffA] [locus\_tag=BN49\_RS25085] [protein=dTDP-4-amino-4,6-dideoxygalactose transaminase] [protein\_id=WP\_002883310.1] [location=complement(4860998..4862128)] [gbkey=CDS]

MIPFNAPPVVGTELDYMQSAMNSGKLCGDGGFTRRCQQWMEQRFGTAKALLTPSCTASLEMAALLLDIQP

GDEVIMPSYTFVSTANAFVLRGAKIVFVDIRRDTMNIDETLIEAAITDKTRAIVPVHYAGVACEMDTIMA

IADKYNLFVVEDAAQGVMSTYKGRALGTIGHIGCFSFHETKNYTAGGEGGATLINDRTLVERAEIIREKG

TNRSQFFRGLVDKYTWRDIGSSYLMSDLQAAYLWAQLEAAERINQQRLALWQNYYDALLPLARAGRIELP

TVPADCGQNAHMFYIKLRDIEDRSRLIAWLKEAEILAVFHYIPLHSCPAGEQFGEFRGEDRYTTQESERL

VRLPLFYNLSVVNQRTVINSLLSYFS

>lcl|NZ\_FO834906.1\_prot\_WP\_004146507.1\_4633 [gene=rffC] [locus\_tag=BN49\_RS25090] [protein=dTDP-4-amino-4,6-dideoxy-D-galactose acyltransferase] [protein\_id=WP\_004146507.1] [location=complement(4862134..4862808)] [gbkey=CDS]

MPVRASIDPLEWENRFFAVNSAIVRFDEHAPRLTPEALAGWSRVQAKIAASDTVRLDALQRLGFQLVEGE

VDLALPVGSPADAGADVAVEADIAPLREQAAQAFAMSRFRAPWYAADASGRFYAQWIENAVRGTFDHQCL

IYRHPEGDIRAFVSLRQITATEARIGLLAGRGAGAQLMQAARYWAASRGLSTLRVATQMGNTAALKRYIL

SGANVESTAYWLYR

>lcl|NZ\_FO834906.1\_prot\_WP\_002883307.1\_4634 [gene=rfbA] [locus\_tag=BN49\_RS25095] [protein=glucose-1-phosphate thymidylyltransferase RfbA] [protein\_id=WP\_002883307.1] [location=complement(4862786..4863667)] [gbkey=CDS]

MKGIILAGGSGTRLHPITRGVSKQLLPIYDKPMIYYPLSVLMLAGIREILIITTPDDLRDFQRLLGDGSE

FGIALHYAVQPTPDGLAQAFIIGEAFLNGEPACLVLGDNIFFGQSFSPKLRSVAARTEGATIFGYQVMDP

ERFGVVEFDDNFRALSLEEKPKQPKSNWAVTGLYFYDGKVTEYAKRVKPSERGELEITSINQMYLEDGAL

TVELLGRGFAWLDTGTHDSLIEASMFVQTVEKRQGFKIACLEEIGWRNGWLDDDGVKRAAKRLEKTGYGQ

YLLDLLRARPRQY

>lcl|NZ\_FO834906.1\_prot\_WP\_016530328.1\_4635 [gene=rffG] [locus\_tag=BN49\_RS25100] [protein=dTDP-glucose 4,6-dehydratase] [protein\_id=WP\_016530328.1] [location=complement(4863686..4864753)] [gbkey=CDS]

MRTILVTGGAGFIGSAVVREIIQHTADRVVVVDKLTYAGNLMSLAPVAQDARFAFEQVDICDRAELDRIF

RQHQPDTVMHLAAESHVDRSIDGPAAFIETNIVGTYTLLEAARSWWNTLATAQKSAFRFHHISTDEVYGD

LHGSDDFFTETTPYAPSSPYSASKASSDHLVRAWLRTYGLPTLITNCSNNYGPYHFPEKLIPLTILNALA

GKPLPVYGNGQQIRDWLYVEDHARVLYLVATRGEPGETYNIGGHNERKNIEVVETICQLLEELAPDKPQG

VAHYRDLIAFVADRPGHDLRYAIDASKIARELGWTPAETFTSGMRKTVAWYLANEAWWRQVQDGSYQGER

LGLQS

>lcl|NZ\_FO834906.1\_prot\_WP\_004181644.1\_4636 [gene=wecC] [locus\_tag=BN49\_RS25105] [protein=UDP-N-acetyl-D-mannosamine dehydrogenase] [protein\_id=WP\_004181644.1] [location=complement(4864750..4866012)] [gbkey=CDS]

MSFSTISVIGLGYIGLPTAAAFASRQKRVVGVDVNQHAVETINRGEIHIVEPDLASVVKTAVEQGYLSAT

TTPVEADAYLIAVPTPFKDRHEPDMVFVESAAKSIAPTLKKGSLVILESTSPVGSTEQMAEWLAEMRPDL

SFPQQVGEAADVNIAYCPERVLPGQVMVELIKNDRVIGGMSPVCSARASELYKIFLEGECVVTNSRTAEM

CKLTENSFRDVNIAFANELSLICADQGINVWELIRLANRHPRVNILQPGPGVGGHCIAVDPWFIVAQNPQ

QARLIRTAREVNDHKPEWVIEQVKAQVADCLNATNKRASELTIACFGLAFKPNIDDLRESPAMEIAAQIA

RWHSGTTQVVEPNIHALPKKLDGLCTLAPLEAALASADVLVMLVDHNQFKAVSGDSVTQAFIVDTKGVWR

>lcl|NZ\_FO834906.1\_prot\_WP\_002883297.1\_4637 [gene=wecB] [locus\_tag=BN49\_RS25110] [protein=UDP-N-acetylglucosamine 2-epimerase (non-hydrolyzing)] [protein\_id=WP\_002883297.1] [location=complement(4866009..4867139)] [gbkey=CDS]

MKVLTVFGTRPEAIKMAPLVHALAKDPHFEAKVCVTAQHREMLDQVLKLFSIVPDYDLNIMKPGQGLTEI

TCRILEGLKPVLESFKPDVVLVHGDTTTTMAASLAAFYQRIPVGHVEAGLRTGDLSSPWPEEGNRTLTGH

LATYHFAPTETSRQNLLRENIADSRITVTGNTVIDALFWVRDRVLGDEALRETLLQRYPFISHGKKMILV

TGHRRESFGLGFEQICQALAEIAHTHPEVQIVYPVHLNPNVSEPVNRILGHIDNVMLIEPQDYLPFVWLM

DRAWLILTDSGGIQEEAPSLGKPVLVMRDMTERPEAVAAGTVCLVGTDSQRIVAEVTRLLEDDAAYQAMS

RAHNPYGDGEACRRILSALKNNQVTL

>lcl|NZ\_FO834906.1\_prot\_WP\_002883296.1\_4638 [gene=wzzE] [locus\_tag=BN49\_RS25115] [protein=ECA polysaccharide chain length modulation protein] [protein\_id=WP\_002883296.1] [location=complement(4867196..4868242)] [gbkey=CDS]

MTQPLPGAQAVNVENELDIRGLFRALWAGKGWIVGGAVLFAAIVLVYTFFARQEWSATAITDRPTVNMLG

GYYSQQQFLRNLDIKADLASVDQPSAMDEAYKEFIMQLASWDTRRDFWLQTDYYKQRQSGNARADAAMLD

DLINNIQFMPGDAAKSINDSVKLTAETGQDANNLLRQYVAFASQRAAGHLNDELKGAWAARTVQMKAQVK

RQEEVAEAIFNRRTHSVEQALKVAQQHNISRSETDVPADQLPDSELFLLGRPMLQARLENLQAVGPEYDL

DYDQNRAMLSTLNVGPTLDPRFQTYRYLRTPEEPVKRDSPRRVFLMVMWGIVGALIGAGVALSRRRVL

>lcl|NZ\_FO834906.1\_prot\_WP\_002883295.1\_4639 [gene=wecA] [locus\_tag=BN49\_RS25120] [protein=UDP-N-acetylglucosamine--undecaprenyl-phosphate N-acetylglucosaminephosphotransferase] [protein\_id=WP\_002883295.1] [location=complement(4868256..4869359)] [gbkey=CDS]

MNLLTAITELISIFLFTTLFIFVARKVAKKIGLVDKPNYRKRHQGLIPLVGGISVYAGICFTFAIADYYI

PHASLYLACAGVLVLVGALDDRFDISVKIRAVIQAAIAVIMMMAGNLHLSSLGFIFGSWELVLGPFGFFL

TLFAVWAAINAFNMVDGIDGLLGGLSSVSFAATGIILWFDGQYSLAMWCFAMIAAILPYILLNLGALGRR

YKVFMGDAGSTMIGFTIIWILLETTQGKTHPISPVTALWIIAIPLMDMVAIMYRRLRKGMSPFSPDRQHI

HHLIMRAGFTSRQAFVLITLAAALLALVGVVAEYTRIVPEWVMLILFLVAFFLYGYCIKRAWKVARLVKR

IRRRIRRHSGNNPKLTK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883293.1\_4640 [gene=rho] [locus\_tag=BN49\_RS25125] [protein=transcription termination factor Rho] [protein\_id=WP\_002883293.1] [location=complement(4869600..4870859)] [gbkey=CDS]

MNLTELKNTPVSELITLGENMGLENLARMRKQDIIFAILKQHSKSGEDIFGDGVLEILQDGFGFLRSADS

SYLAGPDDIYVSPSQIRRFNLRTGDTISGKIRPPKEGERYFALLKVNEVNYDKPENARNKILFENLTPLH

ANSRLRMERGNGSTEDLTARVLDLASPIGRGQRGLIVAPPKAGKTMLLQNIAQSIAYNHPDCVLMVLLID

ERPEEVTEMQRLVKGEVVASTFDEPASRHVQVAEMVIEKAKRLVEHKKDVIILLDSITRLARAYNTVVPA

SGKVLTGGVDANALHRPKRFFGAARNVEEGGSLTIIATALIDTGSKMDEVIYEEFKGTGNMELHLSRKIA

EKRVFPAIDYNRSGTRKEELLTTQEELQKMWILRKIIHPMGEIDAMEFLINKLAMTKTNDDFFDMMKRS

>lcl|NZ\_FO834906.1\_prot\_WP\_002883224.1\_4641 [gene=trxA] [locus\_tag=BN49\_RS25130] [protein=thioredoxin TrxA] [protein\_id=WP\_002883224.1] [location=complement(4871190..4871519)] [gbkey=CDS]

MSDKIIHLTDDSFDTDVLKADGLTLVDFWAEWCGPCKMIAPILDEIAEEYQGKLTVAKLNIDQNPGTAPK

YGIRGIPTLLLFKNGEVAATKVGALSKGQLKEFLDANLA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883222.1\_4642 [gene=rhlB] [locus\_tag=BN49\_RS25135] [protein=ATP-dependent RNA helicase RhlB] [protein\_id=WP\_002883222.1] [location=4871861..4873126] [gbkey=CDS]

MSKTHLTEQKFSDFALHPAVIEALEKKGFHNCTPIQALALPLTLEGRDVAGQAQTGTGKTMAFLTSTFHY

LLSHPAIADRQVNQPRALIMAPTRELAVQIHADAEPLAQATGLKLGLAYGGDGYDKQLKVLESGVDILIG

TTGRLIDYAKQNHINLGAIQVVVLDEADRMYDLGFIKDIRWLFRRMPPATQRLNMLFSATLSYRVRELAF

EQMNNAEYVEVEPEQKTGHRIKEELFYPSNEEKMRLLQTLLEEEWPDRAIVFANTKHRCEDIWGHLAADG

HRVGLLTGDVAQKKRLRILEEFTRGDLDILVATDVAARGLHIPAVTHVFNYDLPDDCEDYVHRIGRTGRA

GASGHSISLACEEYALNLPAIETYIGHSIPVSKYNPDALMTDLPKPLRLTRARPGNGPRRNGPPRNRRRS

G

>lcl|NZ\_FO834906.1\_prot\_WP\_004150419.1\_4643 [gene=gppA] [locus\_tag=BN49\_RS25140] [protein=guanosine-5'-triphosphate,3'-diphosphate diphosphatase] [protein\_id=WP\_004150419.1] [location=4873245..4874753] [gbkey=CDS]

MKSMSSTSLYAAIDLGSNSFHMLVVREVAGSIQTLSRIKRKVRLAAGLNSDNTLSAEAMERGWQCLRLFA

ERLQDIPPTQIRVVATATLRLAVNAGEFLAKAQEILGTPVQVISGEEEARLIYQGVAHTTGGADQRLVVD

IGGASTELVTGTGAQTTSLFSLSMGCVTWLERYFADRSLTKENFDLAEAAAREVLLPVADVLRYHGWKVC

VGASGTVQALQEIMMAQGMDERITLAKLQQLKQRAIQCGRLEELEIEGLTLERALVFPSGLAILIAIFSE

LNIQCMTLAGGALREGLVYGMLHLSVEQDIRSRTLRNIQRRFMIDTEQAQRVGGLASHLLSQLDGSWELD

PLSRDLLLSACALHEIGLSVDFKRAPQHAAYLVNNLDLPGFTPAQKKLIATLLLNQTNAIDLSSLHQQNA

VPPRVAEHLCRLLRLAILFASRRRDDLLPAIQLTAQDEQLTLILPGNWLDEHPLGREMVDQECQWQSYVH

WILRVASGDTLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883211.1\_4644 [locus\_tag=BN49\_RS25145] [protein=LysR family transcriptional regulator] [protein\_id=WP\_002883211.1] [location=4874773..4875699] [gbkey=CDS]

MREELDFKSLRFFSALYRLGNVSPAADALDISQPTGSLLLKKLRDHFADPLFVRVGQRMIPTPRADAIAP

TISTLLQLADNDLAVKPEFLPQQSQRNFTIGMTDISQMTLLPLLQIALQQQAADGITFTVQNLDEQTLNA

LESGKCDLAIGYLTQLPESVYQQHLFDQSYVCLAAENHPRIRAQLRAEDWRQEKHLAIRVEGTAHGDMDK

LLDEHHMPRRIALTLPSFLGTGELVAESDMIAVVPEQVARHITRRYPCRSWPLPFPLAKIAIRQVWHQRL

HRDPGHIWLRSLIATLADPAQQSTSIKI

>lcl|NZ\_FO834906.1\_prot\_WP\_004181642.1\_4645 [locus\_tag=BN49\_RS25150] [protein=amidohydrolase family protein] [protein\_id=WP\_004181642.1] [location=4875830..4876828] [gbkey=CDS]

MRGKIALEEHVSTPENNRLWDSSGEAGRNGTEYMKDVERRLLDRSIQLEEMAQRHIDHVILSLTSPGAQS

ILDKAKAVSFARDTNDFIVENYVKPNPDKFSAFATLALQNPEAAAEELERAVKKLGMKGALINGYTNVKD

SEHGLYLDDESMLVFWDKVNELNVPVYLHPREPLEGPARGIYTGYESLIGSAWGFAQETAVHAIRLMMSG

LFDRYPNLNLVLGHLGEGLVHMLPRTQHRLYRQRFGCGLGKAEKPLMHYLQNNFIVTTSGHFNTHSLNNA

IEVMGADRVMFSVDYPYEDIHQACDWFDPLELEAGLKEKIAWGNASRVFNIK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883185.1\_4646 [locus\_tag=BN49\_RS25155] [protein=DUF554 domain-containing protein] [protein\_id=WP\_002883185.1] [location=4876891..4877613] [gbkey=CDS]

MAIGIFVCSGSLLVGALAGASLNRFIPEHFKKTLPLIAGLISISMGIFFVNKLHNLPPIALAIIVGTIIG

GLLNIEKWIERAGTTLRSPIERIFPAQSSASVGAEDFMNQFIAVLILFCASGTGIFGALTEGMTGDPTIL

LTKSILDFFTAAIFASTLGYIITVIFIPQLIVFVILFFAATFIMALINPSMIADFTACGGIIMLATGFRL

CGIRAFPTANMLPSLILVMPFSAAWQQFIA

>lcl|NZ\_FO834906.1\_prot\_WP\_009309743.1\_4647 [gene=rep] [locus\_tag=BN49\_RS25160] [protein=DNA helicase Rep] [protein\_id=WP\_009309743.1] [location=complement(4877618..4879639)] [gbkey=CDS]

MRLNPGQQQAVEFVTGPCLVLAGAGSGKTRVITNKIAHLIRGCGYQARHIAAVTFTNKAAREMKERVGQT

LGRKEARGLMISTFHTLGLDIIKREYAALGMKSNFSLFDDTDQVALLKELTEGLIEDDKVVLQQLISTIS

NWKNDLKTPAQAAAGAKGERDRIFAHCYGLYDAHMKACNVLDFDDLILLPTLLLQRNKEVRERWQNKIRY

LLVDEYQDTNTSQYELVKLLVGQRARFTVVGDDDQSIYSWRGARPQNLVLLSQDFPALQVIKLEQNYRSS

GRILKAANILIANNPHVFEKRLFSELGYGAELKVLSANNEDHEAERVAGELIAHHFINKTNYKDYAILYR

GNHQSRVFEKMLMQNRIPYKISGGTSFFSRPEIKDLLAYLRVLTNPDDDSAFLRIVNTPKREIGPATLQK

LGEWAMGRNKGLFTASFDMGLSQTLTGRGYESLTRFTHWLREIQQLAEREPVNAVRDLIRGIDYESWLYE

TSPSPKAAEMRMKNVNQLFTWMTEMLEGSEIDEPMTLTQVVTRFTLRDMMERGESDEELDQVQLMTLHAS

KGLEFPYVYLVGMEEGLLPHQSSIDEDNVDEERRLAYVGITRAQKELTFTLCKERRQYGELVRPEPSRFL

LELPQDDLIWEQARKTITPEERMQKGQANVANIRAMLAKAKKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002883181.1\_4648 [locus\_tag=BN49\_RS25165] [protein=peptidylprolyl isomerase PpiC] [protein\_id=WP\_002883181.1] [location=4879752..4880033] [gbkey=CDS]

MAKSAAALHILVKEEKLALEILAKLERGVSFDHLAKRYSKCPSGRNGGDLGEFQQGAMVGPFDQAVFSCP

LLKPYGPVKTKFGYHIIKVLYRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002883180.1\_4649 [gene=ppiC] [locus\_tag=BN49\_RS25170] [protein=peptidylprolyl isomerase PpiC] [protein\_id=WP\_002883180.1] [location=4880085..4880366] [gbkey=CDS]

MAKTAAALHILVKEEKLALDLLEQLKNGADFGKLAKKHSICPSGKRGGDLGEFRQGQMVPAFDKVVFSCP

ELEPTGPLHTQFGYHIIKVLYRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883178.1\_4650 [gene=ilvC] [locus\_tag=BN49\_RS25175] [protein=ketol-acid reductoisomerase] [protein\_id=WP\_002883178.1] [location=complement(4880570..4882045)] [gbkey=CDS]

MANYFNTLNLRQQLAQLGKCRFMARDEFADGASYLQGKKVVIVGCGAQGLNQGLNMRDSGLDISYALRKE

AIAEKRASWRKATENGFKVGTYEELIPQADLVVNLTPDKQHSDVVRSVQPLMKDGAALGYSHGFNIVEVG

EQIRKDITVVMVAPKCPGTEVREEYKRGFGVPTLIAVHPENDPKGEGMAIAKAWAAATGGHRAGVLESSF

VAEVKSDLMGEQTILCGMLQAGSLLCFDKLVAEGTDPAYAEKLIQFGWETITEALKQGGITLMMDRLSNP

AKLRAYALSEQLKEIMAPLFQKHMDDIISGEFSSGMMADWANDDKKLLTWREETGKTAFETAPQYEGKIG

EQEYFDKGVLMIAMVKAGVELAFETMVASGIIEESAYYESLHELPLIANTIARKRLYEMNVVISDTAEYG

NYLFSYACVPLLKEFMTTLQTGDLGTAIAEGAVDNAQLRDVNEAIRSHAIEQVGKKLRGYMTDMKRIAVA

G

>lcl|NZ\_FO834906.1\_prot\_WP\_002883176.1\_4651 [gene=ilvY] [locus\_tag=BN49\_RS25180] [protein=HTH-type transcriptional activator IlvY] [protein\_id=WP\_002883176.1] [location=4882198..4883088] [gbkey=CDS]

MDLRDLKTFLHLAESRHFGRSARAMHVSPSTLSRQIQRLEEDLGQPLFVRDNRTVTLTEAGEELRTFAQQ

TLLQYQQLRHVIDQQGPSLSGELHIFCSVTAAYSHLPPILDRFRAAHPSVEIKLSTGDAADAMEKVVTGE

ADLAIAGKPETLPGSVAFSMLENLAVVLIAPALPCPVRNQVTVERPDWSTVPFIMADQGPVRRRIELWFR

RHKISNPSIYATVGGHEAMVSMVALGCGVALLPEVVLENSPEPVRNRVMILERSDEQTPFELGVCAQKKR

LHEPLIDAFWKILPNH

>lcl|NZ\_FO834906.1\_prot\_WP\_002883174.1\_4652 [gene=ilvA] [locus\_tag=BN49\_RS25185] [protein=threonine ammonia-lyase, biosynthetic] [protein\_id=WP\_002883174.1] [location=complement(4883085..4884629)] [gbkey=CDS]

MADSQPLSGAPEGAEYLRAVLRAPVYEAVQKTPLQKMDKLSSRLDNVILVKREDRQPVHSFKLRGAYAMM

SSLTAEQKSHGVITASAGNHAQGVAFSASRLGVKALIVMPVATADIKVDAVRGFGGEVLLHGANFDEAKA

RAIELAQQQGFTWVPPFDHPMVIAGQGTLALELLQQDAHIDRVFVPVGGGGLAAGVAVLIKQLMPQIKVI

AVEAEDSACLKAALDAGHPVDLPRVGLFAEGVAVKRIGDETFRLCQEYLDDIITVDSDAICAAMKDLFED

VRAVAEPSGALALAGMKKYIAQHNIRGERLAHILSGANVNFHGLRYVSERCELGEQREALLAVTIPEEKG

SFLKFCQLLGGRSVTEFNYRFADAKDACIFVGVRLSRGLEERKEILQLLNDGGYSVVDLSDDEMAKLHVR

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043885.1\_4653 [gene=ilvD] [locus\_tag=BN49\_RS25190] [protein=dihydroxy-acid dehydratase] [protein\_id=WP\_046043885.1] [location=complement(4884632..4886482)] [gbkey=CDS]

MPKYRSATTTHGRNMAGARALWRATGMTDADFGKPIIAVVNSFTQFVPGHVHLRDLGKLVAEQIEAAGGV

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IFVSGGPMEAGKTKLSDKIIKLDLVDAMIQGADPKVSDEQSNQVERSACPTCGSCSGMFTANSMNCLTEA

LGLSQPGNGSLLATHADRKELFLNAGKRIVELTKRYYEQDDASALPRNIASKAAFENAMTLDIAMGGSTN

TVLHLLAAAQEAEIDFTMSDIDKLSRKVPQLCKVAPSTQKYHMEDVHRAGGVLGILGELDRAGLLNREVK

NVLGLTLPQTLEQYDVMVTQDDAVKKMFRAGPAGIRTTQAFSQDCRWDTLDDDRAEGCIRSLEHAYSKDG

GLAVLYGNFAENGCIVKTAGVDDSILKFTGAAKVYESQDDAVEAILGGKVVEGDVVVIRYEGPKGGPGMQ

EMLYPTSFLKSMGLGKACALITDGRFSGGTSGLSIGHVSPEAASGGNIALIEDGDMIAIDIPNRSIQLQL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002883171.1\_4654 [gene=ilvE] [locus\_tag=BN49\_RS25195] [protein=branched-chain-amino-acid transaminase] [protein\_id=WP\_002883171.1] [location=complement(4886543..4887472)] [gbkey=CDS]

MTTKKADYIWFNGEMVPWGEAKVHVMSHALHYGTSVFEGIRCYDSHKGPVVFRHREHMQRLHDSAKIYRF

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DAMVSSWNRAAPNTIPTAAKAGGNYLSSLLVGSEARRHGYQEGIALDVNGYISEGAGENLFEVKDGVLFT

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>lcl|NZ\_FO834906.1\_prot\_WP\_002883170.1\_4655 [gene=ilvM] [locus\_tag=BN49\_RS25200] [protein=acetolactate synthase 2 small subunit] [protein\_id=WP\_002883170.1] [location=complement(4887489..4887746)] [gbkey=CDS]

MMQHQVALQARFNPETLERVLRVVRHRGFHICAMNMETAPDAQNINIELTVASPRPVELLFSQLSKLVDV

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529642.1\_4656 [gene=ilvG] [locus\_tag=BN49\_RS25205] [protein=acetolactate synthase 2 catalytic subunit] [protein\_id=WP\_016529642.1] [location=complement(4887743..4889389)] [gbkey=CDS]

MNGAQWVVHALRTQGVDTVFGYPGGAIMPVYDALYDGGVEHLLCRHEQGAAMAAIGYARATGKTGVCIAT

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AFQVANSGRPGPVLVDIPKDIQMAQGDLDPHFSTVADEMAFPQAEVAQALQMLAQSQQPMLYVGGGVGMA

QAVPALREFLAVTRMPATCTLKGLGVVDADYPYYLGMLGMHGTKAANLAVQECDLLIAVGARFDDRVTGK

LNTFAPHAKVIHMDIDPAELNKLRQAHIGLTGDLNCLLPALQQPLAIDGWRERSVALRAEHAWRYDHPGE

AIYAPLLLKQLSDRKPADSVVTTDVGQHQMWSAQHMTYTRPENFITSSGLGTMGFGLPAAVGAQVARPND

TVICISGDGSFMMNVQELGTVKRKQLPLKIVLLDNQRLGMVRQWQQLFFQERYSETTLTDNPDFLTLASA

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>lcl|NZ\_FO834906.1\_prot\_WP\_175426296.1\_4657 [gene=ilvX] [locus\_tag=BN49\_RS31550] [protein=peptide IlvX] [protein\_id=WP\_175426296.1] [location=complement(4889392..4889442)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_001311244.1\_4658 [gene=ilvL] [locus\_tag=BN49\_RS29595] [protein=ilv operon leader peptide] [protein\_id=WP\_001311244.1] [location=complement(4889530..4889628)] [gbkey=CDS]

MTALLRVISLVVISVVVIIIPPCGAALGRGKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529641.1\_4659 [locus\_tag=BN49\_RS25215] [protein=YifB family Mg chelatase-like AAA ATPase] [protein\_id=WP\_016529641.1] [location=4889983..4891503] [gbkey=CDS]

MSLAIVYTRAALGIEAPLITVEVHLSNGLPGLTMVGLPETTVKEARDRVRSALINSGYAFPAKKITINLA

PADLPKEGGRYDLPIALALLVASEQLNTTRLNQYEFVGELALTGGLRGVPGAIPSAMEAIKAGRRIVVSS

DNAAEVGLIGGSDCLVADHLQEVCAFLAGQTSLSPPLAEAPARDERYEDLLDVIGQQQGKRALEIVAAGG

HNLLLIGPPGTGKTMLASRLPGLLPPLSNQEALESAAIQSLVNLHTAKTRWRQRPFRAPHHSASLAAMVG

GGSIPVPGEISLAHNGVLFLDELPEFERRVLDALREPIESGKIHISRSRAKIDYPARFQLIAAMNPSPTG

HYQGKHNRASPEQTLRYLVRLSGPFLDRFDLSLEIPLPPPGILSQGSQGEESSATVRQRVLAARERQMLR

QNKLNAHLENREMKNCCRLRREDAVWLEQTLTQLGLSIRAWQRLLKVARTIADLAEVEEIERCHLQEALS

YRAIDRMLNHLQKMMA

>lcl|NZ\_FO834906.1\_prot\_WP\_004146520.1\_4660 [locus\_tag=BN49\_RS25220] [protein=DUF413 domain-containing protein] [protein\_id=WP\_004146520.1] [location=complement(4891528..4891866)] [gbkey=CDS]

MAESFTTTNRFFDNKNYPRGFSRHGDFTIKEAQLLERHGYAFNELELGKREPVTEDEKQFVSVCRGEREP

VTEAERVWIKYMARIKRPKRFHTLSGGKPQMEGADDYTESDD

>lcl|NZ\_FO834906.1\_prot\_WP\_004181639.1\_4661 [gene=hdfR] [locus\_tag=BN49\_RS25225] [protein=HTH-type transcriptional regulator HdfR] [protein\_id=WP\_004181639.1] [location=4891985..4892806] [gbkey=CDS]

MDTELLKTFLEVSRTRHFGRAAEALYLTQSAVSFRIRQLENQLGVNLFTRHRNNIRLTTAGEKLLPYAET

LMNTWQAARKEVAHSSRHNEFSIGASASLWECMLNSWLGTLYSAPYNLQFEARIAQRQSLVKQLHERQLD

LLITTESPKMDELSSQLLGNFTLALYCASPAKNRNELNYLRLEWGPDFQQNEVGLIGSDDVPLLTTSSAE

LIYQQLSRLNGCCWLPVRWAKEKHGLHTVMDSATLSRPLYAIWLQNSDKQAQIHEILKNPILE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529411.1\_4662 [gene=murI] [locus\_tag=BN49\_RS25260] [protein=glutamate racemase] [protein\_id=WP\_016529411.1] [location=complement(4898671..4899522)] [gbkey=CDS]

MATNLQDGNTPCLAATPSDPRPTVLVFDSGVGGLSVYNEIRQLLPNLHYIYAFDNVAFPYGEKSEEFIVE

RVVEIVTAVQQRYPLALAVIACNTASTVSLPALREKFAFPVVGVVPAIKPAARLTANGIVGLLATRGTVK

RPYTHELIDRFANECRIEMLGSAELVELAEAKLHGEPVPLEELRRILRPWLRMQEPPDTVVLGCTHFPLL

QEELQRVLPEGTRLIDSGAAIARRTAWLLEHEAPDAKSSDENKAFCMALTAETEQLLPVLRRYGFSTLEK

LPL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529412.1\_4663 [gene=btuB] [locus\_tag=BN49\_RS25265] [protein=TonB-dependent vitamin B12 receptor BtuB] [protein\_id=WP\_016529412.1] [location=complement(4899467..4901305)] [gbkey=CDS]

MIKKASLMTALSVTAFSGWAQDSNSDTLVVTANRFQQPVNTVLAPTDIVTRDDIDRWQSKDLNDVMRRLP

GVDIARNGGMGQSASLYVRGTEARHVLVLIDGVPMARLGISNGVDISQIPISLVQRVEYIRGPRSAVYGS

GAIGGVVNIITMTDSDRSQVNVGMGSNGYQTYDGAINKRFGDTVVTAAGAYQTTKGFNVQPNSPYSGDSD

RDGYRNKLFLGGVQHKFDDNFSGFFRGYGYSANADYDQGNWGYAGGNDEDQSYTQSWDTGLHYHSGIYST

QLIANYQRIKDYNYSSDAGRYAAGTTLDDMEQRYIQWGNNVVVGHGAVSGGVDWKQEKLKSSGTTSTDVY

KRDTTGLYLTGQQQIDSVTLEASGREDHDEQFGWHGTWQTAAGWEFIDGYRTTLSYGTGFLAPSLGQQYG

AERFGIASNPNLKPEESKQWEAGLEGLTGPVDWRLSAYRYEIQNLIDYDNNAYYNVKSATIKGLEWTGNI

TTGPVEHHLTLQYVDPRDDETNKILYRRAKQQVKYELNGQVYDLGWDVTYHYIGKRYDYDYDNSRTVNMG

GLSLWDVGLSYPVTSHLTVRGKIANLFDKDYETVYGYQSAGREYTLSGSYTF

>lcl|NZ\_FO834906.1\_prot\_WP\_002883023.1\_4664 [gene=trmA] [locus\_tag=BN49\_RS25270] [protein=tRNA (uridine(54)-C5)-methyltransferase TrmA] [protein\_id=WP\_002883023.1] [location=4901672..4902772] [gbkey=CDS]

MTPEHLPTEQYEAQLAEKVVRLQTMMAPFAAPVPEVFRSPVSHYRMRAEFRLWHDGDDLYHIIFDQQTRS

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DALRAQGLNVHLIGRATKTKIELDQDYIDERLPVGGREMIYRQVENSFTQPNAAMNIQMLEWALDVTKGA

TGDLLELYCGNGNFSLALARNFDRVLATEIAKPSVAAAQYNIAANHIDNVQIIRMAAEEFTQAMNGVRQF

NRLQGIDLHSYQCETIFVDPPRSGLDSETEKMVQAYPRILYISCNPETLCRNLETLSQTHNVTRLALFDQ

FPYTHHMECGVLLTRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002883021.1\_4665 [locus\_tag=BN49\_RS25275] [protein=YijD family membrane protein] [protein\_id=WP\_002883021.1] [location=complement(4902824..4903183)] [gbkey=CDS]

MKHSVQDKGTLLLALIAGLSINGAFAALFSSIVPFSVFPILSLLLTVYCLHQRYQNRSMPVGLPGLAAAF

FILGVLLYSTVVRAEYPDIGSNFFPAVLSVAMVFWIGYKMRNRKDTAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151856.1\_4666 [gene=fabR] [locus\_tag=BN49\_RS25280] [protein=HTH-type transcriptional repressor FabR] [protein\_id=WP\_004151856.1] [location=complement(4903199..4903834)] [gbkey=CDS]

MMGVRAQQKEKTRRSLVEAAFSQLSAERSFASLSLREVAREAGIAPTSFYRHFRDVDELGLTMVDESGLM

LRQLMRQARQRIAKGGSVIRTSVSTFMEFIGNNPNAFRLLLRERSGTSAAFRAAVAREIQHFIAELADYL

ELENHMPRAFTEAQAEAMVTIVFSAGAEALDVGPEQRRQLEERLVLQLRMISKGAYYWYRREQEKMSHHS

E

>lcl|NZ\_FO834906.1\_prot\_WP\_002883016.1\_4667 [gene=sthA] [locus\_tag=BN49\_RS25285] [protein=Si-specific NAD(P)(+) transhydrogenase] [protein\_id=WP\_002883016.1] [location=4904031..4905431] [gbkey=CDS]

MSHSWDYDAIVIGSGPGGEGAAMGLVKQGARVAVIERYHNVGGGCTHWGTIPSKALRHAVSRIIEFNQNP

LYSDHSRLLRSSFADILNHADSVINQQTHMRQGFYERNHCEILQGNAHFVDEHTLALECHDGTVETVTAE

KFVIACGSRPYHPADVDFHHPRIYDSDSILSLQHEPRHVIIYGAGVIGCEYASIFRGMEVKVDLINTRDR

LLAFLDQEMSDSLSYHFWNSGVVIRHNEEYEKIEGVDDGVIMHLKSGKKLKADCLLYANGRTGNTDTLAL

ENIGLQTDSRGQLKVNSMYQTALPHIYAVGDVIGYPSLASAAYDQGRIAAQALVKGEASAHLIEDIPTGI

YTIPEISSVGKTEQQLTAMKVPYEVGRAQFKHLARAQIVGMSVGTLKILFHRETKEILGIHCFGERAAEI

IHIGQAIMEQKGGGNTIEYFVNTTFNYPTMAEAYRVAALNGLNRLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002883015.1\_4668 [gene=oxyR] [locus\_tag=BN49\_RS25290] [protein=DNA-binding transcriptional regulator OxyR] [protein\_id=WP\_002883015.1] [location=complement(4905414..4906331)] [gbkey=CDS]

MNIRDLEYLVALAEHRHFRRAADSCHVSQPTLSGQIRKLEDELGVMLLERTSRKVLFTQAGLLLVDQART

VLREVKVLKEMASQQGETMSGPLHIGLIPTIGPYLLPHIIPMLHQTFPKLEMYLHEAQTHQLLAQLDSGK

LDCAILALVKESEAFIEVPLFDEPMMLAIYEDHPWANRDRVPMSDLAGEKLLMLEDGHCLRDQAMGFCFE

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RYEHLAEAIRGTMDGHFDKALKQAV

>lcl|NZ\_FO834906.1\_prot\_WP\_016528799.1\_4669 [gene=argH] [locus\_tag=BN49\_RS25295] [protein=argininosuccinate lyase] [protein\_id=WP\_016528799.1] [location=complement(4906590..4907963)] [gbkey=CDS]

MALWGGRFTQAADQRFKQFNDSLRFDYRLAEQDIVGSVAWSKALVTVGVLSAAEQQQLEEALNVLLEEVR

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ETAQQNQDAVMPGYTHLQRAQPVTFAHWCLAYVEMLARDESRLQDALKRLDVSPLGCGALAGTAYEIDRE

QLAGWLGFASATRNSLDSVSDRDHVLELLSDAAIGMVHLSRFAEDLIFFNSGEANFVELSDRVTSGSSLM

PQKKNPDALELIRGKCGRVQGALTGMMMTLKGLPLAYNKDMQEDKEGLFDALDTWLDCLHMAALVLDGIQ

VKRPRCAEAAQQGYANATELADYLVAKGVPFREAHHIVGEAVVEAIAQGKPLEALTLADLQKFSPVIADD

VYPILSLQSCLEKRAAKGGVSPQQVAQAINEAKVRLS

>lcl|NZ\_FO834906.1\_prot\_WP\_004187843.1\_4670 [gene=argB] [locus\_tag=BN49\_RS25300] [protein=acetylglutamate kinase] [protein\_id=WP\_004187843.1] [location=complement(4908063..4908839)] [gbkey=CDS]

MMNPLIIKLGGVLLDSEEALERLFTALVNYREAHQRPLIIVHGGGCVVDELMKQLNLPVQKKNGLRVTPA

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YLPVVSSIGVTDEGQLMNVNADQAATALAATLGADLILLSDVSGILDGKGQRIAEMTAEKAEQLIEQGII

TDGMIVKVNAALDAARALGRPVDIASWRHAEQLPALFNGTPIGTRILA

>lcl|NZ\_FO834906.1\_prot\_WP\_004181637.1\_4671 [gene=argC] [locus\_tag=BN49\_RS25305] [protein=N-acetyl-gamma-glutamyl-phosphate reductase] [protein\_id=WP\_004181637.1] [location=complement(4908846..4909850)] [gbkey=CDS]

MLNTLIVGASGYAGAELVTYINRHPHMNITALTVSAQSNDAGKLISDLHPQLKGIVDMPLQPMSDISEFS

AGVDVVFLATAHEVSHDLAPQFLAAGCVVFDLSGAFRVNDGAFYEKYYGFTHQHPDLLKQAVYGLAEWSA

DALKDAQLIAVPGCYPTAAQLSLKPLIEANLLDLNQWPVINATSGVSGAGRKAAIGNSFCEVSLQPYGIF

NHRHQPEIASHLGAKVIFTPHLGNFKRGILETITCRLKPGVGHAQIAAVYQQAYADKPLVRLYDKGVPAL

KSVEGLPFCDIGFAVQDDHLIVVAAEDNLLKGAAAQAVQCANIRFGFAETQSLI

>lcl|NZ\_FO834906.1\_prot\_WP\_004177969.1\_4672 [gene=argE] [locus\_tag=BN49\_RS25310] [protein=acetylornithine deacetylase] [protein\_id=WP\_004177969.1] [location=4909964..4911115] [gbkey=CDS]

MKNNLPPFIEIYRALIATPSISATEEALDQSNESLINLLAGWFRDLGFNVEIQPVPDTRHKFNLLASTGH

GAGGLLLAGHTDTVPFDDGRWTRDPFTLTEHDNKLYGLGTADMKGFFAFILDALRDVDVTTLKKPLYILA

TADEETSMAGARYFAETTRLRPDCAIIGEPTSLQPIRAHKGHMSNAIRIQGQSGHSSDPARGVNAIELMH

DAIGRIMQLRDLLKERYHFEAFTVPYPTLNLGAIHGGDASNRICACCELHMDIRPLPGMTLNDLNGLLGE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004181636.1\_4673 [gene=ppc] [locus\_tag=BN49\_RS25315] [protein=phosphoenolpyruvate carboxylase] [protein\_id=WP\_004181636.1] [location=4911374..4914025] [gbkey=CDS]

MNEQYSALRSNVSMLGKVLGDTIKDALGENILDRVETIRKLSKSSRAGNEANRQELLTTLQNLSNDELLP

VARAFSQFLNLANTAEQYHSISANGEAASNPEVIARTLRKLKDQPNLNEETIKQAVESLSLELVLTAHPT

EITRRTLIHKMVEVNNCLKQLDNKDIADYEHHQLMRRLRQLIAQSWHTDEIRKHRPSPVDEAKWGFAVVE

NSLWEGVPNYLRELNEQLEANLGYQLPVDFVPVRFTSWMGGDRDGNPNVTADITRHVLLLSRWKATDLFL

KDVQVLISELSMVECTDELRALAGAEGAQEPYRYLMKKLRSQLMETQAWLEARLKGQKLPKPAGLITQNE

QLWEPLYACYKSLQACGMGIIANGELLDTLRRVKSFGVPLVRIDIRQESTRHTEALGEMTRYLGIGDYES

WSEADKQAFLIRELNSKRPLLPRQWEPSEETREVLDTCKVIAEAPRGSIAAYVISMAKTPSDVLAVHLLL

KEAGIGFALPVAPLFETLDDLNNANDVMTQLLNIDWYRGFIQGKQMVMIGYSDSAKDAGVMAASWAQYQA

QDALIKTCEKAGIELTLFHGRGGSIGRGGAPAHAALLSQPPGSLKGGLRVTEQGEMIRFKYGLPEVTISS

LSLYTSAILEANLLPPPEPKAEWRDIMAELSDVSCKMYRGYVRENKDFVPYFRSATPEQELGKLPLGSRP

AKRRPTGGVESLRAIPWIFAWTQNRLMLPAWLGAGAALQKVVEGGKQSELEAMCRDWPFFSTRLGMLEMV

YSKADLWLAEYYDQRLVKPELWALGSELRKLLAADINVVLAIANDSHLMADLPWIAESIQLRNIYTDPLN

VLQAELLHRSRQAEEEGKDPDPRVEQALMVTIAGVAAGMRNTG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530043.1\_4674 [gene=zinT] [locus\_tag=BN49\_RS25320] [protein=metal-binding protein ZinT] [protein\_id=WP\_016530043.1] [location=complement(4914069..4914719)] [gbkey=CDS]

MTRKIPLLALGFGMALASAQAFAHGNHSHGPALTEVERQASEGIFADKDVQDRALSDWEGVWQSVNPYLL

NGDLDPVLEQKAKKPGGKSVEEYRAYYKKGYATAVEQIGIEDDVIEFHVGQTVNSCKYRYSGYKILHYAS

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DEMLHH

>lcl|NZ\_FO834906.1\_prot\_WP\_074185302.1\_4675 [locus\_tag=BN49\_RS25325] [protein=AraC family transcriptional regulator] [protein\_id=WP\_074185302.1] [location=4914744..4915730] [gbkey=CDS]

MATNCYDITYLIWEARATGKRFYRWNNVRYDEKGDALNGRMMDNDINQLIDALLKKQTSLGRVYFAGETR

SPAEPVVQVDFPRLNILLDGQLPDQALGDNAPLLEAHDVLYIPGDSWNCPQWQAPCLLLSILFAKQQLEC

SLQHWNGKAITVVDKRQALRRGPRVGSFLLQALNELRMQPQEQQTARSIVVSLLSHCHDLLGSQAQTSSR

SQALFEAIRQYMDIHYAEPLSRESVAQAFYLSPNYLSHLFQKCGPMGFNEYLNHIRLEQARMLLKGHDMK

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177977.1\_4676 [gene=fsa] [locus\_tag=BN49\_RS25330] [protein=fructose-6-phosphate aldolase] [protein\_id=WP\_004177977.1] [location=4915936..4916598] [gbkey=CDS]

MELYLDTANVAEVERLARIYPLAGVTTNPSIIAAGKVPVWDVLPRLQKAVGPEGTLFAQTMSRDAQGMVE

EAKRLSNAVPGIVVKIPVTAEGLAAIKLLKKEGIPTLGTAVYSASQGLLAALAGAKYVAPYVNRVDAQGG

DGIRMVQELQSLLEMHAPESKVLAASFKTPRQALDCLLAGCEAITLPLDVAQQMLGTPAVESAIEKFEQD

WNNAFGTLNL

>lcl|NZ\_FO834906.1\_prot\_WP\_004146274.1\_4677 [locus\_tag=BN49\_RS25335] [protein=glycerol dehydrogenase] [protein\_id=WP\_004146274.1] [location=4916653..4917756] [gbkey=CDS]

MDRIIQSPGKYIQGAGAIKRLGDYLKPLAERWLVVGDKFVLGFAEEMLRKSLADAGLAAEIAPFGGECSH

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LMLPRNPNMVIVDTQIVAGAPARLLAAGIGDALATWFEARACSRSGATTMAGGKCTQAALALAELCYNTL

LEEGEKAMLAAEQHVVTPALERVVEANTYLSGVGFESGGLAAAHAIHNGMTAIPDAHHYYHGEKVAFGTL

TQLVLENAPVDEIETVAALCHSVGLPITLAQLDIKGDIPTKMRLVAEAACAEGETIHNMPGGVDSDQVYA

ALLVADQYGQRFLQEWE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529657.1\_4678 [locus\_tag=BN49\_RS25340] [protein=DMT family transporter] [protein\_id=WP\_016529657.1] [location=complement(4917820..4918701)] [gbkey=CDS]

MARKSDPLAFGGLALLTLIWSFSWIAMKQVTSYIGAFDFTALRCIFGAVVLWIVMLIRGKALKPTPFGYT

LAIALLQTCGMVGLAQWALMSGGAGKVAILSYTMPFWVVVMAALFLGERMRRWQYIAIGVACVGLILVLQ

PWQLDFTSLKSALLAILSGVSWGAGAIVAKRMYTRYPQVDLLALTTWQMLYAAIVMSVVAWLVPQRAVDW

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LALAMISIKRRGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002882952.1\_4679 [gene=metF] [locus\_tag=BN49\_RS25345] [protein=methylenetetrahydrofolate reductase] [protein\_id=WP\_002882952.1] [location=complement(4918845..4919732)] [gbkey=CDS]

MSFFHANQREALNQSLAEVQGQINVSFEFFPPRTSEMEQTLWKSIDRLSSLKPKFVSVTYGANSGERDRT

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EVGDFDISVAAYPEVHPEAKSAQADLLNLKRKVEAGANRAITQFFFDVESYLRFRDRCVSAGIDVEIIPG

ILPVSNFKQAKKFADMTNVRIPVWMSKMFEGLDNDAETRQLVGANIAMDMVKILSREGVKDFHFYTLNRA

EMSYAICHTLGVRPA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529658.1\_4680 [locus\_tag=BN49\_RS25350] [protein=LysR family transcriptional regulator] [protein\_id=WP\_016529658.1] [location=complement(4919961..4920869)] [gbkey=CDS]

MTTSRLHSLDIRLLRAFAVVAEENNISRAAQRLFISQPPLTRHIRHLEAQLGVTLFQRHSKGLILTDAGR

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QVRKGKLDAALVALPLNTEGLHLHPLPYHEPLIAALPASWPEAARPGLTLSALNHRPLFWFKRERNPGFF

DYTRRIFDRAGYAPTYVEEPAEHDVLLARIARGEGMILLPASFSAIQRQGVAFCPVAEGDAMPLSLGVIY

APHQSESVQQWLSLLDGILATG

>lcl|NZ\_FO834906.1\_prot\_WP\_002882947.1\_4681 [locus\_tag=BN49\_RS25355] [protein=carboxymuconolactone decarboxylase family protein] [protein\_id=WP\_002882947.1] [location=4920961..4921332] [gbkey=CDS]

MSSERYIIGQEMLQRVDGKGGEAVVDSLRDIAPDFARYLIEFPFGDIYARPGLDLRSREIATIAALTALG

NAEPQLKVHIAAGLNVGLTQEEITEAIMQMAVYAGFPAALNGLFAARAVFAAH

>lcl|NZ\_FO834906.1\_prot\_4682 [locus\_tag=BN49\_RS25360] [protein=bifunctional metallophosphatase/5'-nucleotidase] [pseudo=true] [location=complement(4921370..4922926)] [gbkey=CDS]

MKLKAMSAALLLTLPFWACAKDVTIIYTNDLHAHVEPYKVPWIADGKRDIGGWANITTMVKQEKAKNNAT

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DKSFWDKPYTIIEKDGVKIGVIGLHGVFAFNDTVSAATRVGIEARDEVKWLQHYIDELNGKVDLTVALIH

EGVPARQSS\*GGTDVRRALDKDIQTAGQVKGLDVLITGHAHVGTPEPIKVGNTLILSTDSGGIDVGKLVL

DYQEKPHQFTVKHFELKTLYADEWKPDPQTKQVIDGWNKQLDQLVQQVITQSPVELTRAYGISSPLGNLA

ADALLLAAGRSTQMALTNSGGIRNEIPAGAVSMGAVISTFPFPNELVIMDLTGKQLRSLMEHGAGLSNGV

LQVSRGLEMKYDSSKPVGQRVVLFRLNGKPIDDTTVYHIATNSFLADGGDGFVAFTEGQARNTSGGYYVS

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>lcl|NZ\_FO834906.1\_prot\_WP\_023342387.1\_4683 [locus\_tag=BN49\_RS25365] [protein=hypothetical protein] [protein\_id=WP\_023342387.1] [location=4923065..4924201] [gbkey=CDS]

MDTLFTINACKTFGCRNLGLPSAAEYHFPNFRLGYPALYCAACGSYPPLFNEREFRPWLAAYLTDHARRY

GYFCPVCYQRDIIRYGRNPQGTQRLQCRHCKKVWTPKFPHIAPIEAPRRICSVPLIAPFQGNAAGQKLYF

LLSFDAVRGNVIHLTSNFTPFAVGESLRYRWRGGQADREETDDIIQRISLTEMRFLQRSQFDEIQYGSAM

QKRHARGNILRPVIAAHGHFKLLSQRFPEVKTHVIAHECFLRGAAIVAWAPLFRQRQGDLWYVEEEIRNP

ASPAPWQLQGKTHHGWWQNSWQRWTQEENQKMVCRLAGTAEENAFLPDLAASRRFTIWLKNRPAFAQSAL

YSAGRVTQIVASLVQEYNATLTAAAPGG

>lcl|NZ\_FO834906.1\_prot\_WP\_002882944.1\_4684 [locus\_tag=BN49\_RS25370] [protein=bifunctional aspartate kinase/homoserine dehydrogenase II] [protein\_id=WP\_002882944.1] [location=complement(4924176..4926608)] [gbkey=CDS]

MSVIAQAGAKGRQLHKFGGSSLADAKCYLRVAGIMKEYSQAGDMMVVSAAGSTTNQLISWLKLSQSDRLA

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LNQLGMEAAWLDARAFLRAERAAQPQVDEGLSYPLLQQLMAQHPNKRLVVTGFISRNQAGETVLLGRNGS

DYSATQIGALAGASRVTIWSDVAGVYSADPRKVKDACLLPLLRLDEASELARLAAPVLHARTLQPVSASD

IDLQLRCSYTPEQGSTRIERVLASGTGARIVTSHDDVCLVEFQVPAGHDFKLAHKELDALLKRAQLRPLA

VGVHADRKLLQFCYTSEVADSALKLLDEAGLPGELRLRQKLALVAMVGAGVTRNPLHCHRFWQQLKGQPV

EFTWQSEEGISLVAVLRAGPTESLIQGLHQSLFRAEKRIGLMLFGKGNIGSRWLELFAREQTTLSARTGF

EFILAGVVDSKRSLLNYDGLDASRALAFFNDEAVEQDEESLFLWMRAHPYDDLVVLDVTASEQLADQYLD

FASHGFHVISANKLAGASSSDKYRQIHDAFEKTGRHWLYNATVGAGLPVNHTVRDLIDSGDTILGLSGIF

SGTLSWLFLQFDGTVPFTDLVDQAWQQGLTEPDPRVDLSGKDVMRKLVILAREAGYDIEPDQVRVESLVP

AHCEEGSVDHFFENGEELNEQMLQRLEAAREMGLVLRYVARFDANGKARVGVEAVREEHPLAALLPCDNV

FAIESRWYRDNPLVIRGPGAGRDVTAGAIQSDINRLAQLL

>lcl|NZ\_FO834906.1\_prot\_WP\_004150388.1\_4685 [gene=metB] [locus\_tag=BN49\_RS25375] [protein=cystathionine gamma-synthase] [protein\_id=WP\_004150388.1] [location=complement(4926611..4927771)] [gbkey=CDS]

MTRKQATIAVRSGLNDDEQYGCVVPPIHLSSTYNFTGFNEPRAHDYSRRGNPTRDVVQRALAELEGGAGA

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VLVESPSNPLLRVVDIAKICGLAREAGAISVVDNTFLSPALQNPLALGADLVLHSCTKYLNGHSDVVAGV

VIAKDPATVTELAWWANNIGVTGSAFDSYLLLRGLRTLSPRMEVAQRNALAIVEYLKTQPLVKKLYHPSL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002882924.1\_4686 [gene=metJ] [locus\_tag=BN49\_RS25380] [protein=met regulon transcriptional regulator MetJ] [protein\_id=WP\_002882924.1] [location=4928039..4928356] [gbkey=CDS]

MAEWSGEYISPYAEHGKKSEQVKKITVSIPLKVLKILTDERTRRQVNNLRHATNSELLCEAFLHAFTGQP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002882922.1\_4687 [gene=rpmE] [locus\_tag=BN49\_RS25385] [protein=50S ribosomal protein L31] [protein\_id=WP\_002882922.1] [location=complement(4928458..4928670)] [gbkey=CDS]

MKKGIHPNYDEITATCSCGNVMKIRSTVGHDLNLDVCGKCHPFFTGKQRDVATGGRVDRFNKRFSIPGSK

>lcl|NZ\_FO834906.1\_prot\_WP\_021312592.1\_4688 [gene=priA] [locus\_tag=BN49\_RS25390] [protein=primosomal protein N'] [protein\_id=WP\_021312592.1] [location=4928923..4931118] [gbkey=CDS]

MSVAHVALPVPLPRTFDYLLPEGMAVKAGCRVRVPFGKQERIGIVAAVSERSELPLDELKPVAEALDDEP

VFSTTVWRLLMWAAEYYHHPIGDVLFHALPVMLRQGKPASATPLWYWFATEQGQVVDLNGLKRSRKQQQA

LAALRQGKIWRHQVGELEFNEAALQALRGKGLAELACEAPALTDWRSAYSVAGERLRLNTEQATAVGAIH

SAADRFSAWLLAGITGSGKTEVYLSVLENVLVQGRQALVMVPEIGLTPQTIARFRQRFNAPVEVLHSGLN

DSERLSAWLKAKNGEAAIVIGTRSSLFTPFKDLGVIVIDEEHDSSYKQQEGWRYHARDLAVWRAHSEQIP

IILGSATPALETLHNVRQGKYRQLTLSKRAGNARPAQQHVLDLKGQPLQAGLSPALISRMRQHLQADNQV

ILFLNRRGFAPALLCHDCGWIAECPRCDSYYTLHQAQHHLRCHHCDSQRPIPRQCPSCGSTHLVPVGIGT

EQLEQALAPLFPEVPISRIDRDTTSRKGALEEHLAAVHRGGARILIGTQMLAKGHHFPDVTLVSLLDVDG

ALFSADFRSAERFAQLYTQVSGRAGRAGKQGEVILQTHHPEHPLLQTLLYKGYDAFAEQALAERQTMQLP

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530310.1\_4689 [gene=cytR] [locus\_tag=BN49\_RS25400] [protein=DNA-binding transcriptional regulator CytR] [protein\_id=WP\_016530310.1] [location=4931269..4932297] [gbkey=CDS]

MKPKKQVVAATMKDVALKANVSTATVSRALMNPDKVSQATRNRVEQAALEVGYLPQSLGRNMKRNESRTI

LVIVPDICDPFFSEVIRGIEVTAAEHGYLVLIGDCAHQNQKEKTFIDLIITKQIDGMVLLSSRLPFDASV

EEQRNLPPMVMSNEFAPELELPTVHIDNLTAAFNAVNYLHELGHQRIGCIAGPEDIPLCHYRLQGYVQAL

RRSGITVDPHYIARGNFTFEAGANALEQLLAQPVPPTAVFCHSDVMALGALSLAKRRGLKVPDDLSIVGF

DNIALSEFCDPPLTTVSQPRFDIGREGMLLLLEQMQGHNVNSGSRLLDCELIVRGSTQKIRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002882919.1\_4690 [gene=ftsN] [locus\_tag=BN49\_RS25405] [protein=cell division protein FtsN] [protein\_id=WP\_002882919.1] [location=4932391..4933359] [gbkey=CDS]

MAQRDYVRRSQPASSRRKKSTTRSSRNKQSSLPAISPAMVAIAAAVLVAFIGGLYFITHHKKEEAEAMQN

RQAAGNGLPPKPEERWRYIKELESRQPGVRAPTEPTAGGEVMKPEQLTDEQRQLLAQMQADMRQQPTQLT

EVPWNEQTPAQRQQTLQRQRLAQQQQQAQQQQWAQTQAQTVQQQPPRVQQPKPVQQQQPKQTASNQQPYQ

DLLQTPAHTNTTQPRTQAAAPVTRVEEAPKTTAEKKDDRSWMIQCGSFKGAEQAETVRAQLAFEGFASHI

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>lcl|NZ\_FO834906.1\_prot\_WP\_002882918.1\_4691 [gene=hslV] [locus\_tag=BN49\_RS25410] [protein=ATP-dependent protease subunit HslV] [protein\_id=WP\_002882918.1] [location=4933451..4933981] [gbkey=CDS]

MTTIVSVRRNGHVVIAGDGQATLGNTVMKGNVKKVRRLYNDKVIAGFAGGTADAFTLFELFERKLEMHQG

HLVKAAVELAKDWRTDRMLRKLEALLAVADENASLIITGNGDVVQPENDLIAIGSGGPYAQAAARALLEN

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>lcl|NZ\_FO834906.1\_prot\_WP\_002882917.1\_4692 [gene=hslU] [locus\_tag=BN49\_RS25415] [protein=HslU--HslV peptidase ATPase subunit] [protein\_id=WP\_002882917.1] [location=4933991..4935325] [gbkey=CDS]

MSEMTPREIVSELDKHIIGQDAAKRSVAIALRNRWRRMQLNEELRHEVTPKNILMIGPTGVGKTEIARRL

AKLANAPFIKVEATKFTEVGYVGKEVDSIIRDLTDAAIKMVRMQSIDKNRYRAEELAEERVLDVLIPPAK

NNWGQTEPSQEPSAARQAFRKKLREGQLDDKEIEIDLAAAPMGVEIMSPPGMEEMTSQLQSMFQNLGGQK

QKPRKLKIKDAMKLLIEEEAAKLVNPEELKQEAIDAVEQHGIVFIDEIDKICKRGGNTSGPDVSREGVQR

DLLPLVEGCTVSTKHGMVKTDHILFIASGAFQVASPSDLIPELQGRLPIRVELKALTTHDFERILTEPNA

SITVQYKALMATEGVNIEFTEDGIKRIAQAAWQVNETTENIGARRLHTVLERLVEDISYDASEMNGQTVT

IDAEYVSKHLDVLVADEDLSRFIL

>lcl|NZ\_FO834906.1\_prot\_WP\_002882914.1\_4693 [gene=menA] [locus\_tag=BN49\_RS25420] [protein=1,4-dihydroxy-2-naphthoate polyprenyltransferase] [protein\_id=WP\_002882914.1] [location=4935395..4936315] [gbkey=CDS]

MTDISRSQAWLESLRPKTLPLAFAAIIVGTVLAWEQGHFDPWVALLALITAGLLQILSNLANDYGDAVKG

SDKPDRIGPLRGMQKGVITPQQMKRALIVTVVLICLFGLALLCAAWQSVGDFIGFLALGGLSIVAAITYT

VGTRPYGYIGLGDISVLVFFGWLSVLGSWYLQAHNVEAAIFLPATACGLLATAVLNINNLRDIDSDRQNG

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LEKTVKGALLTNLLFVIGIIASKLMA

>lcl|NZ\_FO834906.1\_prot\_WP\_002882913.1\_4694 [gene=rraA] [locus\_tag=BN49\_RS25425] [protein=ribonuclease E activity regulator RraA] [protein\_id=WP\_002882913.1] [location=4936408..4936893] [gbkey=CDS]

MKYDTSELCDIYQEDVNVVEPLFSNFGGRSSFGGQIITVKCFEDNGLLYDLLEQNGRGHILLIDGGGSVR

RALIDADLARLAVQNEWEGLVVYGAVRQVDDLEELDIGIQALAAIPVGAAGEGIGESDVRVNFGGVTFFS

GDHLYADNTGMILSEDPLDIE

>lcl|NZ\_FO834906.1\_prot\_WP\_002882911.1\_4695 [gene=pfkA] [locus\_tag=BN49\_RS25430] [protein=6-phosphofructokinase] [protein\_id=WP\_002882911.1] [location=complement(4936955..4937917)] [gbkey=CDS]

MIKKIGVLTSGGDAPGMNAAIRGVVRAALTEGLEVFGIYDGYLGLYEDRMVQLDRYSVSDMINRGGTFLG

SARFPEFREEHIRAVAIENMKKRGLDALVVIGGDGSYMGAMRLTEMGFPCIGLPGTIDNDIKGTDYTIGF

FTALSTVVEAIDRLRDTSSSHQRISVVEVMGRYCGDLTLAAAIAGGCEFIMVPEVEYTRDDLVAEIKAGI

AKGKKHAIVAITEHMCDVDELASYIEKETGRETRATVLGHIQRGGSPVPYDRILASRMGAYAIELLLQGH

GGRCVGIQNEKLVHHDIIDAIENMKRPFKNDWLDCAKKLY

>lcl|NZ\_FO834906.1\_prot\_WP\_002882907.1\_4696 [gene=fieF] [locus\_tag=BN49\_RS25435] [protein=CDF family cation-efflux transporter FieF] [protein\_id=WP\_002882907.1] [location=complement(4938114..4939016)] [gbkey=CDS]

MNQSYGRLVSRAAIAATAMASALLLIKIFAWWYTGSVSILAALVDSLVDIAASLTNLLVVRYSLQPADEE

HTFGHGKAESLAALAQSMFISGSALFLFLTGIQHLVRPEPLQAAGVGVVVTLIALVSTLALVTFQRWVVR

KTQSQAVRADMLHYQSDVMMNGAILVALGLSWYGWHRADALFALGIGIYILYSALRMGYEAVQSLLDRAL

PDEERQDIITIVTAWPGIRGAHDLRTRQSGPTRFIQIHLEMEDNLPLVQAHVIADQVEQAILRRFPGSDV

IIHQDPSSVVPAAQQGFFER

>lcl|NZ\_FO834906.1\_prot\_WP\_002882903.1\_4697 [gene=cpxP] [locus\_tag=BN49\_RS25440] [protein=cell-envelope stress modulator CpxP] [protein\_id=WP\_002882903.1] [location=complement(4939175..4939678)] [gbkey=CDS]

MRNVIAAVMASTLALSAYSQAAEVVTSVNWLPGDDGGQRGSQSHMFDGISLTEQQRQQLRDLMQRARHDR

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DQLREVARMQKGSAMMLSSSSNTLQPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002882901.1\_4698 [gene=cpxR] [locus\_tag=BN49\_RS25445] [protein=envelope stress response regulator transcription factor CpxR] [protein\_id=WP\_002882901.1] [location=4939828..4940526] [gbkey=CDS]

MNKILLVDDDRELTSLLKELLDMEGFNVLVAHDGEQALALLDDSVDLLLLDVMMPKKNGIDTLKELRQTH

QTPVIMLTARGSELDRVLGLELGADDYLPKPFNDRELVARIRAILRRSHWSEQQQTTEAGSPTLEVDALS

LNPGRQEANFDGQTLELTGTEFTLLYLLAQHLGQVVSREHLSQEVLGKRLTPFDRAIDMHISNLRRKLPE

RKDGHPWFKTLRGRGYLMVSAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002882898.1\_4699 [gene=cpxA] [locus\_tag=BN49\_RS25450] [protein=envelope stress sensor histidine kinase CpxA] [protein\_id=WP\_002882898.1] [location=4940523..4941896] [gbkey=CDS]

MIGSLTARIFAIFWLTLALVLMLVLMLPKLDSRQMTELLESEQRQGIMIEQHVEAELANDPPNDLMWWRR

LFRAIDKWAPPGQRLLLVTSEGRVIGAERNEMQIIRNFIGQADNADHPQKKRYGRLEMVGPFSVRDGEDN

YQLYLIRPASTSQSDFINLLFDRPLLLLIVTMLVSAPLLLWLAWSLAKPARKLKNAADEVAQGNLRQHPE

LEAGPQEFLAAGASFNQMVTALERMMTSQQRLLSDISHELRTPLTRLQLGTALLRRRSGESKELERIETE

AHRLDSMINDLLVMSRNQAKNALVSETVKANQLWNEVLDNAAFEAEQMGKSFTVEYPPGPWPLYGNPNAL

ESALENIVRNALRYSHTKISVSFSVDKDGITVNVDDDGPGVSPEDREQIFRPFYRTDEARDRESGGTGLG

LAIVETAIQQHRGWVKADDSPLGGLRLTIWLPLYKRT

>lcl|NZ\_FO834906.1\_prot\_WP\_002882896.1\_4700 [gene=yiiM] [locus\_tag=BN49\_RS25455] [protein=6-hydroxyaminopurine reductase] [protein\_id=WP\_002882896.1] [location=complement(4941969..4942643)] [gbkey=CDS]

MHYPVNVFVGKIRDYAGSRPSAIDKIQVDGELQLGDLGLDGDQQAEKKIHGGPDRALCHYPREHYADWIR

DFPQQAERFCAPAFGENLSTTGLTEQNVYIGDIFRWGEALIQVTQPRSPCFKLNFHFAINDMAQLMQNSG

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SGKIEDSSRRLWGK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531062.1\_4701 [gene=sodA] [locus\_tag=BN49\_RS25460] [protein=superoxide dismutase [Mn]] [protein\_id=WP\_016531062.1] [location=complement(4942716..4943336)] [gbkey=CDS]

MSYTLPSLPYAYDALEPHFDKQTMEIHHTKHHQTYVNNANAALESLPEFANLSAEELITKLDQLPADKKT

VLRNNAGGHANHSLFWKGLKTGTTLQGDLKAAIERDFGSVENFKAEFEKAAATRFGSGWAWLVLKGDKLA

VVSTANQDSPLMGEAISGASGFPIIVLDVWEHAYYLKFQNRRPDYIKAFWDVVNWDEAAARFAAKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002882892.1\_4702 [gene=rhaT] [locus\_tag=BN49\_RS25465] [protein=L-rhamnose/proton symporter RhaT] [protein\_id=WP\_002882892.1] [location=4943626..4944660] [gbkey=CDS]

MNHAITMGIFWHLIGAASAACFYAPFKKVKHWSWETMWSVGGIVSWLILPWAISATLLPDFWAYYRSFSA

STLLPVFLFGAMWGIGNINYGLTMRYLGMSMGIGIAIGITLIVGTLMTPIINGQFAVLMHTQGGQMTLLG

VLVAVIGVGIVTRAGQLKERKMGIKAEEFNLKKGLLLAVMCGIFSAGMSFAMNAAKPMHDAAAALGVDPL

YAALPSYVVIMGGGALVNLGFCFIRLAKVKNLSVKADFSLAKPLIISNLLLSALGGLMWYLQFFFYAWGH

ASIPAQYDYMSWMLHMSFYVLCGGVVGLVLKEWNNAGRRPVSVLSLGCVVIIIAANIVGLGMAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002882891.1\_4703 [gene=rhaR] [locus\_tag=BN49\_RS25470] [protein=HTH-type transcriptional activator RhaR] [protein\_id=WP\_002882891.1] [location=complement(4944693..4945538)] [gbkey=CDS]

MAGLILRKEEFFPSATQAVAVADRYPQNVFAEHTHEFCELVLVWRGNGLHVLNDRPWRITRGDLFYIRAE

DKHSYASVNDLVLQNIIYCPERLQLNFDWAGAIPGLFGTPWKPHWRMGSTGMAQARQVISQLEHECARRD

AQGNAMAELLFAQLALTLQRHRYATDDPAATQREALLDKLLAALAASLSRPFVLERFCEQEGGSERALRQ

QFRQQTGMTINHYLRQLRICHAQYLLQHTERLIGDIAMQCGFEDSNYFSVVFSREIGMSPGQWRQRSRAA

A

>lcl|NZ\_FO834906.1\_prot\_WP\_002882888.1\_4704 [gene=rhaS] [locus\_tag=BN49\_RS25475] [protein=HTH-type transcriptional activator RhaS] [protein\_id=WP\_002882888.1] [location=complement(4945612..4946448)] [gbkey=CDS]

MTILHSTDFFKAGISTVAIEPRLPQSAFPEHHHDFHEIVIVEQGSGIHVFNGQPYTIGGGSVCFIRDHDR

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HAVASREILFMQLLVLLRKSSLAEEATNNDARLNQLLAWLEDHFAQEICWEEVAAQFSLSLRTLHRQLKQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_004210449.1\_4705 [gene=rhaB] [locus\_tag=BN49\_RS25480] [protein=rhamnulokinase] [protein\_id=WP\_004210449.1] [location=4946759..4948225] [gbkey=CDS]

MSIRHCVAVDLGASSGRVMLASYQPGPRALTLREIHRFTNSLQKVDGFDCWDVDSLEGEIRRGLEKVCEQ

GILIDSIGIDTWGVDYVLLDKQGQRVGLPISYRDDRTQGLLRHAEAQLGRAEIYRRSGIQFLPFNTLYQL

RALVEQQPELVSQAAHALLIPDYFSFRLTGNLNWEYTNATTTQLVNINSDSWDETLLNWTGAPLAWFGKP

THPGNVIGHWICPQGNRIPVVAVASHDTASAVIASPLADRHAAYLSSGTWSLMGFESLTPYTCDAALQTN

ITNEGGAEGRYRVLKNIMGLWLLQRVLKEQNVSDLQGLIARTAALPACRFIIDCNDDRFINPASMSAEIQ

AACRDAGQPVPESDAELARCIFDSLALLYARVLNELAALRGHPFSQLHIVGGGCQNTLLNQLCADACGIA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150375.1\_4706 [gene=rhaA] [locus\_tag=BN49\_RS25485] [protein=L-rhamnose isomerase] [protein\_id=WP\_004150375.1] [location=4948222..4949481] [gbkey=CDS]

MTTQLEQAWEIAKQRYAAVGVDVEEALRQLDRLPVSMHCWQGDDVAGFENPAGSLTGGIQATGNYPGKAR

NAEELRADLEQALSLIPGPKRLNLHAIYLESDAPVARNEIKPEHFKNWVTWAKANKLGLDFNPSCFSHPL

SADGFTLSHANDEIRQFWIDHCKASRRVSAYFGEQLGTPSVMNIWVPDGMKDITVDRFAPRQRLLNALDE

VISEKLDPAHHIDAVESKLFGIGAESYTVGSNEFYMGYATSRQTALCLDAGHFHPTEVISDKISAAMLYI

PRLLLHVSRPVRWDSDHVVLLDDETQAIASEIIRHNLFDRVHIGLDFFDASINRIAAWVIGTRNMKKALL

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>lcl|NZ\_FO834906.1\_prot\_WP\_002882882.1\_4707 [gene=rhaD] [locus\_tag=BN49\_RS25490] [protein=rhamnulose-1-phosphate aldolase] [protein\_id=WP\_002882882.1] [location=4949631..4950461] [gbkey=CDS]

MQTIIDAWFVQGMIKATSDAWLKGWDERNGGNLTLRLDEADIEPYAADFHAKPRYIALSQPMPTLANQPF

IVTGSGKFFRNVQLDPAANLGVVKVDSDGAGYHILWGLTEDAVPTSELPAHFLSHSERIKLTGGKDRVIM

HCHATNLIALTYVLENHSDLFTRKLWEGSTECLVVFPDGVGILPWMVPGTDEIGQATAETMQKHSLVLWP

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>lcl|NZ\_FO834906.1\_prot\_WP\_012737100.1\_4708 [gene=rhaS] [locus\_tag=BN49\_RS25495] [protein=rhamnose ABC transporter substrate-binding protein] [protein\_id=WP\_012737100.1] [location=4950543..4951529] [gbkey=CDS]

MKTKTSLILTVAALALSGSALAEVKIALVAKSLGNGFFEAANVGAQQAAKELGDVKVIYTGPTTTTAEAQ

IDVLNGLIAQGVDAIAISANDPDAVVPVLKKAMQRGIKVVSWDSGVAPAGRQIHLNPSNNALIGETNVKL

AADALQALNVEKGEVAVLSATPTSTNQNIWIEEMKKVLPQYPSVQLVTVAYGDDLSDKSYREAVGLLKSY

PDLKVIVSPSSVGIVAAAQAVKDQGKIGKVYVTGLGLPSEMAGAIKSGASKSFAIWNPIDLGYAATYLAD

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150373.1\_4709 [locus\_tag=BN49\_RS25500] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_004150373.1] [location=4951675..4953186] [gbkey=CDS]

MSASTPLLSLKGITKIFPGVRALENVQLDLWPGKVTALIGENGAGKSTLVKVMTGIYQPEEGEILYKAIP

IHLPTPESAHKVGITAIHQETVLFDELSVSENIFVGQYLYKGLLKTLDWPAMHRRANEILTRLEVQIDPR

ATLKTLSIAQRHMVAIARALAFDAQVVILDEPTAALSQHEILEFYHIVERLKQDGKAILFISHKFDEIFE

LADYYTILRDGVYVSSGAISDITEERMVSMMVGRAISQTYPKVDCTPGETVLEVTDLCHPTEFAHISFRL

RKGEILGFYGLVGAGRTELMQALSGVSRPSSGEIRLNGRTMRFHQPADAIRAGIVCVPEERQKQGAIIAL

PIAQNISLPQLSKLNPNGVLNDAREWRLADEYASRLQVKAFSWRQPVETLSGGNQQKVVIGKWLATQPEV

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IVSAASGIGQEAA

>lcl|NZ\_FO834906.1\_prot\_WP\_004220853.1\_4710 [locus\_tag=BN49\_RS25505] [protein=ABC transporter permease] [protein\_id=WP\_004220853.1] [location=4953183..4954190] [gbkey=CDS]

MMGHAWLKHREALLAVVIILMIGAIGSRAPSFVSPGNLVEMFNDTAILIILALGQMMVLLTKGIDLSMAA

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GGWVNSHQMSADFLSLPRSPLLGLPLLSWCAIAALLLVGYFLRYSRTGRALYTAGGNATAAYYTGINAGK

MQFVSFCLSGALAGFCGYLWISRFAVAYVDVANGFELQVVAACVIGGISTMGGSGRVLGCLCGALFLGVI

NNALPVIGISPFWQMAISGAVIVMAVLLNERGNRGHGRLILRNAALARQKQAVKS

>lcl|NZ\_FO834906.1\_prot\_WP\_002882873.1\_4711 [locus\_tag=BN49\_RS25510] [protein=ABC transporter permease] [protein\_id=WP\_002882873.1] [location=4954187..4955191] [gbkey=CDS]

MSKMMVSEEMKNAPAAPSPLRRLLCWEGFLLAVTLAVFIGNAVASPYFLNIWNLSDATFTFTEKAIVVLP

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PTGAWFSGINVKRHNLVLFALVGLMAGLAAVLLTSRLGSTRPTLAMGWELAVVTMAVLGGVNILGGSGSM

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530955.1\_4712 [gene=fucO] [locus\_tag=BN49\_RS25515] [protein=lactaldehyde reductase] [protein\_id=WP\_016530955.1] [location=4955281..4956429] [gbkey=CDS]

MSFMLALPKISLHGAGAIGDMVKLVAGTQWGKALIVTDGQLVKLGLLDSLFAALDEQQMAYQLFDEVFPN

PTEALVQQGYAAYQAARCDYLIAFGGGSPIDTAKAIKILTANPGPSTAYSGVGKVKNAGVPLVAINTTAG

TAAEMTSNAVIIDSERQVKEVIIDPNLIPDIAVDDASVMLDIPPAVTAATGMDALTHAIEAFVSVGAHPL

TDANALEAIRLINLWLPKAVDDGHDLQAREQMAFGQYLAGMAFNSAGLGLVHALAHQPGATHNLPHGVCN

AILLPIIENFNRPNAVARFARVAQAMGVDTRGMSDEAASMEAINAIRTLSKRVGIPQGFSQLGVSKADIE

GWLDKALADPCAPCNPRPASRDEVRELYLEAL

>lcl|NZ\_FO834906.1\_prot\_WP\_004181618.1\_4713 [gene=rhaM] [locus\_tag=BN49\_RS25520] [protein=L-rhamnose mutarotase] [protein\_id=WP\_004181618.1] [location=4956426..4956740] [gbkey=CDS]

MIRKAFVMQVNPDAHEEYQRRHNPIWPELEAVLKAHGAHHYAIYLDKERHLLFATVEIESEARWEAVAST

EVCQRWWKYMREVMPSNPDNSPLSAELKEVFYLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004210464.1\_4714 [locus\_tag=BN49\_RS25525] [protein=MFS transporter] [protein\_id=WP\_004210464.1] [location=complement(4956778..4958043)] [gbkey=CDS]

MNPTVCTHKNNPNFWIFGLFFFLYFFIMATCFPFLPIWLSDVIGLNKTETGLVFSSLSLFAICFQPILGV

ISDKLGLKKHLMWIVTVLLVLIAPFFLYVFAPLLKTNIWLGALSGGAYIGFAFSAGAGAMEAYIERVSRN

SGFEYGKARTFGCLGWALCATTAGMLFSINPEWVFWMGSAAALLLVVLVAIAKPQASQSAQVMDSLGANR

PAIDLKTAVRMFRQRKMWMFILYVIGVACVYDVFDQQFATFFKSFFATPEAGTRAFGFATTAGEICNAII

MFSSPWIINRIGAKNTLLIAGMVMAARMIGSSFATTAAEVVALKMLHALEVPFLLVGAFKYITGVFDVRL

SATIYLVGFQFAKQVAAIFLSAFAGNMYDRIGFQETYMILGGIALTVTLISAFTLAGKAKTEPLRDNAMT

V

>lcl|NZ\_FO834906.1\_prot\_4715 [locus\_tag=BN49\_RS25530] [protein=alpha-galactosidase] [pseudo=true] [partial=5'] [location=complement(4958085..>4959587)] [gbkey=CDS]

GEVWGVHLAWSGNHRLRAEVKTDGRRYLQAEALYLPGEMALAEGETLWTPYLYASYSANGLNGMSQQFHR

YLRERIIRFPGNKPRPVHLNTWEGIYFDHDPDYIMRMADEAAALGVERFIIDDGWFKGRNDDWAALGDWY

LDEKKYPYGLTPIIDHVKSLSMEFGIWVEPEMINPDSDLYRAHPDWVLALPGYTPLTGRHQFVLNLNIPE

AFDYLLERMSWLLGEHAVDYVKWDMNRELVQPGHQGRAAADAQTRQFYRLLDTLVARFPHIEFESCSSGG

GRIDYEVLKRSHRFWASDNNDALERNTIQRGMSYFFPPEVMGAHIGNRHCHATFRQHSIAFRGLTALFGH

MGLELDPVSADEEERAGYRKYAALHKQWRDVIHHGVQWRIDMPDATTLAHGVVSPDKAQAIFLVSQLAMP

DYTLMAPLRLAGLEASARYQVTLLDHPNIQITGEGGHTMRKLPAWMTTPQTVSGEWLQQAGLALPILDPE

SAILIGLQRV

>lcl|NZ\_FO834906.1\_prot\_WP\_129015090.1\_4716 [locus\_tag=BN49\_RS29615] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_129015090.1] [location=join(4959679..4959994,4959994..4960907)] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLPRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_4717 [locus\_tag=BN49\_RS25540] [protein=alpha-galactosidase] [pseudo=true] [partial=3'] [location=complement(<4960918..4961544)] [gbkey=CDS]

MSDSLIHLQSAGADIVIKTRPFAEIVYWGPHLSHFSPQDADSLTRPVANGRLDVDSPVTLMAELGHGLFG

APGIEGHRQGLDASPLFTTSEVRHEGQTLTLVSEDPQAGLRLQSEIALDASGVLSVRHGVTNLRVSPWQV

DRLAVTLPVAERAREVMAFHGRWIREFQPHRLTLEHDSFVLENRRGRTSHEHFPALITGSRAFSEMQGD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530962.1\_4718 [locus\_tag=BN49\_RS25545] [protein=substrate-binding domain-containing protein] [protein\_id=WP\_016530962.1] [location=complement(4961660..4962655)] [gbkey=CDS]

MSLKAIAKQLGISVTTVSRALNGYDDVSQETRARVEAEAQRRGYRPNTFARRLKMGTIDAVGLVFPVRPA

PLNNNVFLEMVGEISHELARHDIDLLLIADDEQADKHGYMRMVQGRRVDALIVAHTLDDDPRLAQLQASG

FPFLALGRSRLAQPYAWFDFDNYAGTCRATRHLIQQGHQRIALLGENNNQAFILQRRNGYLDALREAGLS

DAWLRSVPATRRGGYQATLELLRLPEPPTAIITDCNTHGDGAAMALAHLGRLTGDNRVALVVYDGLPQDS

IIETDVAAVIQSTRQGVGRQISDMVRRLIAGEDLATLQVLWQPEFIPGETA

>lcl|NZ\_FO834906.1\_prot\_WP\_002882865.1\_4719 [locus\_tag=BN49\_RS25550] [protein=XRE family transcriptional regulator] [protein\_id=WP\_002882865.1] [location=complement(4962743..4963291)] [gbkey=CDS]

MTQPISVIAKSLVRERARTGLSLAEVARRAGIAKSTLSQLESGNGNPSLETLWSLCVALDIPFARLLEPQ

VNKTQVIRRGEGTKVVAEQANYQAILLAACPPGARRDIYLLLTQPGADRISHPHPPGSVEHIIVTQGRAR

VGLTSAPEELGEGDYICYPADQEHVFQALEPDTQALLIAEQN

>lcl|NZ\_FO834906.1\_prot\_WP\_004195589.1\_4720 [locus\_tag=BN49\_RS25555] [protein=AzlC family ABC transporter permease] [protein\_id=WP\_004195589.1] [location=4963391..4964050] [gbkey=CDS]

MKQTLSSLSGDTIKAIVLVCLAVGVVGMSYGSLAVAYGFPLWVPLLLSVSVLAGASEFMFIGIVASGGSP

LAAAAAGLLVNARHIPFGVTVRELVGRRALSFIGCHIMNDESVVFGLSQPTPAQRKAAYWLCGAGVALIW

PLGTLTGAAVGKLLPAPETIGLDAVFPAILLALVIPAFKNRTTLIRAASGAALALAAVPFVPTGLPVLLS

LFGLLSRKK

>lcl|NZ\_FO834906.1\_prot\_WP\_002882863.1\_4721 [locus\_tag=BN49\_RS25560] [protein=AzlD domain-containing protein] [protein\_id=WP\_002882863.1] [location=4964050..4964373] [gbkey=CDS]

MGNMTLFIAGIAILSLGTYLMRLGGAKLGNRLAFSERSQALLSDAATVLLFSVALATTFYEGAHFAGMAR

VLGVAFAVFLAWRKVPLIGVIIAAAVVTALLRLAGMP

>lcl|NZ\_FO834906.1\_prot\_WP\_004895164.1\_4722 [locus\_tag=BN49\_RS25565] [protein=hypothetical protein] [protein\_id=WP\_004895164.1] [location=complement(4964370..4964963)] [gbkey=CDS]

MNRHLTPGCKTAILINGIPASGKSTITRLLAETFSLPVLTIDGIKEPFMARLAPVDRPMNRQLGCAAYEV

IWSIVGASPASMVWLIDAWFGFQPRETLQRLLQQAGVEQVIEVWNHISPELAVARYASRLATRPPGHPGE

EYLPELAQLAGRAQPMSLGPVLTIDQRHPLQIEPVIQWLVGTIAGQHSGFTDYAYSS

>lcl|NZ\_FO834906.1\_prot\_WP\_002882861.1\_4723 [locus\_tag=BN49\_RS25570] [protein=PTS sugar transporter subunit IIA] [protein\_id=WP\_002882861.1] [location=complement(4964960..4965397)] [gbkey=CDS]

MTIKELLIEADAIQVGVVESDWQRVIKLAARPLEAKGFISTEYSQAVIDNTLNHGAYYVFDEGIAIPHAR

PECGVRRNCFSLVVLEKPIPFADSEKADIVIMFGARDSNAHIEEGIRSIVALLDNNDTMAKLRTARSREE

VVALL

>lcl|NZ\_FO834906.1\_prot\_WP\_002882858.1\_4724 [locus\_tag=BN49\_RS25575] [protein=hypothetical protein] [protein\_id=WP\_002882858.1] [location=complement(4965407..4965676)] [gbkey=CDS]

MFESLKTLWKKEQNPLQDYDQQSRQLAEEIARLEGELQRQPDNSDVQKTLMLTYNRALSVYAKSKSHRQD

IDALFLQIDNLRNIIRRNI

>lcl|NZ\_FO834906.1\_prot\_WP\_002882856.1\_4725 [locus\_tag=BN49\_RS25580] [protein=class II fructose-bisphosphate aldolase] [protein\_id=WP\_002882856.1] [location=complement(4965735..4966577)] [gbkey=CDS]

MSLYNFNEILKIAQERDFKAIGSFNLHCIEMLPAFFKAAQNSRSPLMIQISTGTAEYLGYRLLVDAVRSL

ADSENIPTCLHLDHCSDIKAIETAMNAGFSSVMYDGSHLSLEENIGNTRIVVEMARPRNITVEGELGAIG

GSEDGKAVAAEDICFTTVEDATRFVKETQVDMLAVSVGTVHGLYTGKAQIQHARLKAISEATGVPLVLHG

GTGVSDEDMRLAVTEGINKVNVGTEMNVQWVDRCKSTFEKGKVNDSVRKFLIPANQAVTAVLMEKMALFK

>lcl|NZ\_FO834906.1\_prot\_WP\_004150366.1\_4726 [locus\_tag=BN49\_RS25585] [protein=PTS sugar transporter subunit IIC] [protein\_id=WP\_004150366.1] [location=complement(4966564..4967931)] [gbkey=CDS]

MNSFVAFIVKDLLGQASILIAFIAMLGLILQKKSPGKTAEGTFKTLLGFLIMMAGINIIVATLTFLNDIF

TQGFGMKGYITDVAAIAGLANRELGSEVALTLLVIFAVNIIIARLTPLKYIFLTGQALLWMATIGAVIGY

KSGLTGVPLILTGGIFGGVMAVLMPALAQPVVRRITGSDDVALGHFCTIGYLVQAAVAKVVGKGSRSTED

LELPDNFKFLQDTYLAMAVVMVPMYLIPAIAAGPQYIAQFSGGINYLMYAFMQSIQFVAGVFVLYSGVRL

LLNELVPAFRGIAMRIVPDAKPALDCPVLFPYAPNAVIVGFLATTVGSIIGMLVFPMFGLAMILPGLLTN

FFAGGTAGVFGNALGGRRGAMIGGVIHGLFITFLPAILVPMLESYGFTGVTFSDSDVISSGLVLGHAFQN

NWLFVALFIVFVAALAWFVNGKSAKPKGESVHESV

>lcl|NZ\_FO834906.1\_prot\_WP\_004151864.1\_4727 [locus\_tag=BN49\_RS25590] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_004151864.1] [location=complement(4967924..4968238)] [gbkey=CDS]

MLKILCVCGCGLGSSFAIEMTAKAVLKKLEIPAHIEHTTVSEAGAFKSDMILTQKTFADILTADASEEEI

KRVVVLNKLTDKEEIETKIVAFLKERHLKVADYE

>lcl|NZ\_FO834906.1\_prot\_WP\_002882831.1\_4728 [locus\_tag=BN49\_RS25595] [protein=6-phosphofructokinase] [protein\_id=WP\_002882831.1] [location=complement(4968250..4969230)] [gbkey=CDS]

MKIGIVISGGDVSGMNNFIFQIARQANADITLFNGGIPGLLEKSHQDMAWRDLVDYSITAVPIITSGRTS

RKLQRSEYESIAKKLKSLRIDVLIMAGGDGSLQFLNTLSEFEINCFGVGMTIDNDVYGSDYTIGFSTACE

QIIKEVSRLRNTGRALPGRVFMVEILGGYCGELTLQSAIKCNADIALIPEAQMPLAVLAERITRKLSTQN

SVVILCSEGYTKEYSPGFQGAIDTMIKQLEPQIGVRIRKTIVGYGLRSGDPTCEEIYQGTIMASEVVRCI

QSGMKNKAIIINSSNKPIPIDLVSMKKRLVDTEGHHYKLAKQLNII

>lcl|NZ\_FO834906.1\_prot\_WP\_002882830.1\_4729 [locus\_tag=BN49\_RS25600] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_002882830.1] [location=complement(4969633..4969845)] [gbkey=CDS]

MKSIKTFVAVIAMAASFASFAAETVTATASTMDGAEAKIAAQAQAAGASSYKITEAFTGNRVHMTAELNK

>lcl|NZ\_FO834906.1\_prot\_WP\_002882828.1\_4730 [gene=fdhD] [locus\_tag=BN49\_RS25605] [protein=formate dehydrogenase accessory sulfurtransferase FdhD] [protein\_id=WP\_002882828.1] [location=complement(4969974..4970810)] [gbkey=CDS]

MNKKPLEQIKNVTNVTGYRQVSLWKREDLQHPQPDELAEEVPVALVYNGISHVVMMASPKDLEQFAVGFS

LSEGIIEHRREIFGMDVVAVCNGLEVQIELSSRRFMGLKARRRALAGRTGCGVCGVEQLNDIGKPVQPLP

FTQSFDLANLDQALAHLNDFQPVGRLTGCTHAAAWVRLTGELAGGFEDVGRHVALDKLLGRRAEVGEGWQ

HGAALVSSRASYEMVQKAAMCGVEILFAVSAATTLAVEVAERCNLTLVGFCKPGRATVYTHPQRLIAG

>lcl|NZ\_FO834906.1\_prot\_WP\_085921749.1\_4731 [gene=fdnG] [locus\_tag=BN49\_RS25615] [protein=formate dehydrogenase-N subunit alpha] [transl\_except=(pos:586..588,aa:Sec)] [protein\_id=WP\_085921749.1] [location=4970967..4974017] [gbkey=CDS]

MQVSRRQFFKICAGGMAGTTAAALGFAPATALAETRQYKLLRTRETRNTCTYCSVGCGLLMYSLGDGAKN

AKASIFHIEGDPDHPVNRGALCPKGAGLVDFIHSESRLKFPEYRAPGSDKWQQISWDEAFDRIAKLMKED

RDANFIAQNDAGTTVNRWLTTGMLCASASSNETGYLTQKFTRALGMLAVDNQARVUHGPTVASLAPTFGR

GAMTNHWVDIKNANLVVVMGGNAAEAHPVGFRWAMEAKIHNGAKLIVIDPRFTRTASVADFYTPIRSGTD

ITFLSGVILYLLNNEKFNREYTEAYTNASLIVREDYSFDDGLFSGYNAEKRQYDKTSWNYELDENGFAKR

DTTLQHPRCVWNLLKQHVSRYTPDVVENICGTPKADFLKVCEYIAETSAPDKTASFLYALGWTQHSIGAQ

NIRTMAMIQLLLGNMGMAGGGVNALRGHSNIQGLTDLGLLSTSLPGYMSLPNEKQADLQTYLTANTPKPL

LKDQVNYWGNYPKFFVSMMKAFFGDKATAENSWGYDWLPKWDKSYDVLQYFEMMNQGKVNGYICQGFNPV

ASFPNKNKVVASLSKLKFLVTIDPLNTETSTFWQNHGESNDVDPAKIQTEVFRLPSTCFAEENGSIVNSG

RWLQWHWKGADAPGIAVTDGEILAGIFTRLRKMYAEEGGPAPEPVLNMTWNYSTPHEPASEEVAMESNGK

ALADITDPATGAVIVKKGQQLSSFAQLRDDGTTSSGCWIFAGSWTPEGNQMARRDNADPSGLGNTLGWAW

AWPLNRRILYNRASADPQGKPWDPKRQLLKWDGAKWGGVDIPDYSAAAPGSDVGPFIMQPEGMGRLFAID

KMAEGPFPEHYEPFETPLGTNPLHPNVVSNPAARVFKGDLEQMGKAEKFPYVGTTYRLTEHFHYWTKHAL

LNAIAQPEQFVEIGEKLANKLGIGHGDTVKVSSNRGYIKAKAVVTKRIRTLKVDGKDIDTIGIPIHWGYE

GVAKKGFIANTLTPFVGDANTQTPEFKAFLVNVEKV

>lcl|NZ\_FO834906.1\_prot\_WP\_002882822.1\_4732 [gene=fdxH] [locus\_tag=BN49\_RS25620] [protein=formate dehydrogenase subunit beta] [protein\_id=WP\_002882822.1] [location=4974030..4974932] [gbkey=CDS]

MAYQSQDIIRRSATNGFTPAPQARDHQQEVAKLIDVTTCIGCKACQVACSEWNDIRDEVGHNVGVYDNPA

DLTAKSWTVMRFSEVEQNDKLEWLIRKDGCMHCADPGCLKACPSEGAIIQYANGIVDFQSEQCIGCGYCI

AGCPFDVPRLNPEDNRVYKCTLCVDRVTVGQEPACVKTCPTGAIHFGSKEDMKTLAGERVAELKTRGYDN

AGLYDPAGVGGTHVMYVLHHADKPNLYHGLPENPEISQTVKFWKGIWKPLAAVGFAATFAASIFHYVGVG

PNRAEEEEDNLHEEKDEVRK

>lcl|NZ\_FO834906.1\_prot\_WP\_002882818.1\_4733 [gene=fdoI] [locus\_tag=BN49\_RS25625] [protein=formate dehydrogenase cytochrome b556 subunit] [protein\_id=WP\_002882818.1] [location=4974929..4975564] [gbkey=CDS]

MKRRDTIVRYTAPERINHWVTAFCFVLAAVSGLGFFFPSFNWLMHILGTPQLARILHPFVGVVMFASFII

MFFRYWHHNLINRDDIFWAKNIRKIVVNEEVGDTGRYNFGQKCVFWAAIIFLVLLLVSGVIIWRPYFAPA

FSIPVIRFALMLHSFAAVALIVVIMVHIYAALWVKGTITAMVEGWVTKTWAKKHHPRWYREVRQKQEKSS

E

>lcl|NZ\_FO834906.1\_prot\_WP\_004150358.1\_4734 [gene=fdhE] [locus\_tag=BN49\_RS25630] [protein=formate dehydrogenase accessory protein FdhE] [protein\_id=WP\_004150358.1] [location=4975561..4976490] [gbkey=CDS]

MSIRIIPQDELGSSEKRTAEAIPPLLFPRLKNLYNRRAERLRELAANNPLGDYLRFAALIAHAQEVVLYD

HPLQMDLTARIKAASEQGKPPLDIHVLPRDKHWHKLLHSLIAELKPEMSGPALAVIENLEKASEQELEQM

ASALFVSDFASVSSDKAPFIWAALSLYWAQMASLIPGKARAEYGEQRQFCPVCGSMPVSSIVQIGTTQGL

RYLHCNLCETEWHVVRVKCSNCEQSRDLHYWSLDNEQAAVKAESCGDCGTYLKIMYQEKDPKVEAVADDL

ASLVLDARMEQEGFARSSINPFMFPGEGE

>lcl|NZ\_FO834906.1\_prot\_WP\_002882817.1\_4735 [locus\_tag=BN49\_RS25635] [protein=type II toxin-antitoxin system VapC family toxin] [protein\_id=WP\_002882817.1] [location=complement(4976664..4977047)] [gbkey=CDS]

MTSGSALFDTNILIDLFSGRREAKQALEAWPPQNAISLITWMEVMVGAKKYHQEQRTRMALSTFNIINIS

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150355.1\_4736 [locus\_tag=BN49\_RS25640] [protein=ribbon-helix-helix domain-containing protein] [protein\_id=WP\_004150355.1] [location=complement(4977047..4977289)] [gbkey=CDS]

MMAERDMGRILLDLSDDVIQRLDDLKVQRNIPRAELLREAVEQYLEKQDRAKDTISSALGLWQDCEEDGM

EYQRQLRKEW

>lcl|NZ\_FO834906.1\_prot\_WP\_004178029.1\_4737 [locus\_tag=BN49\_RS25645] [protein=alpha/beta hydrolase] [protein\_id=WP\_004178029.1] [location=4977491..4978408] [gbkey=CDS]

MALEKGIASLVEAFIAAGRPSSRDQHIDDRRAGYIASAVLAGETETRVRVEDITLEGMHFRVVSPPTADG

LLPTLIYYHGGCFVSGGFATHDNQLRQLAWFSGCRVIAVQYRLAPEYPFPAAHDDAERGATIIHQHAKQL

GVDASRITLAGDSAGGHLALVTALRLKAAGTWQPAQLILIYPMLDATASMASYASNGEDYIITRDTLLSG

YEMYLAATPATHPDASPLWREDFHGLPPVHILTAEFDPLRDEGEVLYRRLTEQGVESSCQRYLGVIHGFF

QLGGVSNAARDAMRDIAWRVASPGR

>lcl|NZ\_FO834906.1\_prot\_WP\_004178031.1\_4738 [gene=fabY] [locus\_tag=BN49\_RS25650] [protein=fatty acid biosynthesis protein FabY] [protein\_id=WP\_004178031.1] [location=complement(4978422..4979363)] [gbkey=CDS]

MYHLRVPQTAEELESYYQFRWEMLRKPLHQPKGSERDAWDAMAHHQMVVDEEGNLVAVGRLYINAENEAS

IRFMAVHPSVQDKGLGTLMAMTLESVARQEGVKRVTCSAREDAVEFFAKLGFVNQGEITTPTTTPIRHFL

MIKPVASLDDILHRGDWCAQLQQAWYQHIPLSEKMGVRIQQYTGQKFITTMPEAGNQNPHHTLFAGSLFS

LATLTGWGLIWLMLRERHLGGTIILADAHIRYSQPISGRPSAIADLGSLSGDLDRLARGRKARVQMQVEL

FGDDKQGAVFEGIYIVLPAKPFGSYEEGGNEEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002882809.1\_4739 [gene=dtd] [locus\_tag=BN49\_RS25655] [protein=D-aminoacyl-tRNA deacylase] [protein\_id=WP\_002882809.1] [location=complement(4979408..4979845)] [gbkey=CDS]

MIALIQRVSRASVTVADEVTGEIGPGLLVLLGVEKDDDEQKANRLCERVLGYRIFSDAEGKMNLNVQQAG

GSVLVVSQFTLAADTERGMRPSFSKGAAPDRAEALYEYFVARCRQQEMHTQTGRFAADMQVSLVNDGPVT

FWLQV

>lcl|NZ\_FO834906.1\_prot\_WP\_002882807.1\_4740 [locus\_tag=BN49\_RS25660] [protein=virulence factor BrkB family protein] [protein\_id=WP\_002882807.1] [location=complement(4979842..4980702)] [gbkey=CDS]

MLKTVHQKLLHHTRPLLAWLKLLWRRIDEDHMTTLAGNLAYVSLLSLVPLIAVVFALFAAFPMFSEVSVQ

IRHFIFANFIPATGDVIQGYIEQFVANSSRMTAVGAFGLIVTSLLLMYSIDSALNTIWRSTRSRPKVYSF

AVYWMILTLGPLLAGASLAISSYLLSLRWASDLDGVIDNLLRLFPLILSWAAFWLLYSIVPTTQVRNRDA

VIGALVAALLFEAGKKAFALYITTFPSYQLIYGVISVVPILFVWVYWTWCIVLLGAEITVTLGEYRKLET

EETEQP

>lcl|NZ\_FO834906.1\_prot\_WP\_046043904.1\_4741 [gene=yihX] [locus\_tag=BN49\_RS25665] [protein=glucose-1-phosphatase] [protein\_id=WP\_046043904.1] [location=complement(4980696..4981295)] [gbkey=CDS]

MLYIFDLGNVIVDIDFNRVLGAWSDLTRIPLATLKQHFTMGEVFHQHERGELSDEDFAAAMCHEMNMPLS

YEQFAHGWQAVFVALRPEVITIMHKLRAQGHRVVVLSNTNRLHTTFWPDEYPEVRAAADRIYLSQEMGLR

KPEAQIYLRVLEEEGFSAADTVFFDDNVDNIAGANRLGITSILVTGKETIPDYFAKQLC

>lcl|NZ\_FO834906.1\_prot\_WP\_002882755.1\_4742 [gene=typA] [locus\_tag=BN49\_RS25670] [protein=ribosome-dependent GTPase TypA] [protein\_id=WP\_002882755.1] [location=complement(4981431..4983254)] [gbkey=CDS]

MIENLRNIAIIAHVDHGKTTLVDKLLQQSGTFDARTEAQERVMDSNDLEKERGITILAKNTAIKWNDYRI

NIVDTPGHADFGGEVERVMSMVDSVLLVVDAFDGPMPQTRFVTKKAFAHGLKPIVVINKVDRPGARPDWV

VDQVFDLFVNLDATDEQLDFPIVYASALNGIAGLDHEDMADDMTPLYQAIVDRVPAPDVDLDGPLQMQIS

QLDYNNYVGVIGIGRIKRGKVKPNQQVTIIDSEGKTRNGKVGKVLTHLGLERIESDVAEAGDIIAITGLG

ELNISDTICDPQNVEALPALSVDEPTVSMFFNVNTSPFCGKEGKFVTSRQILDRLNKELVHNVALRVEET

EDADAFRVSGRGELHLSVLIENMRREGFEMAVSRPKVIFREIDGRKQEPFENVTLDVEEQHQGSVMQALG

ERKGDLKNMNPDGKGRVRLDYVIPSRGLIGFRSEFMTMTSGTGLLYSTFSHYDDVRPGEVGQRNNGVLIS

NGQGKAVAFALFGLQDRGKLFLGHGAEVYEGQIIGIHSRSNDLTVNCLTGKKLTNMRASGTDEATVLVPP

VKMTLEQALEFIDDDELVEVTPTSIRIRKRHLTENDRKRAMRGAKEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002882753.1\_4743 [gene=glnA] [locus\_tag=BN49\_RS25680] [protein=glutamate--ammonia ligase] [protein\_id=WP\_002882753.1] [location=4983633..4985042] [gbkey=CDS]

MSAEHVLTMLNEHEVKFVDLRFTDTKGKEQHVTIPSHQVNAEFFEEGKMFDGSSIGGWKGINESDMVLMP

DASTAVIDPFYEEPTLIIRCDILEPGTLQGYDRDPRSIAKRAEEYLRATGIADTVLFGPEPEFFLFDDIR

FGASISGSHVAIDDIEGAWNSSTKYEGGNKGHRPGVKGGYFPVPPVDSSQDIRSTMCMIMEEMGLVVEAH

HHEVATAGQNEVATRFNTMTKKADEIQIYKYVVHNVAHRFGKTATFMPKPMFGDNGSGMHCHMSLAKNGT

NLFSGDKYAGLSEQALFYIGGVIKHAKAINALANPTTNSYKRLVPGYEAPVMLAYSARNRSASIRIPVVT

SPKARRIEVRFPDPAANPYLCFAALLMAGLDGIKNKIHPGEAMDKNLYDLPPEEAKEIPQVAGSLEEALQ

ALDADREFLTAGGVFTNDAIDAYIALRMEENDRVRMTPHPVEFELYYSV

>lcl|NZ\_FO834906.1\_prot\_WP\_004146229.1\_4744 [gene=glnL] [locus\_tag=BN49\_RS25685] [protein=nitrogen regulation protein NR(II)] [protein\_id=WP\_004146229.1] [location=4985231..4986280] [gbkey=CDS]

MATGTLPDAGQILNSLINSILLVDDDLAVHFANPAAQQLLAQSSRKLFGTPLPELLSYFSLNIGLMQESL

QAGQGFTDNEVTLVIDGRSHILSLTAQRLPEGFILLEMAPMDNQRRLSQEQLQHAQQVAARDLVRGLAHE

IKNPLGGLRGAAQLLSKALPDPALTEYTKVIIEQADRLRNLVDRLLGPQHPGMHVTESIHKVAERVVKLV

SMELPDNVKLIRDYDPSLPELPHDPDQIEQVLLNIVRNALQALGPEGGEIILRTRTAFQLTLHGVRYRLA

ARIDVEDNGPGIPPHLQDTLFYPMVSGREGGTGLGLSIARSLIDQHSGKIEFTSWPGHTEFSVYLPIRK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529056.1\_4745 [gene=glnG] [locus\_tag=BN49\_RS25690] [protein=nitrogen regulation protein NR(I)] [protein\_id=WP\_016529056.1] [location=4986289..4987698] [gbkey=CDS]

MQRGIAWIVDDDSSIRWVLERALTGAGLSCTTFESGNEVLDALTTKTPDVLLSDIRMPGMDGLALLKQIK

QRHPMLPVIIMTAHSDLDAAVSAYQQGAFDYLPKPFDIDEAVALVDRAISHYQEQQQPRNAPISSPTADI

IGEAPAMQDVFRIIGRLSRSSISVLINGESGTGKELVAHALHLHSPRSKAPFIALNMAAIPKDLIESELF

GHEKGAFTGANTVRQGRFEQADGGTLFLDEIGDMPLDVQTRLLRVLADGQFYRVGGYAPVKVDVRIIAAT

HQNLEQRVQEGKFREDLFHRLNVIRVHLPPLRERREDIPRLARHFLQIAARELGVEAKQLHPETETALTR

LAWPGNVRQLENTCRWLTVMAAGQEVLTQDLPSELFETTIPDSPTQMQPDSWATLLGQWADRALRSGHQN

LLSEAQPEMERTLLTTALRHTQGHKQEAARLLGWGRNTLTRKLKELGME

>lcl|NZ\_FO834906.1\_prot\_WP\_004152951.1\_4746 [locus\_tag=BN49\_RS30755] [protein=YshB family small membrane protein] [protein\_id=WP\_004152951.1] [location=4987809..4987919] [gbkey=CDS]

MFESLVSMISSGAAASHTPQTAVAAVLCAALVGLFS

>lcl|NZ\_FO834906.1\_prot\_WP\_016529057.1\_4747 [gene=hemN] [locus\_tag=BN49\_RS25695] [protein=oxygen-independent coproporphyrinogen III oxidase] [protein\_id=WP\_016529057.1] [location=complement(4987955..4989328)] [gbkey=CDS]

MSEQIIDWDLALIQKYNYSGPRYTSYPTALEFSPQFGAAEFDAAVARYPQRPLSLYVHIPFCHKLCYFCG

CNKIVTRQQHKADQYLDVLEQEIIHRAPLFATRQVKQLHWGGGTPTYLNKAQISRLMDLLRSHFHFSAEA

EISIEVDPREIELDVLDHLRAEGFNRLSMGVQDFNKEVQRLVNREQDEAFIFDLLNHAREIGFTSTNIDL

IYGLPKQTPKSFAFTLQKVAELNPDRLSVFNYAHLPTLFAAQRKIKDADLPSAEQKLEILQETIGSLTTA

GYQFIGMDHFARPDDELAVAQRHGVLHRNFQGYTTQGDTDLLGMGVSAISMIGDSYAQNQKELKQYYQQV

AEQGNALWRGIALTRDDCLRRDVIKALICNFQLDIAAVEAQWDVDFASYFAEDLKLLAPLAHDGLVAVDD

KVIQVTAKGRLLIRNICMCFDAYLRQKARMQQFSRVI

>lcl|NZ\_FO834906.1\_prot\_WP\_016529058.1\_4748 [gene=yihI] [locus\_tag=BN49\_RS25700] [protein=Der GTPase-activating protein YihI] [protein\_id=WP\_016529058.1] [location=complement(4989517..4990023)] [gbkey=CDS]

MKKPTSATRGKSGRKSREELNQEARDRKWQKKHRGHAAGSRANGGDAASAGKKQRQAQDPRVGSKKPIPL

GVSESSAPAPKQHKPKSEKPMLSPQAELELLENDERLDALLERLEEGGTLNAEEQSWVDAKLDRIDELMQ

QLGLSYDDEDEEEEERQEDMMRLLKGGN

>lcl|NZ\_FO834906.1\_prot\_WP\_002882734.1\_4749 [gene=yihA] [locus\_tag=BN49\_RS25705] [protein=ribosome biogenesis GTP-binding protein YihA/YsxC] [protein\_id=WP\_002882734.1] [location=4990607..4991239] [gbkey=CDS]

MTNWNYQLTHFVTSAPDIRHLPADTGIEVAFAGRSNAGKSSALNTLTNQKNLARTSKTPGRTQLINLFEV

AEGKRLVDLPGYGYAQVPEEMKIKWQRALGEYLEKRLCLKGLVVLMDIRHPLKDLDQQMIEWAVESDIQV

LVLLTKADKLASGARKAQVNMVREAVLAFNGDVQVEPFSSLKKSGVDKLRQKLDSWFNEIPPQEAVEDAE

>lcl|NZ\_FO834906.1\_prot\_WP\_032420753.1\_4750 [gene=polA] [locus\_tag=BN49\_RS25710] [protein=DNA polymerase I] [protein\_id=WP\_032420753.1] [location=complement(4991587..4994379)] [gbkey=CDS]

MVQIPENPLILVDGSSYLYRAYHAFPPLTNSAGEPTGAMYGVLNMLRSLILQYQPTHAVVVFDAKGKTFR

DELFEHYKSHRPPMPDDLRAQIEPLHKMVKAMGLPLMAVPGVEADDVIGTLAREAERAGRPVLISTGDKD

MAQLVTPGITLINTMTNTILGPDEVVTKYGVPPELIIDFLALMGDSSDNIPGVPGVGEKTAQALLQGLGG

LDTLYAEPEKIAELSFRGAKTMAAKLEQNKDVAYLSYQLATIKTDVELELTCEELEVQPPAADDLLALFR

QYEFKRWTTDVEAGKWLQAKGGKPAAKPAVPAATAEAEEEVEAATALSAEHYVTILDEATLLTWIDKLKQ

APLFAFDTETDSLDNISANMVGLSFAVEPGVAAYVPVAHDYLDAPDQIPRERVLTLLKPLLEDEKVLKVG

QNLKYDRGILANYDIELRGIAFDTMLESYILDSVAGRHDMDSLSDRWLKHKTITFEEIAGKGKNQLTFNQ

IALEEAGRYAAEDADVTLQLHLKMWPKLQQHEGPLNIFQHIEMPLVPVLSRVERNGVKIDPAVLHAHSQE

IAQRLVELEQRAHEIAGEAFNLSSTKQLQTILFEKQGIKPLKKTPGGAPSTSEEVLEELALDYPLPKVIL

EYRGLAKLKSTYTDKLPLMINPKTGRVHTSYHQAVTATGRLSSTDPNLQNIPVRNEEGRRIRQAFIAPED

YVIVSADYSQIELRIMAHLSRDKGLLTAFAEGKDIHRATAAEVFGLPLDSVSSEQRRSAKAINFGLIYGM

SAFGLARQLNIPRKEAQKYMDLYFERYPGVLEYMERTRAQAKEQGYVETLDGRRLYLPDIKSSNGARRAG

AERAAINAPMQGTAADIIKRAMIAVDEWLRSEKPRVRMIMQVHDELVFEVHKDELDAVSKKIHELMENST

TLAVPLLVEVGSGENWDQAH

>lcl|NZ\_FO834906.1\_prot\_WP\_004150336.1\_4751 [locus\_tag=BN49\_RS25715] [protein=acyltransferase] [protein\_id=WP\_004150336.1] [location=4994776..4995675] [gbkey=CDS]

MSRLLAAITLPLSIALTILVTIICSVPIIVAGLIKLLVPIPAVWRSISVFCNFMMYCWCEGLALLLHLNP

WLKWDVQGLEGLNKKNWYLLISNHHSWADIVVLCVLFRKHIPMNKYFLKQQLAWVPFIGLACWALDMPFM

RRYSRSYLIRHPERRGKDVETTRRSCEKFRAHPTTIVNFVEGSRFTEEKKRETRSPYHNLLPPKAAGIAM

ALNVLGSQFDKLLNVTLCYPDNHTRPFYDMLSGRLTRIVVRINLVPIGEELHGDYVNDKNFKRSFQRWLN

GLWEEKDRQLTDIMRDKER

>lcl|NZ\_FO834906.1\_prot\_WP\_016531304.1\_4752 [gene=dsbA] [locus\_tag=BN49\_RS25720] [protein=thiol:disulfide interchange protein DsbA] [protein\_id=WP\_016531304.1] [location=complement(4995723..4996346)] [gbkey=CDS]

MKKVWLALAGMILAFSASAAQITDGKQYITLDKPIAGEPQVLEFFSFYCPHCYQFEEVLHVSDNVRQKLP

EGTKMTKYHVEFLGPLGKDLTQAWAVAIALGVDDKITAPMFEAVQKNQTVQSVADIRKVFVDAGVKGEDY

DAAWNSFVVKSLVAQQEKAAADLQLQGVPAMYVNGKYQLNPQGMDTSNMDVFVAQYADTVKQLVEKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004187940.1\_4753 [locus\_tag=BN49\_RS25725] [protein=serine/threonine protein kinase] [protein\_id=WP\_004187940.1] [location=complement(4996374..4997360)] [gbkey=CDS]

MHDKAFTFQTLRPDTIIDGLFDLGMRVDSGLTPLNSYENRVYQFQDEERHRYVVKFYRPERWSAEQILEE

HQFALQLVEDEVPVAAPLLFNDSTLHQHQGFYFAVFPSLGGRQFEADNLDQMEWVGRYLGRLHQTGRKQR

FTARPEIGVQEYLLEPRQVFEQATLIPSGLKADFLKATDKLIAAVMEQWHGRGNTLRLHGDCHAGNILWR

DGPLFVDLDDARTGPAIQDLWMLLNGDKAEQRMQLETIVEAYEEFSPFNSDEIALIEPLRAMRLVYYLAW

LLRRWDDPAFPVNFPWLTGEDYWRGQTSTFLEQVKVLQEPPLQLTPMY

>lcl|NZ\_FO834906.1\_prot\_WP\_002882612.1\_4754 [locus\_tag=BN49\_RS25730] [protein=YihD family protein] [protein\_id=WP\_002882612.1] [location=complement(4997436..4997705)] [gbkey=CDS]

MKCKRLNEVIELLQPAWQKEPELNLMQFLQKLAKEAGYDGELSDLSDDILIYHLKMRDSSKDAVIPGIQK

DYEEDFKTALLRARGVIKE

>lcl|NZ\_FO834906.1\_prot\_WP\_004178039.1\_4755 [gene=mobA] [locus\_tag=BN49\_RS25735] [protein=molybdenum cofactor guanylyltransferase MobA] [protein\_id=WP\_004178039.1] [location=4997777..4998358] [gbkey=CDS]

MQSEAITGVVLAGGRATRMGGIDKGLQALNGRPLWRHVAEALAPQVDELVISANRHLEQWRASGYPVFRD

IQEGYQGPLAGMLAVMQQVASPWFVFCPCDTPFIPSFLVERFIQQRGDAPVVWAHDGERDHPAVALVHRQ

IIPELEAYLAHGERRVMVFMRQMGGRPVNFSDVKTAFINVNTLEDLQQMQEPS

>lcl|NZ\_FO834906.1\_prot\_WP\_032104071.1\_4756 [gene=mobB] [locus\_tag=BN49\_RS25740] [protein=molybdopterin-guanine dinucleotide biosynthesis protein MobB] [protein\_id=WP\_032104071.1] [location=4998355..4998861] [gbkey=CDS]

MIPLLAIAAWSGTGKTTLLKRLIPELCALGLRPGLIKHTHHDMDVDKPGKDSYELRKAGAAQTIVASEQR

WALMTETPEKPELDLTWLVNRMDASKLDLVLVEGFKHEPVPKILLFRQNSGHRVEELVIDEHTIAVASDV

SIATSLPLLDLNDVPQIATFIVSWLERQ

>lcl|NZ\_FO834906.1\_prot\_WP\_009309849.1\_4757 [locus\_tag=BN49\_RS25765] [protein=cupin domain-containing protein] [protein\_id=WP\_009309849.1] [location=5004737..5005858] [gbkey=CDS]

MAYQLNINWPEFLEKYWQKQPVVLKNAFPDFVDPITPDELAGLAMEPEVDSRLVSLKNGKWQASNGPFEH

FDGLGETGWSLLAQAVNHWHMPAAELVRPFRVLPDWRLDDLMISFSVPGGGVGPHIDQYDVFIIQGMGSR

RWRVGDKLPMRQFCPHPALLHVDPFPPIIDEDLQPGDILYIPPGFPHDGITHETALNYSVGFRGPNGRDL

ISSFADYVLENDLGGEHYSDPDLTCREHPGRVEEYELERLRTMMIDMIRQPEDFKQWFGSFVTTPRHELD

IAPAEPPYEEEEVLDALLGGEKLSRLSGLRVLHIGDSFFVHSEQLDTTDAEALDALCRYTSLGQEELGSG

LQNPAFVSELTRLINQGYWYFEE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529513.1\_4758 [gene=kacT] [locus\_tag=BN49\_RS25770] [protein=type II toxin-antitoxin system toxin KacT] [protein\_id=WP\_016529513.1] [location=complement(5005906..5006439)] [gbkey=CDS]

MEQQLTIEMIADAFSYDITGLDCGEEALNTFLKEHLKRQHDGQILRGYALVSGDTVPRLLGYYTLSGSCF

ERGMLPSKTQQKKIPYQNAPSVTLGRLAIDKSVQGQGWGEMLVAHAMRVVWGASKAVGIYGLFVEALNEK

AKAFYLRLGFIQLVDENSNLLFYPTKSIEQLFTDDES

>lcl|NZ\_FO834906.1\_prot\_WP\_002887278.1\_4759 [gene=kacA] [locus\_tag=BN49\_RS25775] [protein=type II toxin-antitoxin system antitoxin KacA] [protein\_id=WP\_002887278.1] [location=complement(5006450..5006716)] [gbkey=CDS]

MPALKKQRIDLRLTDDDKSIIEEAAAISNQTITQFVVASASERAAEVIEQHRRMVLNEQSWSLVMEAITQ

PPAPNDRLKRAAKRLQTR

>lcl|NZ\_FO834906.1\_prot\_WP\_046043909.1\_4760 [locus\_tag=BN49\_RS25780] [protein=Cu(+)/Ag(+) sensor histidine kinase] [protein\_id=WP\_046043909.1] [location=complement(5006819..5008252)] [gbkey=CDS]

MAAKRPFSLATRLTFFISLATIIAFFAFTWIMIHSVKAHFEERDVHDLRQLSTTLETVLDHADYPPARRL

EIVKNIIAGYANVFICLDDGQGNILFQSPNGPDLSHMLSTPGLAMQLRDGNVISWTDPQPRAMAHDNHPM

ETRAWRLIMLPLGKQADGKPAYHLLMALSIDFHLHYINELKAKLISAASIISLLIIAIVLFVVYQGHKPI

RQISRQIQNITSRDLDVRLDPQAVPVELERLALSFNHMLERIEDVFTRQSNFSADIAHEIRTPITNLVTQ

TEIALSQSRSQQELEEVLYSNLEEFSRMSRMVSDMLFLAQADNNQLIPEQQALDLAEEVHKVFEFFEAWA

EEKAVALRFVGSPCRVTGDPLMLRRAISNLLSNAIRYTPAGQAVTIQLSESAETVRLVVENPGTSIAAEH

LPRLFDRFYRVDPSRQRKGEGSGIGLAIVKSIVGAHHGSVAAQSDLRSTRFIVVLPK

>lcl|NZ\_FO834906.1\_prot\_WP\_002887273.1\_4761 [gene=cusR] [locus\_tag=BN49\_RS25785] [protein=copper response regulator transcription factor CusR] [protein\_id=WP\_002887273.1] [location=complement(5008242..5008925)] [gbkey=CDS]

MKILIVEDEKKTGEYLTKGLTEAGFVVDLADNGLNGYHLAMTSDYDLLILDIMLPDVNGWDIVRMLRAAG

KGMPILLLTALGTIEHRVKGLELGADDYLVKPFAFAELLARVRTLLRRGAAVIVESQFQAADLSVDLVSR

KVTRGATRITLTSKEFTLLEFFLRHQGEVLPRSLIASQVWDMNFDSDTNAIDVAVKRLRAKIDNDFEPKL

IQTVRGVGYMLEVPDGR

>lcl|NZ\_FO834906.1\_prot\_WP\_016530864.1\_4762 [locus\_tag=BN49\_RS25795] [protein=efflux transporter outer membrane subunit] [protein\_id=WP\_016530864.1] [location=5009097..5010482] [gbkey=CDS]

MRSIQLLTLSMIFALTGCLSLAPDYQRPAAPVPQQFSLSQNKLVTATAGYQETGWRTFFVDPQVKSLIST

ALANNRDLRMATLKVQEARAQYRVTGADRYPQLNGDGSTTYGGKLKGDTTTSSDYAAGLNLSYDLDFFGR

LKNLSESDRQNFFASEEARRAVHILLIANVSQSYFNQRLAAAQLQVANDTLQNYQQSYAFVEKQLLTGST

TVLALEQARGMIESTRADIAKRQGQLAQANNALQLLLGSYQRLPDDSASSAVDLKGVILPPSLSSAILLQ

RPDILEAEHSLLAANANIGAARAAFFPSITLTSSLSGSSSELSSLFNASGAMWNFIPKIELPIFNAGRNQ

ASLDLAEIRQQQQVVNYEQKIQSAFKEVADALALRQSLADQIAAQERYLASLNITLQRATALYRHGAVSY

IEVLSAQRDIFTTRQTLLELNYSRQANEITLFTALGGGWME

>lcl|NZ\_FO834906.1\_prot\_WP\_004192220.1\_4763 [gene=cusF] [locus\_tag=BN49\_RS25800] [protein=cation efflux system protein CusF] [protein\_id=WP\_004192220.1] [location=5010500..5010844] [gbkey=CDS]

MNSLSKIALFTLLSGAVFAAQAAAPHAGMAMHEQHAAAQAQSISGKGVIKAIDMDNKKITIAHEAIPAVN

WPPMTMRFTITPQTQLNNVKDGDSVDFTFVQQGNLSLLQDIRAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_046043912.1\_4764 [locus\_tag=BN49\_RS25805] [protein=efflux RND transporter periplasmic adaptor subunit] [protein\_id=WP\_046043912.1] [location=5010889..5012151] [gbkey=CDS]

MASLTLKNTALILGSMLIGGALTAVLYARWAPTHSAAPAAEQQRKVLFWYDPMYPNTRFDKPGKSPFMDM

DLVPKYADEEHAAAGAPGVRIDPTQTQNLGVKTAAVTRGPLRYAQTFPANISYNEYQYVIMQARAAGFIN

KVYPLTVGDKVKQGTPLLELTIPDWVEAQSEYLLLQETGGTDTQVEGILERLRLAGMPDDDIRRLKATRK

IQTRFTLKAPIDGVITAFDLRAGMNIAKDNVVAKIQGMDPVWVSVAVPESITWLIKDASQFSIQVPAWPG

KTFRISKWTLLPSVDSATRTLQLRLQVNNPDEALKPGMNAYLQLTSESAPMLLIPSKALIDSGSEQRVIT

VDNEGRFVPKIVQVFHESNGVTAIRSGLQEGEKVVASGLFLIDSEANIAGALERMRAQAPDAAAPAAHAH

>lcl|NZ\_FO834906.1\_prot\_WP\_046043914.1\_4765 [locus\_tag=BN49\_RS25810] [protein=CusA/CzcA family heavy metal efflux RND transporter] [protein\_id=WP\_046043914.1] [location=5012163..5015312] [gbkey=CDS]

MIEWIIRRSVANRFLVMMGALFLSLWGTWTIVHTPVDALPDLSDVQVIVKTSYPGQAPQIVENQVTWPLT

TTMLSVPGARTVRGFSQFGDSYVYVIFEDGTDPYWARSRVLEYLNQVQGKLPAGVSAEMGPDATGVGWVF

EYALVDRSGKHDLAELRSLQDWFLKYELKTIPNVSEVASVGGVVKEYQIVVDPMKLTQYDISLGEVKSAL

DASNQEAGGSSVELAEAEYMVRASGYLQTLDDFKNIVLKTGDNGVPVYLGDVARVQIGPEMRRGIAELNG

EGEVAGGVVILRSGKNAREMISAVKEKLASLQSSLPEGVEVVTTYDRSQLIDRAIDNLSYKLLEEFIVVA

LVCALFLWHVRSALVAIISLPLGLCFAFIMMHFQGLNANIMSLGGIAIAVGAMVDAAIVMIENAHKRLEE

WEHQHPGEKLSNDIRWKIITEASVEVGPALFISLLIITLSFIPIFTLEGQEGKLFGPLAFTKTWSMAGAA

LLAIVAIPILMGFWIRGRIPAESSNPLNRFLIRIYHPLLLKVLHWPKTTLLIALLSILTVVWPLNRVGGE

FLPQINEGDLLYMPSTLPGISAAQAADMLQKTDKLIMTVPEVARVFGKTGKAETATDSAPLEMVETTIQL

KPQDQWRPGMTMEKIVDELDKTVRLPGLANLWVPPIRNRIDMLSTGIKSPIGIKVSGTNLADIDAIAEQI

EGVARSVPGVTSALAERLGGGRYLNIDIHREKAARYGMTVGDVQLFVSSAIGGAMVGETVEGVERYPINI

RYPQSYRDSPETLRQLPILTPLKQQIVLGDVAEVKVVTGPPMLKTENARPTSWIYIDARDRDMVSVVHDL

QQAIGKEVKLKPGISVSYSGQFELLERANQKLKLMVPMTLMIIFVLLYLAFRRVGEALLIITSVPFALVG

GIWFLYWMGFHLSVATGTGFIALAGVAAEFGVVMLMYLRHAIEAEPSLENPQTFSVDKLDEALYQGAVLR

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043916.1\_4766 [locus\_tag=BN49\_RS25815] [protein=DUF1294 domain-containing protein] [protein\_id=WP\_046043916.1] [location=5015385..5015732] [gbkey=CDS]

MNLNLVCYSLLLLTAVGSALLPYPLAMWFLLSSLLTWLIYGADKLAARKAWRRVPETTLLVLGLAGGWPG

AILGQQCFRHKTQKQSFRTRFFISVALNVAALAGLYVVYTHLLSR

>lcl|NZ\_FO834906.1\_prot\_WP\_002887259.1\_4767 [locus\_tag=BN49\_RS25820] [protein=lipocalin family protein] [protein\_id=WP\_002887259.1] [location=complement(5015742..5016275)] [gbkey=CDS]

MKLWPVVTGVAIALTLVACKSPTPPKGVQPISGFDASRYLGKWYEVARLENRFERGLEQVTATYGARSDG

GISVVNRGYDPVKKRWNESDGKAYFTGAPTTAALKVSFFGPFYGGYNVIRLDDDYQYALVSGPNRDYLWI

LSRTPTIPAAVKQDYLNTARELGFDVDRLVWIRQTPR

>lcl|NZ\_FO834906.1\_prot\_WP\_004192228.1\_4768 [locus\_tag=BN49\_RS25825] [protein=MerR family transcriptional regulator] [protein\_id=WP\_004192228.1] [location=5016392..5017120] [gbkey=CDS]

MPYSIGEFARLCGINATTLRAWQRRYGLLKPLRTDGGHRLYSDDDVQQALKILDWVKKGVPVSQVKPLLS

RPGARRTNNWLTLQETMLQRLKEGKIESLRQLIYDAGREYPRQELVTEVLRPLRSQVSANVPAIMTLREI

LDGIIIAYTSFCLEGDKKAPGDNFLITGWHLTDACEIWLEALKRTGQGHRIDVLPVPPAALAPEIFPQRN

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>lcl|NZ\_FO834906.1\_prot\_WP\_002887256.1\_4769 [locus\_tag=BN49\_RS25830] [protein=nuclear transport factor 2 family protein] [protein\_id=WP\_002887256.1] [location=5017352..5017786] [gbkey=CDS]

MSTSPSVIRRFVEYYAGLDAQPPAALATLYHPDATLSDPFGQHQGLFAIQRYFTHLLANVEQCRFTIDTP

LCDGQRFAVTWTMHWSHPRIAGGETLALPGCSVVDIAGEQVLHQRDYYDAGEMIYEHLPLLGWAVRGVKR

RVRS

>lcl|NZ\_FO834906.1\_prot\_WP\_004872509.1\_4770 [locus\_tag=BN49\_RS25835] [protein=SDR family NAD(P)-dependent oxidoreductase] [protein\_id=WP\_004872509.1] [location=5017783..5018502] [gbkey=CDS]

MMTVLITGASSGIGAGLAKSFAADGHLVIACGRDASRLAALQQFSPNISVRLFDMTDRDACRQALTGCFA

DLIILCAGTCEYLDHGQVDAALVERVMATNFLGPVNCLAALQTQLEAGDRVVLVSSMAHWLPFPRAEAYG

ASKAALSWFANSLRLDWEPKGVAVTVVSPGFVDTPLTRKNDFAMPGRVSVDRAVAAIRHGLAKGKNHIAF

PTGFSLALRLLASLPSGIQRLLLRRMVRS

>lcl|NZ\_FO834906.1\_prot\_WP\_046043918.1\_4771 [locus\_tag=BN49\_RS25840] [protein=FAD-dependent oxidoreductase] [protein\_id=WP\_046043918.1] [location=5018499..5019758] [gbkey=CDS]

MNIAIIGSGIAGLTCAWRLAGHHQVTLFEAGATPGGHTATVDVSTPQGTWAIDTGFIVYNDRTYPRFMGL

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GATLESFLARHRFSPFFARHYILPMGAAIWSSSLQEMRRFPLPLFLRFFENHGLLDIRDRPQWYVVPGGS

REYVRALLARLGDRLDLRLNAPVQQVDRHPAGVTLRLASGEAHFDQVIFACHSAHALAMLAAPTDSEREV

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043920.1\_4772 [locus\_tag=BN49\_RS25845] [protein=DUF1365 domain-containing protein] [protein\_id=WP\_046043920.1] [location=5019760..5020482] [gbkey=CDS]

MNSCLYQGVLRHRRLQPKAHHFVYHLFMAWLDLDELDKLPEAGIRRNRLAAAAWYDADYPLGAPLKAQAL

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LEKAFHVSPFNPMDMVYHWRFNAPGKTLHMHIENHQASKVFDATLALSRVPLTRANLRGLLLRLPLMTLK

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043923.1\_4773 [locus\_tag=BN49\_RS25850] [protein=cyclopropane-fatty-acyl-phospholipid synthase family protein] [protein\_id=WP\_046043923.1] [location=5020479..5021699] [gbkey=CDS]

MTDPVFALEPDVPRNVRLARWLLFRLLSGLREGSLTVREGAQTFHFGDPAAALRAEARVCAPEVYWRLLT

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YDLGNEFYAHFLDDDLLYSSALFTDDQQDLTQAQRAKMARLCDQLALTPGDHLLEIGTGWGALAEYAARH

YGCRVTTTTLSREQHRWATERMARAGLQDRVEVLLCDYRDLRGEYDKLVSVEMIEAVGQRYLPAFFRTCQ

ARLRPGGKMALQAITIQDQRYRDYSKSVDFIQRYIFPGGFLPSITAMSELMTRHTDFVVRNLFDMGPDYA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004186827.1\_4774 [locus\_tag=BN49\_RS25855] [protein=DUF2878 domain-containing protein] [protein\_id=WP\_004186827.1] [location=5021696..5022181] [gbkey=CDS]

MTRPAQHLLMALAFDVYWTLVVMLRERGLLIWLTLAIFAWLRLPAASRPPALLLAAAGCGLDACWALAGL

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AMACGWLVLMLLFHLGMGRQK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043924.1\_4775 [locus\_tag=BN49\_RS25860] [protein=hypothetical protein] [protein\_id=WP\_046043924.1] [location=5022178..5022702] [gbkey=CDS]

MRFALLLLWLTILAPAAHAADWLTWRRVGEATLTWGPFTVYHSQLRTPNGRYDGPQQDRALIITYRRDID

REALVEATRDQWQAQGILQQEPRSEAWLRMLQGIWPDVAPGSQLAFVVSVGEGQFWYRASAAQTAFTPLG

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>lcl|NZ\_FO834906.1\_prot\_WP\_015959356.1\_4776 [locus\_tag=BN49\_RS25865] [protein=DUF3833 domain-containing protein] [protein\_id=WP\_015959356.1] [location=5022699..5023250] [gbkey=CDS]

MKRILTLGLALLMLILAGCSTEVTEYRQQQPALDIFHYFQGRTEAWGMVQDRSGKQLRRFHVEIDGDVVG

DTLTLHERFVYDDGEKQQRIWRIRRTGDNRYQGTAGDIEGVASGQAAGNAFHWRYSMNVEASGSRWLLHF

DDWMFLQDGSHLFNKTEMKKFGITVATVTLFFTRTTAEERTAP

>lcl|NZ\_FO834906.1\_prot\_WP\_004178436.1\_4777 [locus\_tag=BN49\_RS25870] [protein=DUF523 and DUF1722 domain-containing protein] [protein\_id=WP\_004178436.1] [location=5023247..5024206] [gbkey=CDS]

MNTQPVIGISGCLTGSAVRFDGGHKRMGFVMDELAQWVAFKPVCPEMAIGLPVPRPALRLVQTPVGEIRM

RFSHAPHEDVTEKMADFASAHLATLGELSGFIVCAKSPSCGMERVRLYDEKGNRGRKEGVGLFTGALMAR

YPWLPVEEDGRLHDPLLRENFVERVFALHELNALRARGLTRHGLLAFHSRYKLQLLAHHQAGYREIGPFV

ASLHEWEDLEAFFEVYREKLMAILKQPASRKNHTNVLMHIQGYFRDQLNSRQRGELREVILNYRAGLLPI

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043926.1\_4778 [locus\_tag=BN49\_RS25875] [protein=carbohydrate porin] [protein\_id=WP\_046043926.1] [location=complement(5024511..5025893)] [gbkey=CDS]

MTMIKKLPLTMAVIAAFFPLTSVMAQEFTQEQIDAIVAKAVDKALADRQAKIDAAANKKVDVITNPETTA

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LNVMFDHWSDEVNLKKAYVGVTNVLESNPNAYIWAGRDFHQRPQQGINDYFWMNHDGQGAGVKNFDIGGV

QFDVAAVSQVKSCSPEVMADETNPSRITCTGSSDIGDNGHYALTTKTHNIKAGPIDVEVYANYGFDSKAV

DSDARLEAWQGGLVLSHTNDSGVNKVILRYSDNSDNSVYNKTDDLTTVYASFEGSHKFTQQAQIEYLLAF

HDYDNGKDNTDNRKNYGAIVRPMYFWNDVYSTWLEAGYQRVDYDQGGDNHGWKLTLSQNIAIGMGPEFRP

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>lcl|NZ\_FO834906.1\_prot\_WP\_004186818.1\_4779 [gene=xylA] [locus\_tag=BN49\_RS25885] [protein=xylose isomerase] [protein\_id=WP\_004186818.1] [location=complement(5026165..5027484)] [gbkey=CDS]

MQTYFDQVDRVRFAGPKTDNPLAFRHYNPDEIVLGKRMADHLRFAACYWHNFCWNGADMFGAGSFERPWQ

AAGDALEMAKRKADVAFEFFYKLNVPYYCFHDVDVSPEGASLKEYLHNFAIMTEVLAEKQQQTGVKLLWG

TANCFTHPRYGAGAATNPDPEVFAWAATQVVTAMNATHQLGGENYVLWGGREGYESLLNTDLRQEREQIG

RFLQMVVEHKHKIGFGGTLLIEPKPQEPTKHQYDYDVATVYGFLKQFGLENEIKVNIEANHATLAGHSFH

HEIASAIALGIFGSVDANRGDAQLGWDTDQFPNSVEENTLVMYEILKAGGFTTGGLNFDAKVRRQSTDKY

DMFYGHIGAMDVMALSLKLAARMIEDGKLDQGLAKRYAGWQGELGQKIMSGQMSLDNIARYAEQHNLNPQ

PQSGRQELLENLVNTYIFG

>lcl|NZ\_FO834906.1\_prot\_WP\_072140513.1\_4780 [locus\_tag=BN49\_RS25890] [protein=MFS transporter] [protein\_id=WP\_072140513.1] [location=5027912..5029351] [gbkey=CDS]

MHSRHDEYHKLTRGERIGYGMGDFAQNLVFGTIGGFLALHMLTVNTISTATAGFIFLFVRIINVFWDPMV

GTYVDKRTSKAGKYRPWLLRAGVPLVILSALLFAPIPGVKGSVAFAFIIYLALDLVYSLVNIPYGSLNAS

LTRDPESIDKLTSTRMMLANSANLLVYTLFPMFVQMAAPKDRSLKDTGFFGLELNLGNYTDPSANYAWFG

VYAIYMIIGAVALFICYKCTKERVVATAEQTANVKTTDLFHELRHNRPLVILGMFFMLAFTFMFFMNTVN

GFFNQYVVGHSEWMGAVGLVASIPGIAFPIFWPKLKKIFGKKGFFHLFLAMFIVGELLTYVWSREGMHDA

LWLAYIATFIKQWGLTSATGFMWALVPEVIAYGELKSGKRNAAIINAIMGLFFKIGFTIGGAIPLWLLAV

YGFNESGAVQSASAIDGIIMTAVWIPIALAAISMVIMQVYPISDKHVTDINRQLDEIRV

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MSLIQNPILRGFNADPSIIRVEDTYYIANSTFEWFPGVRLHESKDLKNWNLLPSPLSTTTLLDMKGNPSS

GGIWAPALSWADGQFWLVYTDVKITEGAFKDMTNYLTTAKDIRGPWSDPIKLNGVGFDASLFHDDDGRKY

IVQQTWDHREYHHPFDGITLTELDTKTLKLMPETARTIYRGTAVALVEGPHLYKLNGYYYLFAAQGGTVF

THQEVVARSKTLEADSFETEPGDVFLTNVDTPDSYIQKQGHGALVSTPEGEWYYASLCARPWNRPGESIY

DPRGWSTLGRETAIQKVYWDDEGWPRIEGGHGGKTFVEGPKDAIFTESASDNSQQDDFTSPALDPNWNTL

RVPFTAKMGTTGDGKLTLIGQGSLANTHDLSLIARRWQAFYFDAAVKVKFEPFSYQQMAGLTNYYNDRHW

SFVFLTWNEINGKVIEVGENNRGKYTSYLKDNAIKVPDGVEYVWFRTKVRKQTYSYEYSFDGVSFTEIPV

LLDAAVLSDDYVLQSYGGFFTGAFVGLAAVDYAGYGTQAEFYQFEYQERGDRLAADGSYSWEAGETRDK

>lcl|NZ\_FO834906.1\_prot\_WP\_004222324.1\_4782 [locus\_tag=BN49\_RS25900] [protein=ROK family protein] [protein\_id=WP\_004222324.1] [location=complement(5031268..5032380)] [gbkey=CDS]

MDSQSECLELRGSQRLLLELIRRHAPVTRAELARLSGLTAGAITQQCRELMFLGLVVEGERNTGQRGQPS

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RILGIGYAVPGFLKADGRKRHCVPSLESWRDADLQQTFADNLPWPTWVENNANAAAVGELYSGEWNAYSD

LTFIDLGYGIGAGIISGHKMLRGGFCNAGEVGMAFPSGTPRPSYKDLLATLDREGFTENQLPELIAEQHP

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>lcl|NZ\_FO834906.1\_prot\_WP\_004222322.1\_4783 [locus\_tag=BN49\_RS25905] [protein=glycerophosphoryl diester phosphodiesterase] [protein\_id=WP\_004222322.1] [location=complement(5032396..5033226)] [gbkey=CDS]

MAFNFHRAAEGIVLANSHRGFSTCAPENTFPAFEAARLAGTHCIEIDVHLTVDNQLVVTHDHRIDRVSSG

DGFVEEMTYLQLLACDFGMKFHPSFIGTHIPLLADVLCWAVENDMGLIVEVKQRNRHDKFVSVLVELLHE

QPEAINHIQLLGFNHVLINQVKAQIPQLALQVVTLERYNNQLAAVQQSNASCVCFEFEFAHIGDLRAYKE

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>lcl|NZ\_FO834906.1\_prot\_WP\_014599027.1\_4784 [locus\_tag=BN49\_RS25910] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_014599027.1] [location=5033440..5034507] [gbkey=CDS]

MSKLVLEQVTKTFGEFYAAREISFCAEEGEFVTLLGPSGCGKTTLLKMIGGFHQPDSGRILIGDKTVNAL

PPEKRNTAMCFQSYALFPHLNVAHNICFGLKQKKATIGEQQARLAEALKQVGLESQRLKMPGQLSGGQQQ

RVALARAMITRPDVILFDEPLSNLDAKLRESVRFEIKELQRLYQLTSIYVTHDQAEALAMSDKIVVLNAG

NVEQIGQPEEIYYRPANRFVADFIGAANIDTAQVTPAEQPGYYRVRCALGEFYVFSERPPRAEHCYICWR

PEDAQYVGQPQAGDNHFTLTLDKMAFMGNLTEAWGHNNAGLSVRLQLIKKPPIAPGERVCFRLTENAIHF

LEPVS

>lcl|NZ\_FO834906.1\_prot\_WP\_004222316.1\_4785 [locus\_tag=BN49\_RS25915] [protein=ABC transporter permease] [protein\_id=WP\_004222316.1] [location=5034504..5035370] [gbkey=CDS]

MKNWRNELFAWLLMLSGLGTILLLMGSTFYVVIAQSLGWFNLEGDSHFSLEYWRNMLQDEVLQSALFYSV

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SEPLRMQNDDFGWGVVILQIWKNLPLALILVGGAVNAIRNDVLDAASNLGANRWRSFTGVVVPLTLPAVQ

VTLILVFIGALGDFAFFSVAGPRNTYSLSRLMQATAMEYGEWNSAAVIAVIIMVTAAICTLLIALLITPF

ATRKGELK

>lcl|NZ\_FO834906.1\_prot\_WP\_009309830.1\_4786 [locus\_tag=BN49\_RS25920] [protein=ABC transporter permease] [protein\_id=WP\_009309830.1] [location=5035367..5036203] [gbkey=CDS]

MSHTANGRRVVTISLIFFMVANLIWLGMPFGMAILWSLVDAAHPWSYPDIFPPVLSFSRWLLVWEKTSLA

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FISIVIGHTVLTLPYSIRIMSAGFKAVPQDLIDASRDLGSGVWGTFSNAYLPLLKPSLLAALIFCLVRSL

EEFSISYVLGAPDFITVPTILYSFLGYSFVRPDAAVVSMILVIPNVILMAIIEKLLKGNYLSQSTGKA

>lcl|NZ\_FO834906.1\_prot\_WP\_016528884.1\_4787 [locus\_tag=BN49\_RS25925] [protein=extracellular solute-binding protein] [protein\_id=WP\_016528884.1] [location=5036225..5037292] [gbkey=CDS]

MKKTVIIMAGGLLCSSLTMAAEKADWDKVLEQAKQEGNVTFHVWYLQSQWRIFVQEFEKQYGIKVRIPEG

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QTGFAYDPKQIGNQALPQTLDQLQSFINANPKRFGYNDPNNGGAGEAFIQRIVTITGGDFNSKTDSIDPT

VVKRWQKGWLWFAANRDNITLTASGADSLTRLNDGELMLIPIWEDHLVGLQKTGAITPRLKFYVPEFGMP

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EVMTQ

>lcl|NZ\_FO834906.1\_prot\_WP\_032447996.1\_4788 [locus\_tag=BN49\_RS25930] [protein=ParB family protein] [protein\_id=WP\_032447996.1] [location=5037577..5039052] [gbkey=CDS]

MNSKITSQVVQSHLMQSCFDQQSSSAEGCARPSKETAMIVTLDQLRPYEFNPRVMRNPNYDDIKASIRQR

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LAENDLHGKLSFIERALGISKARELYQHVEQYQLSQRELAERLRKDGYPINQSQISRMEQTLEYLHPYIP

QVLYAGLGRPQIEKLLSMRTAALRIWEQHATDDLGSFENIFSSALSLFNDQPEEFCFELVQDELLGLLSQ

ALNVDYNLLMLDLDPSEQKRLALLGPTQESPLYIQKEASAARSTVYRRKPSSKRKTVLSAPDSPLGSTLM

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MIPTINHAILSQVVQAIKAGNLRYCEALGFNHDELNKLCSLSYDELLYLTNTSSHFLKVTVNHDVLRKML

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>lcl|NZ\_FO834906.1\_prot\_WP\_014599026.1\_4790 [locus\_tag=BN49\_RS25940] [protein=YdcF family protein] [protein\_id=WP\_014599026.1] [location=5040242..5041357] [gbkey=CDS]

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PEERQQATGKLHQQLQQHFPNQTAKYDAILDAADKVLQDTNIIHFDMPKVAHPGRYHAIVVLGYQLDKEG

NPQEPLKGIMAQALKVAKQYPDSKIIVTGGVPRNNRVEAEVMWKYFTENGIAPSRIIPEVLSYDTVQNAN

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YRSTYRDVLRLYRQEYPGFAM

>lcl|NZ\_FO834906.1\_prot\_WP\_016528883.1\_4791 [locus\_tag=BN49\_RS25945] [protein=porin] [protein\_id=WP\_016528883.1] [location=5041382..5042527] [gbkey=CDS]

MQKRIIAGLITGLITANSQAVTLYENKEQGANLDLTGSLRMMLENSSKRGRTDGDSDSKLKDQGTRIGLK

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SYYSYEYGSSGALYFGGGKIARVGGGDNNFIKRESNTIRFMSERWHGLKVATSYTMQTGTNINDIDNAWA

MALLYDSPWDLTLNAGIAQQTTNGSTDANVKSGYTDVKADKENIWGIGMKYNIPQINLSLALDYGGYQIK

NGNKGSSKGYTAYQDTINVDLFGAGAKWTWDKWGIYGVYGLRDGDAAADNYQETRTIFGTDYTFNKQFIL

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>lcl|NZ\_FO834906.1\_prot\_WP\_020802331.1\_4792 [locus\_tag=BN49\_RS25950] [protein=histidine-type phosphatase] [protein\_id=WP\_020802331.1] [location=5042538..5043836] [gbkey=CDS]

MMKAYTLSLIALALTSSLAQAATADLVLDKVVTLNRHGIRPQMDTAKIQAMSPETFPHFQGKDGELTMHG

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RNIELEGPLFWGNELGETFRLQYAEGLPLEQVAFGHVKNTDDLTRLNKLHQIKFDLILHDPYIAARAGSQ

LLSQILYTLEKGSGFHDPNASPEIAASAPDARMVMYFGHDSNLTPLQTLLNVSWHLKGYPKDDTPPGSTL

MFERYRDSKTHQTYIGLTFMTQSLDQMRRLEPLNVKNPPLQQKLNLHCKNSPDGWLCPIDEFAAQINSRL

DKTAMIAQNYAE

>lcl|NZ\_FO834906.1\_prot\_4793 [locus\_tag=BN49\_RS25955] [protein=HNH endonuclease] [pseudo=true] [partial=3'] [location=complement(<5044123..5044305)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_4794 [locus\_tag=BN49\_RS25965] [protein=transposase] [pseudo=true] [partial=5',3'] [location=<5044465..>5045085] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177598.1\_4795 [locus\_tag=BN49\_RS25970] [protein=polysaccharide pyruvyl transferase family protein] [protein\_id=WP\_004177598.1] [location=complement(5045355..5046164)] [gbkey=CDS]

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VFITDDMAFYLDLNKYLSLKPVYKKQANCFRTDSESLTGDYKENNHDISLTWNGDYWDNEFLARNSTRCM

INFLEEYKVVNTDRLHVAILASLLGKEVNFYPNSYYKNEAVYNYSLFNRYPKTCFITAS

>lcl|NZ\_FO834906.1\_prot\_WP\_004222296.1\_4796 [locus\_tag=BN49\_RS25975] [protein=glycosyltransferase] [protein\_id=WP\_004222296.1] [location=5046262..5048484] [gbkey=CDS]

MKKILIMTPDIEGPVRNGGIGTAFTALATTLAKKGYDVDVLYTCGDYSESSVSKFSDWSRIYSTFGINLL

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LWADEGNYQLPYDQNHLELYYMEKMVVEMADEVVSPSQYLIDWMLSKHWNVPEERHVILNCEPFQGFVTR

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QTKNLGLAVNVISDYDRTNANEYIKRKNVLVIIPSLVENSPYTVYECLINNVNFLASNVGGIPELIPQEH

HAEVLFIPTPVDLYGKIHYRLKNINIKPGLAESQDNIKEAWFVAVERKNNRTFKKIDEANSPLVSVCITH

FERHHLLQQALASIKSQTYQNIEVILVDDGSTTEDSHRYLNLIENDFNSRGWKIVRSSNNYLGAARNLAA

RHASGEYLMFMDDDNVAKPFEVETFVTAALNSGADVLTTPSDLIFGEEFPSPFRKMTHCWLPLGPDLNIA

SFSNCFGDANALIRKEVFEKVGGFTEDYGLGHEDWEFFAKISLQGYKLQIVPEPLFWYRVANSGMLLSGN

KSKNNYRSFRPFMDENVKYNYAMGLIPSYLEKIQELESEVNRLRSINGGHSVSNELQLLNNKVDGLISQQ

RDGWAHDRFNALYEAIHVQGAKRGTSLVRRVARKVKSMLK

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IESFNGSLRDECLNIHWFLSLEDAQDKLDNWRREYNHERTHSSLNDMTPAEFIRSLRKDEDL

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MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

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RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

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\*RSYGFPRIHIQLRREGWPVNH

>lcl|NZ\_FO834906.1\_prot\_WP\_227504835.1\_4800 [locus\_tag=BN49\_RS29640] [protein=PAAR domain-containing protein] [protein\_id=WP\_227504835.1] [location=5051714..5052127] [gbkey=CDS]

MAIGHFLFRGDKTACGGRILEGCPNHQFFEKDMACEGHKVTCGKHPGHYRICGGLDSDEIHGKRVAGTLH

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FVMDALSTGRRIKCLTCVDDFTKECLTVTVAFGISGVQVSRILDSIALFRGYPATIRTDQGPEFTCRALD

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>lcl|NZ\_FO834906.1\_prot\_4802 [locus\_tag=BN49\_RS26030] [protein=integrase arm-type DNA-binding domain-containing protein] [pseudo=true] [partial=3'] [location=complement(<5053346..5054056)] [gbkey=CDS]

MALSDVKVRSAKPEAKAYKLTDGEGMVLLVHPNGSKYWRLRYRFGGKEKMLALGKYPEVSLADARARRDE

ARKLLANDVDPSENKKAVKVEQEQEAITFEVVARDWHASNQKWSASHSARVLKSLEDNLFAVIGKRNIAE

LKTRDLLVPIKAVESSGRLEVAARLQQRTTTIMRYAVQSGLIDYNPAQEIAGAVATAKRQHRAALELNRI

PELLHRIDHYTGRPLTRLAVELTLLVF

>lcl|NZ\_FO834906.1\_prot\_WP\_046043933.1\_4803 [locus\_tag=BN49\_RS26040] [protein=carbonic anhydrase] [protein\_id=WP\_046043933.1] [location=5054932..5055612] [gbkey=CDS]

MTTLKPLLARNRSWALQKCQHDPDYFEKWIDGQRPHSLWIGCSDSRVPAEVLTGSQPGELFVHRNIANML

DPTDDNVMSVLQYALHYLEVERVVLCGHYGCGGVQAALSLPTLPLAQESSALARRIGQLRHTLHHEIAQI

ADGCGVAASPGASARASTDAERSRHALDALVEANVRAQFARLLESEPVQTVLASGRPLSLHGCVYDLASG

HLTTLVEHLSPQEHAP

>lcl|NZ\_FO834906.1\_prot\_WP\_016529159.1\_4804 [locus\_tag=BN49\_RS26045] [protein=SulP family inorganic anion transporter] [protein\_id=WP\_016529159.1] [location=5055609..5057078] [gbkey=CDS]

MNTLRQDSLAGIVVFLVALPLCLGIAQASGLPPFVGLLTGIIGGLVVTALSPSRFAVSGPAAGLVTIVVA

AIESLGSFSVFLMALVLAGVLQLLFGILRAGRFISLVPASVIKGMLAAIGILLIMQQIPVALGTAEETGL

ADVVQGNAAFSVKAIAVAAGGLLVLWLWGSPLIRRVKSLRWIPGPLIAVLLGCVTTLLLTHFAPQQLAAL

PRITLPAFGSLGDLLGELESPAWNAWRNPSVWVVAVTLALVASLETLLSQEALKKLRPQNPPPSPNREMV

AQGVGNLLSGVLGAMPITAVIVRSSVNVSNGAQSKLSIFIHGVLLLICGLWFSGLLTLIPLASLAAVLLY

TGYKLATPRLFIEQFRQGAAQYVPFLATIGGIIAFGMLAGIGIGLATQMAFSLWRSHRHSLQLARYDDHY

VLRIQQNLTFMHNPHLLALLAKIPEKSVVIIEHDSVGYLDPDVRAVLDDFAENAPQRGIRLNQWPLASR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529158.1\_4805 [locus\_tag=BN49\_RS26050] [protein=NAD(P)-dependent alcohol dehydrogenase] [protein\_id=WP\_016529158.1] [location=5057190..5058209] [gbkey=CDS]

MSIIKSYAAKEAGADLSLWEYDAGELQPEDVEVEVEYCGICHSDLSMIDNEWGMSSYPLVAGHEVIGRVA

ALGSAAQDKGLKIGQKVGIGWTARSCGHCDACISGNQINCLEGSVPTILNRDGFANKLRADWQWVIPLPD

SIDLASAGPMLCGGITVFKPLLTHHVTATSRVGVIGIGGLGHIAIKLLRAMGAEVTAFSSNPAKEQEVLA

MGADRVVNSRDPEALKALAGQFDLIINTVAVDLDWQPYFQALAYGGNFHTVGAVMKPFPVPAFTLIGGDR

SISGSATGNPSELRTLMKFAGRSKVAPTTELFPMSQINEALKHVREGKARYRAVLKADF

>lcl|NZ\_FO834906.1\_prot\_WP\_171819484.1\_4806 [locus\_tag=BN49\_RS26055] [protein=sugar ABC transporter permease] [protein\_id=WP\_171819484.1] [location=5058340..5059224] [gbkey=CDS]

MRVTMRKTWLPWLILSPSLLFLLLFTWFPLGRSVYDSLFDTRMASDGAQYVGLDNFARLFADGVFWQSLV

NNLLYILLTVVPGVTLALLLAVALSENHRVNRWLRTAFFFPTIIPMVSAAALWLFIFMPDLGLLDHYLAK

LFGPMNNNWLGRSNSALLALALIGVWKFAGYYMLFFLAGLQSIPASTREAALMEGATRTQVFFKVTLPLL

RPTLSFVITTALIYSITQIDHVAVMTRGGPDNATSVLLYYIQNLAWDTHDLGKASAATFLTLAGLFAFSL

INLKLLEKGAHYER

>lcl|NZ\_FO834906.1\_prot\_WP\_046043935.1\_4807 [locus\_tag=BN49\_RS26060] [protein=carbohydrate ABC transporter permease] [protein\_id=WP\_046043935.1] [location=5059214..5060101] [gbkey=CDS]

MSAEISPLLVRTPAAARPLWLRLRRSSPFTLTVLMCCLALLWVSPFIWMLATSFSATTFGDDMASLLPRL

PLTLDNFRDAWQSADWLSLYANTLIFTFGTFFVQLLTITTAGYVFACHEFRGKQTLFLLFLVQLMIMPVV

MMVPNMLTLKTFGLLNTLTGVMMPYFTSAFGVFLMRQAFLAIPKELEEAALMEGCRWWLVLFRVLLPMSW

PSVLAFATVSITYHWNEYLWPLMMLNDPDKQVLTVGLVSFAMGAESGGQWGTIGAGTLMVCLPLMLAFIL

FQKQFLRSFGFSGIK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529155.1\_4808 [locus\_tag=BN49\_RS26065] [protein=phosphodiesterase] [protein\_id=WP\_016529155.1] [location=5060112..5060936] [gbkey=CDS]

MLLAHISDTHFRSRGEKLYGFIDVNAANADVVSQLNALRERPNAVVVSGDIVNCGRPEEYQVARQILGSL

NYPLYLIPGNHDDKAHFLEHLHPLCPQLGNDAQNMRYAVDDFATRLLFIDSSHAGTSKGWLTDETIGWLE

AQLFEGGDKPATIFMHHPPLPLGNAQMDPIACENGHRLLALVERFPSLTRIFCGHNHSLTMTQYRQALIS

TIPGTVHQVPYCHEDTRPYYDLSPASCLMHRQVGEQWVSYQHSLAHYAGPWLYDENISCPTEER

>lcl|NZ\_FO834906.1\_prot\_WP\_016529154.1\_4809 [locus\_tag=BN49\_RS26070] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_016529154.1] [location=5060942..5062015] [gbkey=CDS]

MLSLQNISKRFDGKPALSALSLDIHEGEFVVLVGPSGCGKSTLLRLLAGLEPVSEGQIWLHDENITATTP

RERNFAMIFQNYALFPHLSVRDNITFGMKVRKEEKSSWQPRVDKVAQMLQLEALLDRKPAKLSGGQRQRV

AMARAIVRNPRLFLMDEPLSNLDARLRSEVRDSIMALHQQLKTSTIYVTHDQTEAMSMADRIVVMNGGHV

QQVGRPEYLYANPANLFVAGFIGSPAMNLLSLPCANGEVLLGEQRHPLPPRHRDQTRVWLGVRPEHITDR

VEEGHLRLPATVLQRELMGADYLLHVSTPIGTLRFSRRHRGTVPEKGESLPIGFSPADVHLFHAETQHNL

LMECNHV

>lcl|NZ\_FO834906.1\_prot\_WP\_016529153.1\_4810 [locus\_tag=BN49\_RS26075] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_016529153.1] [location=5062008..5063318] [gbkey=CDS]

MFKPFTLVAVGLSLALSGAALAKEKIDFMFPAPVDGKLTMEMTRVIKQFNDSQQDVEVRGIFTGNYDTTK

IKAESAQKAGQPPALVIMSANFTTDLALKDEILPMDELFKYGDQKAGDFLHKEFWPAMHKNAQVMGTTYA

IPFHNSTPILYYNKTMFDRAGIKQPPQTWAELLADAKKLTDESTGQWGIMLPSTNDDYGGWIFSALVRAN

GGKYFNEDYPGEVYYNSPTAIGALRFWQDLIYKDKVMPSGVLNSKQISAAFFSGKLGMAMLSTGALGFMR

ENSKDFELGVAMLPAKEQRAVPIGGASLVSFKGISEAQKKAAYQFLTYLVSPDVNGAWSRFTGYFSPRKA

SYDTPEMKAYLQQDPRAAIALEQLKYAHPWYSTWETVAVRKAMENQLAAVVNDAKVTPEAAVQAAQKEAD

ALMKPYVDKTALAEVK

>lcl|NZ\_FO834906.1\_prot\_WP\_002886970.1\_4811 [gene=iolE] [locus\_tag=BN49\_RS26080] [protein=myo-inosose-2 dehydratase] [protein\_id=WP\_002886970.1] [location=complement(5063463..5064362)] [gbkey=CDS]

MNKDNVKLAIAPIGWTNDDMPELGSENTFQQIVSEMALAGFTGSEVGSKYPRDPAVLKPMLDIRGIQICN

AWFSTFFANGQREKTIDEFVNHMNFLHAMGAKVIGCSEQSGSIQGLDKPILGDAKPCFSDEEWQRVAEGY

NTLGRLAAEKGMQVCLHHHMGTGIQTTAEIDKFMSLVDERVFLLFDTGHAWYSEGGEAPMLAILKKYLPR

INHVHLKDVRPPVIDQVRRDGLSFLDGVKKGTFTVPGDGVIDFRPVFKLLDDFGYKGWMVVEAEQDPALA

NPFEYAVKARKYIRETAGI

>lcl|NZ\_FO834906.1\_prot\_WP\_004152193.1\_4812 [locus\_tag=BN49\_RS26085] [protein=sugar phosphate isomerase/epimerase] [protein\_id=WP\_004152193.1] [location=complement(5064386..5065270)] [gbkey=CDS]

MKIAFDVDVIKDLGITRMVHQVAEWGYKYIEQSPHPQINPFYKHPRASREIMAEYKQALRDTGLELSSFI

CVYRWSGPDELRRQAAVKNWKRLVEIAVEMGVQVINTEFSGDPNQPEICDEMFYRSMEELLPIFEREGIR

VEIQAHPWDFCEENNETVDIVKSFRSDNVKYVYSVPHTFFYDKGVGDVASMLRYAGSDLSHVLIADTRNH

TKHCRYIVNPPGVDAVVHQHVGVGEGDVDFDALFRTLREMKFAEQTFKVGGEPIVATSLFGYPEKMKYQA

VETRELIERELLRR

>lcl|NZ\_FO834906.1\_prot\_WP\_029602447.1\_4813 [locus\_tag=BN49\_RS26090] [protein=Gfo/Idh/MocA family oxidoreductase] [protein\_id=WP\_029602447.1] [location=complement(5065312..5066325)] [gbkey=CDS]

MSLKLGVIGAGAIGKEHIRRCTQVLQGATVVAVSDINADNARAAVALPGVQAEVYADGHDVINASDVDAI

LVTSWDPTHEEYTLAAIAAGKPVFCEKPLAMTAEGCRRIVDAEMKAGRRLVQVGFMRPYDEGYLALKKVI

DDGDIGAPLMLRCAHRNQSVGENYTTDMAITNTLIHELDVLRWLLNDDYRSVQVRFPRSTSHTHARLKDP

QIVSFETKKGTLIDVEVFVNCQYGYDIQCEVVGETGIARLPEPSAVQMRKSASLSTAILTDWKDRFIKAY

DVELQAFINDVKAGQLQGPSAWDGYAASVAADACIKAQGTSEPVEVTLPECPAFYKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004152191.1\_4814 [gene=iolD] [locus\_tag=BN49\_RS26095] [protein=3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase (decyclizing)] [protein\_id=WP\_004152191.1] [location=complement(5066372..5068312)] [gbkey=CDS]

MGKLRLTTAQALVKFLDNQYLEVDGVELKFVKGIFAIFGHGNVLGLGQALEQDSGDMRVYQGRNEQGMAH

AATGFARQALRRQIIACTSSIGPGAANMITAAGTASANRIPLLLLPGDVFATRQPDPVLQQIEQSYDLSI

STNDAFRAVSKYWDRITRPEQLMSACINAMRVLTDPAETGAVTLCLPQDVQGEAWDYPESFFARRVHRLD

RRPASAAQLADAVAAIKASRKPLIVCGGGVKYSGAGEALSRFAERYGVPFAETQAGKGTVVSSHPLNVGG

VGETGCLAANLLAKEADLVIGVGTRFSDFTTASKWIFQHPEVRFLNINVSNFDAWKLDGIAMLADAREAM

TALDAALADSGWQAGWGAQIESVQSRQLKETQRVYQAVWQEKSFVPEIDDHLDRESVYREFRQITDSTLT

QSSVLGVLNETLPAEAVIVAAAGSLPGDLQRVWRNRAENTYHVEYGYSCMGYEVNAALGVKLAQPQSEVY

SLVGDGSFMMLHSELVTSLQERAKINVVLFDNMANGCINNLQMEHGMDSFGTEFRYRQPETGQLQGGLVP

VDFATIAAGYGCKTWRVTTLDELRHALDAARRETVSTLIDIKVLPKTMVHKYGSWWNVGVAQTALSERIR

KVAQMINEKRAQARDY

>lcl|NZ\_FO834906.1\_prot\_WP\_023302396.1\_4815 [gene=iolC] [locus\_tag=BN49\_RS26105] [protein=5-dehydro-2-deoxygluconokinase] [protein\_id=WP\_023302396.1] [location=5068818..5070731] [gbkey=CDS]

MNAAVKRLDVICIGRVAVDLYAQQIGSRLEDVASFAKYLGGSSGNVAFGTAIQGLKSAMLARVGDEHNGR

FLRETLNRAGVDTEYLITDKSRLTALVMLGIKDQETFPLIFYRDNCADMALTPDDISEEYIASSRALAVT

GTHLSHANTRAAVLKALEYARRHGLRTALDIDYRPVLWGLTSLGDGETRFIESGPVTSQLQEVLHLFDLV

VGTEEEFHIAGGSTDTLTALKNVRNATKATLVCKRGPMGCVVLEGDIPDSWDQVPLQQGVRVEVLNVLGA

GDAFMSGLLRGWLNDEGWEQACRYANACGALVVSRHGCAPAMPTKVELDDYLQRAESVPRPDVDERLNHL

HRVTSRRQQWPELCIFAFDHRKQLADLARETGRDEACIPQLKLLLLAAAEAAAQEAGLDQRSGILADGTY

GQRALNAITGKGWWIGRPIELPSSRPLRLEHGNIGSQLIDWPLEHVVKCLVFYHPDDPAALRAEQDALLL

EVWQACNKSGHELLLEVILPENGPDKDERHYHTMLEHFYQLGIKPDWWKLPPLSSASWQQITALIEREDQ

WSRGILILGLDAPSDKLRAGFAEAAAHPMIKGFAVGRTIFGQPSRRWMQGELSDEALIEEVKHNYLTLIG

YWREARR

>lcl|NZ\_FO834906.1\_prot\_WP\_004152190.1\_4816 [locus\_tag=BN49\_RS26110] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_004152190.1] [location=5070883..5071740] [gbkey=CDS]

MANNPTQLTILQDEIRRRYDTLSKRLKQVARYILDNSNSVAFDTVASIAQQADVPPSTLIRFANAFGFSG

FNEMKQMFKQHLMEETANYTERARLFRQTTSDESSPPETPTEILNMFTMVNNQALQQLAMQTSSDDLERA

VALLGEAENIYVIGLRRSFSVASYLTYALRHLDRKAFLIDGLGGMFTEQLSLVGPKDVVVAVSFSPYARE

VVELVELGAQRKARQIAITDSQVSPLAAFSDVCFVVREAQVDGFRSQVASLCLAQTLAVSLALNSSQESE

AKQKA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177654.1\_4817 [gene=iolB] [locus\_tag=BN49\_RS26115] [protein=5-deoxy-glucuronate isomerase] [protein\_id=WP\_004177654.1] [location=complement(5072736..5073545)] [gbkey=CDS]

MSLLAKSRKEGQIQHITPQSAGWRYIGFDVWMLKKGQTVTLESGDRELCLVLVAGLASVKTQHADFPNLG

KRMSPFERTPPWSVYVPPQDKVEVTADSDLELAVCSAPGKGSFPARLIRPEDVGVEHRGKGRNQRRVHNI

LPDSAEADCLLVVEVYTDEGATSSWPSHKHDTAQPGKETQLEETYYHRFDPPQGFAFQRVYTDDRSLDAC

MAPYNHDVVMVPRGYHPVAAIAGYDSYYLNVMAGPDRKWLFTWEDDHAWINTPEYPRHD

>lcl|NZ\_FO834906.1\_prot\_WP\_016528794.1\_4818 [locus\_tag=BN49\_RS26120] [protein=CoA-acylating methylmalonate-semialdehyde dehydrogenase] [protein\_id=WP\_016528794.1] [location=complement(5073564..5075069)] [gbkey=CDS]

MTITGNFIGGKTVISSSNETMPVYDPATGKAVREVTVSTAQEVSEAIQVARDAFDSWSRTTPLRRARVLF

NFKMLLEQHVEELAGIIVSEHGKVWSDALGELTRGMEVVEFACGIPHLIKGEYSSDVGTGVDSYSLMQPL

GVVAGITPFNFPAMVPMWMFPLALACGNSFVLKPPALAPTAAVRLAELLKEAGLPDGVFNVVHCSNEDAE

QLYTDPRIAAVSFVGSSGVAEYIYKTASAYGKRVQAFGAAKNHAIVMPDADLDATVNAIMGGAFGSAGER

CMALPVVVAVGDETADKLIARLKPLVEALKVGPGCMRGQEENEMGPVVSDTHQKKVLGYIDKGESEGAKL

VVDGRKLRVPGYDAGYYVGGTLFDHVTPEMTIWREEIFGPVLGIVRAADYDSALELVNSHEFGNGSAVFT

SNGHTAREFVHDVQAGMVGVNVPVPVPMAFHSFGGWKRSVFGALNVHGPDGVRFYTRMKTATVRWPAGQQ

TVSEFSMPTLG

>lcl|NZ\_FO834906.1\_prot\_WP\_016528793.1\_4819 [locus\_tag=BN49\_RS26125] [protein=TIM barrel protein] [protein\_id=WP\_016528793.1] [location=5075421..5076242] [gbkey=CDS]

MAIAMQRFCINRKIAPALSIEAFFRLVNRLGLNKVELRNDLPSGKVTDDLSHQQVRELAARYHIEILTIN

AVYPFNRRSEEVRQLTESLLKEAQAIGAKSLVLCPLNDGSEVPASETLGALRDLAPLFAFYGIHGLVEPL

GFPQSSLRSAHQAQTLIHDARVPFKLLIDTFHHHLYPQAVDEFSQVEVADIGLVHLSGVDDSRPREQLTD

AERIMLTPQDRLGTCEQVKALEARGYQGVYAFEPFAPELAQWSEADIEREIEQSIALIQRHCA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043939.1\_4820 [locus\_tag=BN49\_RS26130] [protein=DUF853 domain-containing protein] [protein\_id=WP\_046043939.1] [location=5076341..5077843] [gbkey=CDS]

MSSPLLIARTLDNALYLLPAMANRHGLITGATGTGKTVTLQKLAESFSEIGVPVFMADVKGDLTGIAAAG

QSSEKLQARLEKIGVSEWEPHANPVVLWDIFGEKGHPVRATVSDLGPLLLARLLNLNEVQSGVLNIIFRI

ADDRGLLLLDFKDLRAITQFIGDNAKSFQNQYGNINSASIGAIQRGLLTLEQQGAEHFFGEPMLDIADWM

RVDASGKGVINILSAEKLYQMPKLYAASLLWMLSELYERLPEAGDLDKPKLVFFFDEAHLLFNDAPQVLL

DKIEQVIRLIRSKGVGVYFVSQNPADIPDAVLGQLGNRVQHALRAFTPKDQKAVKTAAQTMRANPAFSTE

QAIQELGTGEALISFLDEKGSPSVVERAMVIAPCSRMGPVSDDERNGLLNHSPLYGKYEEEVDRESAFEM

LQQGVQVATGQQSAPPAKGQQNGDDDGLLGGLKDILFGSTGPRGGKRDGIVQTAAKSAVRQVTNQIVRGM

LGSLLGGRKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002886956.1\_4821 [gene=lptG] [locus\_tag=BN49\_RS26135] [protein=LPS export ABC transporter permease LptG] [protein\_id=WP\_002886956.1] [location=complement(5077892..5078974)] [gbkey=CDS]

MQAFGVLDRYIGKTIFNTIMMTLFMLVSLSGIIKFVDQLKKSGQGSYDALGAGLYTILSVPKDIQIFFPM

AALLGALLGLGMLAQRSELVVMQASGFTRLQVALAVMKTAIPLVLLTMAIGEWVAPQGEQMARNYRAQQM

YGGSLLSTQQGLWAKDGHNFVYIERVKGNDELGGVSIYAFNPERRLQSVRYAASAKFDSENKVWRLSQVD

ESDLTDPKQVTGSQMVSGTWKTNLTPDKLGVVALDPDALSISGLHNYVKYLKSSGQDPGRYQLNMWSKIF

QPLSVAVMMLMALSFIFGPLRSVPMGVRVVTGISFGFIFYVLDQIFGPLTLVYGIPPIIGALLPSASFFL

ISLWLMMRKA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043941.1\_4822 [gene=lptF] [locus\_tag=BN49\_RS26140] [protein=LPS export ABC transporter permease LptF] [protein\_id=WP\_046043941.1] [location=complement(5078974..5080071)] [gbkey=CDS]

MIIIRYLVRETLKSQLAILFILLLIFFCQKLVRILGAAVDGDIPTNLVLSLLGLGIPEMAQLILPLSLFL

GLLMTLGKLYAESEITVMHACGLSKAVLIKAAMILALFTGAVAAVNVMWAGPWSSRHQDEVLAEAKVNPG

MAALAQGQFQQASDGNAVMFIESVNGNRFHDVFLAQLRPKGNARPSVVVADSGELSQQKDGSQVVTLNKG

TRFEGTAMLRDFRITDFNNSQAIIGHQAVSADPDDTEQMDMRTLWKTHTDRARAELHWRFTLVATVFIMA

LMVVPLSVVNPRQGRVLSMLPAMLLYLVFFLLQTSIKSNGGKGKMDPAIWMWAINLLYFALAVLLNLWDT

VPMRRFRARFNKGAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002886954.1\_4823 [gene=pepA] [locus\_tag=BN49\_RS26145] [protein=leucyl aminopeptidase] [protein\_id=WP\_002886954.1] [location=5080461..5081972] [gbkey=CDS]

MEFSVKSGSPEKQRSACIVVGVFEPRRLSPIAEQLDKISDGYISALLRRGELEGKPGQTLLLHHVPNILS

ERILLIGCGKERELDERQYKQVIQKTINTLNDTGSMEAVCFLTELHVKGRNNYWKVRQAVETAKETLYSF

DQLKTNKSEPRRPLRKMVFNVPTRRELTSGERAIQHGLAIAAGIKAAKDLGNMPPNICNAAYLASQARQL

ADTYSKNVITRVIGEQQMRELGMNAYLAVGNGSQNESLMSVIEYKGNPAEDARPIVLVGKGLTFDSGGIS

IKPAEGMDEMKYDMCGAAAVYGVMRMVAELQLPLNVIGVLAGCENMPGGRAYRPGDVLTTMSGQTVEVLN

TDAEGRLVLCDVLTYVERFEPEAVIDVATLTGACVIALGHHITGLMSNHNPLAHELIGASELAGDRAWRL

PLADEFQDQLESNFADMANIGGRPGGAITAGCFLSRFTRKYNWAHLDIAGTAWRSGKAKGATGRPVALLS

QFLLNRAGFNGEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002886953.1\_4824 [gene=holC] [locus\_tag=BN49\_RS26150] [protein=DNA polymerase III subunit chi] [protein\_id=WP\_002886953.1] [location=5082092..5082535] [gbkey=CDS]

MKNATFYLLDNDATVDGLSAVEQLVCDIAAERWRNGKRVLIACEDEQQAIRLDEALWSRPPESFVPHNLA

GEGPRGGAPVEIAWPQKRNSSPRDILISLRLNFADFATAFTEVIDFVPYEDNLKQLARERYKAYRMAGFN

LNTATWK

>lcl|NZ\_FO834906.1\_prot\_WP\_004894670.1\_4825 [locus\_tag=BN49\_RS26155] [protein=valine--tRNA ligase] [protein\_id=WP\_004894670.1] [location=5082535..5085390] [gbkey=CDS]

MEKTYNPQDIEQPLYEHWEKQGYFKPNGDESQESFCIMIPPPNVTGSLHMGHAFQQTIMDTMIRYQRMQG

KNTLWQAGTDHAGIATQMVVERKIAAEEGKTRHDYGRDAFIDKIWQWKAESGGTITRQMRRLGNSVDWER

ERFTMDEGLSNAVKEVFVRLYKEDLIYRGKRLVNWDPKLRTAISDLEVENRESKGSMWHIRYPLADGAKT

ADGKDYLVVATTRPETLLGDTGVAVNPEDPRYKDLIGKFVVLPLVNRRIPIVGDEHADMEKGTGCVKITP

AHDFNDYEVGRRHQLPMINILTFDGDIRESAEVYDTKGNESDVYSSEIPAEFQKLERFAARKAVVAAVDA

LGLLEEIKPHDLTVPYGDRGGVVIEPMLTDQWYVRADVLAKPAVEAVENGDIQFVPKQYENMYFSWMRDI

QDWCISRQLWWGHRIPAWYDNDGNVYVGRSEDEVRQENNLSADVALRQDEDVLDTWFSSALWTFSTLGWP

ENTDALRQFHPTSVMVSGFDIIFFWIARMIMMTMHFIKDENGKPQVPFKTVYMTGLIRDDEGQKMSKSKG

NVIDPLDMVDGITLPELLEKRTGNMMQPQLADKIRKRTEKQFPNGIEPHGTDALRFTLAALASTGRDINW

DMKRLEGYRNFCNKLWNASRFVLMNTEDQDCGFNGGEMVLSLADRWIIAEFNHTVKAYREALDNFRFDIA

AGILYEFTWNQFCDWYLELTKPVMNGGSEAELRGTRHTLVTVLEGLLRLAHPIIPFITETIWQRVKAICG

ITADTIMLQPFPQYDASQVDDAALADTEWLKQAIVAVRNIRAEMNIAPGKPLELLLRGCSKDAERRVNDN

RSFLLNLARLESITVLPADDKGPVSVTKIVDGAELLIPMAGLINKEDELARLAKEVAKIEGEIGRIESKL

ANEGFVARAPEAVIAKEREKLEGYAEAKAKLIEQQAVIAAL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529394.1\_4826 [locus\_tag=BN49\_RS26160] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_016529394.1] [location=5085511..5086014] [gbkey=CDS]

MNTSVPAATLLRRITAADNAAIARVIRQVSAEYGLTADKGYTVADPNLDELYELYSQPGSAYWVVEQEGE

VVGSGGVAPLACSEPDICELQKMYFMTSARGQGLAKKLALLALDYAREQGFKRCYLETTAFLTEAIGLYE

HLGFEHIDGPLGCTGHVDCEVRMLKTL

>lcl|NZ\_FO834906.1\_prot\_WP\_016529393.1\_4827 [locus\_tag=BN49\_RS26165] [protein=hydroxylase for synthesis of 2-methylthio-cis-ribozeatin in tRNA] [protein\_id=WP\_016529393.1] [location=complement(5086277..5087041)] [gbkey=CDS]

MDYPQILSPIISFLHCPTPQAWIDEARKPENLPLLLTDHMVCELKAAQNAMLLVRRYVADKADADELLAC

LKPYEDFTYRRGPEPDFVALHKRINKSAMPQTDDPWGRQLLDSMILLIKEELHHFWQVREMMLARDIPYV

KITASNYARGLRREVRSHEPVMLIDKLICGAYIEARSCERFAALAPWLDDDLQKFYLSLLRSEARHYQDY

LDLAQKIAGEDISERVRQLGEAEAALILRPEAEFRFHSGVPVAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002886947.1\_4828 [gene=rraB] [locus\_tag=BN49\_RS26170] [protein=ribonuclease E inhibitor RraB] [protein\_id=WP\_002886947.1] [location=complement(5087100..5087522)] [gbkey=CDS]

MANPEHLEEQREETRLIIEELLEDGSDPDALYTIEHHLSADDFETLEKVAVEAFKLGYEVTEPEELEVEE

GDMVICCDILSECALNADLIDAQVEQLMTLAEKYDVEYDGWGTYYEDPNGEDGDDDDEEYVDEDDDGVRH

>lcl|NZ\_FO834906.1\_prot\_WP\_046043943.1\_4829 [gene=argF] [locus\_tag=BN49\_RS26175] [protein=ornithine carbamoyltransferase] [protein\_id=WP\_046043943.1] [location=5087686..5088690] [gbkey=CDS]

MSAFYQKHFLKLLDFTPAEITALLELAAKLKADKKNGIEVQKLAGKNIALIFEKDSTRTRCSFEVAAYDQ

GARVTYLGPSGSQIGHKESIKDTARVLGRMYDGIQYRGHGQEVVETLAQYAGVPVWNGLTNEFHPTQLLA

DLLTMKEHLPGKAFNQMTLVYAGDARNNMGNSMLEAAALTGLDLRLVAPSACWPEAALVETCTALAKQQG

GNITLTEDIAAGVKGADFIYTDVWVSMGEAKEKWAERIALLRDYQVNSAMLALTGNPQVKFLHCLPAFHD

DQTTLGKQMAADYGLHGGMEVTDEVFESAASVVFDQAENRMHTIKTVMVATLSK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529390.1\_4830 [locus\_tag=BN49\_RS26180] [protein=YhcH/YjgK/YiaL family protein] [protein\_id=WP\_016529390.1] [location=complement(5088752..5089204)] [gbkey=CDS]

MIIGNIHHLQPWLPAALREAIEHVIAQVSEATPLGKHDIDGDNLFYLISEDTTEPQAARRAEYHARYLDI

QIVLRGSEGMTFSTLPPGEPQTDWLAEKDIAFLAEGQQEKTVILNEGDFVVFYPGEVHKPLCAVGAPAKV

RKAVVKMLMA

>lcl|NZ\_FO834906.1\_prot\_4831 [gene=pyrL] [locus\_tag=BN49\_RS29665] [protein=pyr operon leader peptide] [pseudo=true] [location=5089399..5089537] [gbkey=CDS]

MANCVRHSVLARLNADAGLPFFFPLLIGFPKPLI\*GAFFLPRRQEI

>lcl|NZ\_FO834906.1\_prot\_WP\_002886928.1\_4832 [gene=pyrB] [locus\_tag=BN49\_RS26185] [protein=aspartate carbamoyltransferase] [protein\_id=WP\_002886928.1] [location=5089540..5090475] [gbkey=CDS]

MANPLYQKHIISINDLSREDLELVLATAAKLKANPQPELLKHKVIASCFFEASTRTRLSFETSMHRLGAS

VVGFSDSANTSLGKKGETLADTISVISTYVDAIVMRHPQEGAARLATEFSGGVPVLNAGDGANQHPTQTL

LDLFTIQETQGRLENLNVAMVGDLKYGRTVHSLTQALAKFNGNRFYFIAPDALAMPQYILDMLDEKGIAW

SLHSAIDDVMAEVDILYMTRVQKERLDPSEYANVKAQFVLRAADLEGARANMKVLHPLPRIDEITTDVDK

TPHAWYFQQAGNGIFARQALLALVLNSELAL

>lcl|NZ\_FO834906.1\_prot\_WP\_002886927.1\_4833 [gene=pyrI] [locus\_tag=BN49\_RS26190] [protein=aspartate carbamoyltransferase regulatory subunit] [protein\_id=WP\_002886927.1] [location=5090489..5090950] [gbkey=CDS]

MTHDNKLQVEAIKRGTVIDHIPAQVGFKLLTLFKLTETDQRITIGLNLPSGEMGRKDLIKIENTFLTDEQ

VNQLSLYAPQATVNRIDDYEVVGKSRPSLPDRIDSVLVCPNSNCISHAEPVSSSFAVKKRADDIALKCKY

CEKEFSHYVVLAN

>lcl|NZ\_FO834906.1\_prot\_WP\_002886926.1\_4834 [gene=ridA] [locus\_tag=BN49\_RS26195] [protein=2-iminobutanoate/2-iminopropanoate deaminase] [protein\_id=WP\_002886926.1] [location=5091103..5091489] [gbkey=CDS]

MSKTIATENAPAAIGPYVQGVDLGSMIITSGQIPVDPKTGSVPEDVSAQARQSLNNVKAIVEAAGLTVGD

IVKTTVFVKDLNDFATVNATYEAFFTEHNATFPARSCVEVARLPKDVKIEIEAIAVRR

>lcl|NZ\_FO834906.1\_prot\_WP\_009309303.1\_4835 [gene=mgtA] [locus\_tag=BN49\_RS26200] [protein=magnesium-translocating P-type ATPase] [protein\_id=WP\_009309303.1] [location=complement(5091562..5094270)] [gbkey=CDS]

MLKNYTRQLFAQLSRHLPRRLVQRDPLPDARHLASGPIPESLGQHCLNVAAMDDQEIWRAFDSHPEGLNE

GEVAAKILKHGDNQIPAQKPSPWWVHLWTCYRNPFNLLLTVLGIVSYSTEDLFAAGVIALMVGISTLLNF

IQEARSTKAADALKAMVSNTATVLRVVNEQGESRWLELPIDQLVPGDIIRLSAGDMIPADLRILQARDLF

VAQASLTGESLPVEKVARSRDPLQQNPLECDTLCFMGTNVVSGSAQAIVFATGGRTWFGQLAGRVSEQES

EPNAFQKGISRVSMLLIRFMLVMAPVVLLINGYTKGDWWEAALFALSVAVGLTPEMLPMIVTSTLARGAV

KLSKQKVIVKHLDAIQNFGAMDILCTDKTGTLTQDKIVLENHTDVSGKVCERVLHAAWLNSHYQTGLKNL

LDTAVLDGVELDAARGLAERWQKVDEIPFDFERRRMSVVVKEDDAAHQLICKGALQEILNVSTQVRYNGD

IVPLDDTMLRRIRRVTDTLNRQGLRVVAVATKYLPAREGDYQRADESDLILEGYIAFLDPPKETTAPALK

ALKASGITVKILTGDSELVAAKVCHEVGLDAGEVVIGSQIEAMSDDELAALAKRTTLFARLAPLHKERIV

TLLKREGHVVGFMGDGINDAPALRAADIGISVDGAVDIAREAADIILLEKSLMVLEEGVIEGRRTFANML

KYIKMTASSNFGNVFSVLVASAFLPFLPMLPLHLLIQNLLYDVSQVAIPFDNVDDEQIRKPQRWNPADLG

RFMVFFGPISSIFDILTFGLMWWVFHANTVEMQTLFQSGWFIEGLLSQTLIVHMIRTRRIPFVQSRAAWP

LFAMTLVVMAVGIALPFSPLASYLQLQALPLSYFPWLVAILAGYMVLTQAVKGFYSRRYGWQ

>lcl|NZ\_FO834906.1\_prot\_WP\_219340445.1\_4836 [gene=mgtL] [locus\_tag=BN49\_RS31555] [protein=mgtA regulatory leader peptide MgtL] [protein\_id=WP\_219340445.1] [location=complement(5094416..5094469)] [gbkey=CDS]

MDPDPTPHPRWSNLSFR

>lcl|NZ\_FO834906.1\_prot\_WP\_004192384.1\_4837 [gene=treR] [locus\_tag=BN49\_RS26205] [protein=trehalose operon repressor TreR] [protein\_id=WP\_004192384.1] [location=5094650..5095597] [gbkey=CDS]

MQNRLTIKDIARLSGVGKSTVSRVLNNESGVSERTRERVEAVMQQHGFSPSRSARAMRGQSDKVVAIIVT

RLDSLSENLAVQTMLPAFYEQGYDPIMMESQFSPALVEEHLGMLARRNIDGVVLFGFTGIDEAMLAPWRD

TLVLMARDAPGFASVCYDDEGAITLLMQRLYDRGHRHISFLGVPHSDVTTGERRHLAYLAFCKKHRLTPT

AALPGLGMKQGYDTVASVLTAETSALVCATDTLALGASKYLQQQGRDALQLASVGSTPLMKFLHPEILTV

DPGYAESGRRAARQLIEQIAGSVDPRQIVIPAALN

>lcl|NZ\_FO834906.1\_prot\_WP\_004186710.1\_4838 [gene=treB] [locus\_tag=BN49\_RS26210] [protein=PTS trehalose transporter subunit IIBC] [protein\_id=WP\_004186710.1] [location=5095728..5097146] [gbkey=CDS]

MSKVNQQDIDKLIELVGGRGNIATVSHCITRLRFVLNDPAIARPKEIEQLRMVKGCFTNAGQFQVVIGTE

VGDYYKALLATTGQTSADKEQVKQAARQNMKWHEQLISHFAEIFFPLLPALISGGLILGFRNVIGDLPMS

NGQTLAQMHPSLKTIYDFLWLIGEAIFFYLPVGICWSAVKKMGGTPILGIVLGVTLVSPQLMNAYLLGQQ

VPEVWNFGLFTIAKVGYQAQVIPALLAGLALGFIETRLKRIVPDYLYLVIVPVCSLILAVFLAHAIIGPF

GRLIGDGVAFAVRHLLTGSFAPIGAALFGFLYAPLVITGVHQTTLAIDMQMIQSMGGTPVWPLIALSNIA

QASAVVGIIIASRKQNEREISVPAAISAYLGVTEPAMYGINLKYRFPMLCAMIGSGLAGLLCGLNGVLAN

GIGVGGLPGILSIQPTYWQVYAMAMAIAVVVPIILTSVVYQRKYRQGTLQIV

>lcl|NZ\_FO834906.1\_prot\_WP\_004210626.1\_4839 [gene=treC] [locus\_tag=BN49\_RS26215] [protein=alpha,alpha-phosphotrehalase] [protein\_id=WP\_004210626.1] [location=5097198..5098853] [gbkey=CDS]

MNHLPHWWQNGVIYQIYPKSFQDTTGSGTGDLRGVTARLDYLQKLGVDAIWLTPFYVSPQVDNGYDVANY

TAIDPSYGTMADFDALVTEAKARGIRIVLDMVLNHTSTEHEWFRQSLNKESPYRQFYIWRDGEPDALPNN

WRSKFGGNAWQWHADSGQYYLHLFAIEQADLNWENPAVRAELKKVCEFWADRGVDGLRLDVVNLISKDQT

FPCDLDGDGRRFYTDGPRVHEFLQEMSRDVFTPRNLMTVGEMSSTSLEHCQQYAALDGRELSMTFNFHHL

KVDYPGGEKWTLARPDYVALKALFRHWQQGMHNRAWNALFWCNHDQPRIVSRFGDEGEYRVTAAKMLAMV

LHGMQGTPYIYQGEEIGMTNPHFSSISDYRDVESHNMFIERAAQGQSPDELLAILASKSRDNSRTPMPWH

AGENGGFSDGEPWIGLGDNYQEINVEAALADPDSVFYAYQQLITLRKTLPLLTWGDYEDLLPEHPSLWCY

RRQWQGQTLVVAANLSRELQAWQPAEAPGEWKMIISNYAETTPRPTGLTLRPFEAIWWLQG

>lcl|NZ\_FO834906.1\_prot\_WP\_004146783.1\_4840 [gene=celB] [locus\_tag=BN49\_RS26220] [protein=PTS cellobiose transporter subunit IIC] [protein\_id=WP\_004146783.1] [location=complement(5098909..5100261)] [gbkey=CDS]

MSNTSWIERYVMPAALRIAGQKHVLSVRDGIILNMPFMLIGSFFLIFAYLPIPGYADMMSSLFGEVWRDK

MLYPVKATYDIMALISSFGIAYRLAEKYRTLDPLSAGAMSLVAFMMTIPQNTLFTPVHGAAEVIKGVIPV

SMVGSQGLFVAIVISLLSTEIYRLVASRNLVIRMPDGVPPAVAKSFLALIPGFCVLAVVLALRLAVEASP

FGDINSMIATLIGIPMHHVGGTLPGMIISVILIGILWTLGLHGDAIVLVFIQPVWLSNMSENLTAFQNGQ

PIPHIITQQFYDLWIAPGGTGALLGLVIFMLLRSRSQQMKQLGKIAAPGALFNISEPMVFGIPLVMNPYF

FLPFILTPVLLVIVSYTAMATGLVAPPAGIALPFTTPIFISGYLATGGHISGTVLQVVNLAISLVVYYPF

FRAWDRLKAKEEHASAQPQASAAIADADRA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529386.1\_4841 [locus\_tag=BN49\_RS26225] [protein=6-phospho-beta-glucosidase] [protein\_id=WP\_016529386.1] [location=complement(5100288..5101595)] [gbkey=CDS]

MQALKIAVIGGGSSYTPELIEGIIVRYEQLPVTELALVDVESGREKVEIIAALTRRMLKHKGLEQVAVSV

HFTLDEAIRGASFVLTQLRVGQLAARAADERLGLKYHLLGQETTGVGGFAKALRTIPVILEVARKVEQLA

PEAFILNFTNPAGIVTEAVSRYSKAKIIGLCNVPINMQHMIVGMLGAQESEVKLRFAGLNHMVWVHKVLQ

GREDVTGKVIDMLCDGKALSMNNIKELPWPAEFLRALKAIPCPYHRYFWLTPAMLAEEIAAAKTKGTRAE

QVMKVEQELFALYTDPQLEEKPEQLSFRGGAYYSEVAVELINAIYNNLGAEMVVNTRNNGAIHGLDDDAV

VETNSIIDAQGARPLAFGPLPPAMNGLTQQVKAFERLTIEAAVHGCRESALLALVTNPLVGNVTDAQALL

DEVLTINRQWLTQFN

>lcl|NZ\_FO834906.1\_prot\_WP\_012737232.1\_4842 [locus\_tag=BN49\_RS26230] [protein=PTS sugar transporter subunit IIB] [protein\_id=WP\_012737232.1] [location=complement(5101686..5101994)] [gbkey=CDS]

MPRIVLCCAAGMSTSMLVNKMKAEAQQRALALEIYAVAVAEFERELPNADVILLGPQVKYEAGRLTALAA

PQGKAVAVIDMADYGMMRGAAVLDKALALLEH

>lcl|NZ\_FO834906.1\_prot\_WP\_002886906.1\_4843 [locus\_tag=BN49\_RS31220] [protein=hypothetical protein] [protein\_id=WP\_002886906.1] [location=5102079..5102252] [gbkey=CDS]

MKIIFTDVIEAQFLRIFIARVSPFTALTIGNMRRECYKERQSIIEKYFQMRVLPKGT

>lcl|NZ\_FO834906.1\_prot\_WP\_002886905.1\_4844 [locus\_tag=BN49\_RS26240] [protein=MurR/RpiR family transcriptional regulator] [protein\_id=WP\_002886905.1] [location=5102255..5102998] [gbkey=CDS]

MDIVGQLQEGMRRFSAQESRVATFILQNLSFTASASIDELAASAGVSPATITRFARSVGCDDIRDLRKQL

AQASERRASWLTPDSAALPVAWRDKLSSLGVTLTRQLGHTAEAAVEKCKSRLLSARAVHCFALGAQDVTL

AALLQHQLLPSGIAINLCQDAALMRLTASTLNDDHLLLVLATAEANPVLQSATLQARTQGVTIIALTPEQ

HALGDMASAILPLPADPQQARYALLLLVDLLNDTLIA

>lcl|NZ\_FO834906.1\_prot\_WP\_046043947.1\_4845 [gene=nrdD] [locus\_tag=BN49\_RS26250] [protein=anaerobic ribonucleoside-triphosphate reductase] [protein\_id=WP\_046043947.1] [location=5103355..5105493] [gbkey=CDS]

MTPHVMKRDGCKVPFNSERIQEAILRAAKAAGVDDADYCATVAEVVSQQMQGRAQVDINEIQTAVENQLM

SGPYKQLARAYIEYRHDRDSQREKRGRLNQEIRGLVEQTNSALLNENANKDSKVIPTQRDLLAGIVAKHY

ARQHLLPHDVVMAHERGMIHYHDLDYSPFFPMFNCMLIDLKGMLTQGFKMGNAEIEPPKSISTATAVTAQ

IIAQVASHIYGGTTINRIDEVLAPFVSESFKKHRKIAEEWQIPDAEGYARARTEKECYDAFQSLEYEVNT

LHTANGQTPFVTFGFGLGTSWESRLIQQSILRNRIAGLGKNRKTAVFPKLVFAIRDGLNHKFGDPNYDIK

QLALECASKRMYPDILNYDQVVKVTGSFKTPMGCRSFLGVWENENGEQVHDGRNNLGVISLNLPRIALEA

KGDEAAFWTLLDERLQLARKALITRIARLEGVKARVAPILYMEGACGVRLKADDDVSEIFKNGRASISLG

YIGIHETINALYGNQHMYDSEALREKGVAIVQRLRDAVDLWKEETGYGFSLYSTPSENLCDRFCRLDTAE

FGVVEGVTDKGYYTNSFHLDVEKKVNPYDKIDFEAPYPPLANGGFICYGEYPNIQHNLKALEDVWDYSYQ

HVPYYGTNTPIDECYECGFTGEFECTSKGFTCPKCGNHDAARVSVTRRVCGYLGSPDARPFNAGKQEEVK

RRVKHLGNGQIG

>lcl|NZ\_FO834906.1\_prot\_WP\_004178375.1\_4846 [gene=nrdG] [locus\_tag=BN49\_RS26255] [protein=anaerobic ribonucleoside-triphosphate reductase-activating protein] [protein\_id=WP\_004178375.1] [location=5105822..5106286] [gbkey=CDS]

MNYHQYYPVDIVNGPGTRCTLFVSGCVHECPGCYNKSTWRVNSGMPFTAEMADRIIADLNDTRIKRQGLS

LSGGDPLHPQNVADILKLVQRVRAECPGKDIWVWTGYKLDELNEAQMQVVNLINVLVDGKFVQDLKDPAL

IWRGSSNQVVHHLR

>lcl|NZ\_FO834906.1\_prot\_WP\_002886902.1\_4847 [locus\_tag=BN49\_RS26260] [protein=type II toxin-antitoxin system RelE/ParE family toxin] [protein\_id=WP\_002886902.1] [location=complement(5106290..5106574)] [gbkey=CDS]

MTYELEFDPRAWREWQKPGETVKKQFKNKLQQIVQNPRIESARLSDLPDCYKIKLKASGYRLVYQVRDSV

VVVYVIAIGKREKAAVYHQANKRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002886901.1\_4848 [locus\_tag=BN49\_RS26265] [protein=type II toxin-antitoxin system RelB/DinJ family antitoxin] [protein\_id=WP\_002886901.1] [location=complement(5106564..5106806)] [gbkey=CDS]

MATLNVRLDDKLKKEAYAVLEKLDMTPTEAVRLLFQYIAENGRMPVKSMTISDGEAALLRTVRERLENPR

PGVKVSLDDL

>lcl|NZ\_FO834906.1\_prot\_WP\_004152270.1\_4849 [locus\_tag=BN49\_RS26270] [protein=BglG family transcription antiterminator] [protein\_id=WP\_004152270.1] [location=complement(5106884..5108794)] [gbkey=CDS]

MRFPNQRLAQLFTLLRNETLPQDELAQRLSVSTRTVRADITALNTLLAQYGAQFILNRGSGYQLKIDNPT

SFQALEETAPKAQHVPRTAQDRITFLLVRFLTSAFSIKLEDLADEWFVSRATLQNDMVEVRERFQRYQLT

LETRPRHGMKLFGSEVSIRACLTDLLWELTQQGDIAPPIGAEAFAAEVPALLEPVLQETLTRHHIRLTDA

GERFVCLYGAVVVRRVSEGYPLADFSAEDVAQNVRDAARELTGELQRLAGKPLSPAEEEWLCVHIAARQV

QDVDPETISADDDEALVNYILRYINSQYNYNLLDDAQLHADLLTHIKTMITRVRYQIMIPNPLLDNIKQH

YPMAWDMTLAAVSSWGKYTPYTISENEIGFLVLHIGVGLERHYNIGYQRQPQVLLVCDTSNAMVRMIEAI

LQRKYPQLEIAATISQREYEQRDAIEADFVISTVRIGEKDKPVVTIAPFPTDYQLDQIGKLVLVDRTRPW

MLNKYFDAAHFRVVDKPMDQQTLFAELCQQLLEEGFVDAEFHASVVEREAIVSTMLGDGIALPHSLGLLA

KKTVVYTVIAPQGIAWGDETAHLIFLLAISKREYEEAMAIYDIFVTFLRERAMSRLAATRSFDEFKTVAM

ECVSRF

>lcl|NZ\_FO834906.1\_prot\_WP\_004178372.1\_4850 [locus\_tag=BN49\_RS26275] [protein=lactonase family protein] [protein\_id=WP\_004178372.1] [location=complement(5108817..5109971)] [gbkey=CDS]

MPVARHLLVASLSLFAAAAGAAQTHYAWVGTYNPNGEGLYRFTVDAKTGALRDKTLVSSLPNVAQLTVSR

DGKTLYAASEVEKGVVQAWRIEKNGELTALNQVASGGAGPVYLSLTPDGKHLLVANYVSGSIAVLPVQED

GSLAEAVDRHQDEGPAGAERPAAAVEGSFAISDHNGPHAHMIAADPSGKYVYSTDLGLDRIYQYRLDSAS

GKLTPNDPPFIAASSPGAGPRHFVFTPQGDGLWLINEEASTLTFYHLDKQSGLLREGKTVSALPEGYKGT

SFAAGLVLSNDGKQLYVANRLHNSIAHFTVLADGSLSHQEDIWTRGDYPRTLTLDNQGQWLYVMNQRSDN

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>lcl|NZ\_FO834906.1\_prot\_WP\_002886899.1\_4851 [locus\_tag=BN49\_RS26280] [protein=KDGP aldolase family protein] [protein\_id=WP\_002886899.1] [location=complement(5110038..5110778)] [gbkey=CDS]

MKLTPNFYRDRVCLNVLAGSKDNAREIYDAAEGHVLVGVLSKNYPDVASAVADMRDYAKLIDNALSVGLG

AGDPNQSAMVSEISRQVQPQHVNQVFTGVATSRALLGQNETVVNGLVSPTGTPGMVKISTGPLSSGAADG

IVPLETAIALLKDMGGSSIKYFPMGGLKHRAEFEAVAKACAAHDFWLEPTGGIDLENYSEILKIALDAGV

SKIIPHIYSSIIDKASGNTRPADVRQLLEMTKQLVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016531236.1\_4852 [locus\_tag=BN49\_RS26285] [protein=DgaE family pyridoxal phosphate-dependent ammonia lyase] [protein\_id=WP\_016531236.1] [location=complement(5110775..5111893)] [gbkey=CDS]

MPSIFEKYHLKQVINTSGRMTALGVSTPRPEVVEAAMAGMNQYFEMKDLVNKTGEYIAKLLDVEGATVVS

CASAGIAQSVAAVLVKDSDWLLENLHVTPIENNEIVLPKGHNVNFGAPVGTMVALGGGKLVEAGYANECS

AQQLAAAITPRTAAILYIKSHHCVQKSMLNVAQAAEVARQHNLPLIVDAAAEEDLQCYYRMGADLVIYSG

AKAIEGPTSGLVIGKTQYVEWVKRQSMGIGRAMKVGKEGILGLTCAIEHYLTASKESGEQMVAKMTPFIE

QLNALNGVTARVVWDSAGRDIARAEIKFDEVTTGVKTGDLVNALKQGEYAIYFRGYKANEGIIEADVRSV

NAEQLAVVARRIAEVLNKEKQA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531235.1\_4853 [locus\_tag=BN49\_RS26290] [protein=amidohydrolase/deacetylase family metallohydrolase] [protein\_id=WP\_016531235.1] [location=complement(5111877..5113010)] [gbkey=CDS]

MFDLLLRRARLVDDTLTDIAIQDGKIAALGEISAPSRKTIELNGKVYVSAGWIDSHVHCYPNSPIYHDEP

DSVGIATGVTTVIDAGSTGADDVDDFYQLTRKAATEVYALLNISRVGLIAQNELANMANIDAAAVKQAVQ

RHPDFIVGLKARMSSSVVGENGITPLARAKAIQQENDDLPLMVHIGNNPPNLDEIADLLSSGDIITHCYN

GKPNRILNPAGELRSSITRALQRGVRLDVGHGTASFSFEVARRAIALGILPHIISSDIYCRNRIDGPVRS

LALVMSKFLAIGMTLPQVIDCVTVSAAEGLRLSRKGRLEVGFDADLTLFRLEHRPTLLVDAEKESLQADN

ILVPLAAIRAGKGYLTEQGSAEHAFDF

>lcl|NZ\_FO834906.1\_prot\_WP\_004152267.1\_4854 [locus\_tag=BN49\_RS26295] [protein=DUF4310 family protein] [protein\_id=WP\_004152267.1] [location=complement(5113116..5113760)] [gbkey=CDS]

MEQNKGFWYADWSFPIFVGLLSSGVFAGTHMYYLYGIGAFNEVAFVAMLKSGIDTGVYGAVAAFGASFLF

ARIIEGSLVGILDIGGAIQTGIGLGVPALLLGAGFVFPVANFAASLVTGLVLGLAVGYIIILARKFTINQ

SDSTYGADVMMGAGNASGRFLGPLIILSAMTASIPIGIGSLVGALLFYIWQKPITGGAILGAMILGSIFP

VAIS

>lcl|NZ\_FO834906.1\_prot\_WP\_002886897.1\_4855 [locus\_tag=BN49\_RS26300] [protein=DUF4311 domain-containing protein] [protein\_id=WP\_002886897.1] [location=complement(5113774..5114550)] [gbkey=CDS]

MFLIILIKSLIIGGLVGVGVGAGAARMFHAPTTQGMGAFRTLGELNSCEGDPASHFSFGLGFFFNAWASS

VAAGSFTQDVDHRIIPNWGAAALMLKNRNVGETLHDPKKMAISCGIIGMIVVAFLNLTASSVPEALQVTA

VKVLVPAANLLVNTVMPVIFWLAAIDAGKKSGFWATIFGGAAQLIMGNAVPGLVLGILIGKGVEESGWNR

VTKVMMVAIVALFVLSGFFRGFDMKMIESFHLTVPNWLDMIHNSLSGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002886896.1\_4856 [locus\_tag=BN49\_RS26305] [protein=DUF4312 family protein] [protein\_id=WP\_002886896.1] [location=complement(5114572..5114871)] [gbkey=CDS]

MKEQFTTTVRVAGKGESKSRAFADALNHVQAAVMKSSSRILLRIEPQDVTVVHAREAVRKEAFLFFFLRR

ERRTYSVELDVTVNVTAIDLDKVDFVTQT

>lcl|NZ\_FO834906.1\_prot\_WP\_002886895.1\_4857 [locus\_tag=BN49\_RS26310] [protein=hypothetical protein] [protein\_id=WP\_002886895.1] [location=complement(5114874..5115236)] [gbkey=CDS]

MEQITVVIGDRLGKGQKVAAGAEKAGARAVVVPGVAADMKLGDIMKAENATFGISFCGSGGAGAITAQTK

YGYKAKYGMRSIDEGVTAINEGCNVLGFGFMDKEELGERLVEAWKKKYGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002886894.1\_4858 [locus\_tag=BN49\_RS26315] [protein=PRD domain-containing protein] [protein\_id=WP\_002886894.1] [location=complement(5115247..5115585)] [gbkey=CDS]

MNNGAVINDVGEQAAQTERLADKMLQQVFALLSRHDIVPNDVQEQMLTSHVRAMAHRSISGEPLPEVDAS

LFEEISEDSMMLAREVVAQFGNLPDEEAWLLSVHFEVAKDNL

>lcl|NZ\_FO834906.1\_prot\_WP\_002886893.1\_4859 [gene=cybC] [locus\_tag=BN49\_RS26320] [protein=cytochrome b562] [protein\_id=WP\_002886893.1] [location=complement(5115875..5116261)] [gbkey=CDS]

MRKKLLAMLAVSAFALGSASAFADLGEDMDTLAENLQVVQKTSDAGELKAALNKMRTAAVDAQKETPPKL

EGKAADSAEMKDYRHGLDILIGQIDGALKLANEGKVKEAQAAAEEFKTTRNTYHKKYR

>lcl|NZ\_FO834906.1\_prot\_WP\_004152265.1\_4860 [gene=pmbA] [locus\_tag=BN49\_RS26325] [protein=metalloprotease PmbA] [protein\_id=WP\_004152265.1] [location=complement(5116298..5117650)] [gbkey=CDS]

MALAMKVISQVAQQRKTLEEAVTTALELAAGKSDGAEVSVSKTTGIGVSTRYGEVENVEFNSDGALGITV

YHQNRKGSASSTDLSPDAIARTVQAALDIARYTSPDPFAGVADKDLLAFDAPDLDLFHPAEVSPDDAIEL

AARAEQAALKADKRITNTEGGSFNSHYGIKVFGNSHGMLQSYCSTRHSLSSCVIAEDDGDMERDYAYTIG

RAIEDLQSPEWVGEECARRTLSRLAPRKLSTMKAPVIFANEVATGLFGHLVGAIAGGAVYRKSTFLLDSL

GKQILPEWLTIEEHPHLLKGLASTPFDSEGVRTERRDIVKDGVLTQWLLTNYSARKLGMKSTGHAGGIHN

WRINGRGLSFAKMLKEMGTGLVVTELMGQGVSGVTGDYSRGASGFWVENGEIQYPVSEITIAGNLKEMWR

NIVTIGDDIETRSNIQCGSVLLPEMKIAGQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004177664.1\_4861 [locus\_tag=BN49\_RS26330] [protein=ribosome-associated protein] [protein\_id=WP\_004177664.1] [location=5117746..5118297] [gbkey=CDS]

MTKQPEDWLDDVPGDDVEDEDDEIIWVSKSEIKRDAEELKRLGAELVDLGKNALDKIPLDTDLRDAIELA

QRIKKEGRRRQLQLIGKMLRNRDVDPIRQALDKLKNRHNQQVALFHKLEQIRDRLIDDGDDAVAEVLNLW

PDADRQQLRSLIRNAKKEKEGNKPPKSARLIFQYLRELAENEG

>lcl|NZ\_FO834906.1\_prot\_WP\_014342865.1\_4862 [locus\_tag=BN49\_RS31225] [protein=hypothetical protein] [protein\_id=WP\_014342865.1] [location=complement(5118627..5118743)] [gbkey=CDS]

MFLALTIQLDKSGYKQTYRRVDEGIQAMRRESPCWRKP

>lcl|NZ\_FO834906.1\_prot\_WP\_016531712.1\_4863 [locus\_tag=BN49\_RS26340] [protein=aldose 1-epimerase family protein] [protein\_id=WP\_016531712.1] [location=5118928..5120142] [gbkey=CDS]

MKKTLVLTTIALLVSGSAVAKTWVLTNAEEGMDKGNWQINSDQLKVKDHAFSIEQKVLHGGKQEGSKILT

IHSKDGLTITLSPTRGMNLLHIEGFGSRMGWDSPVKEVVNPAFINLESRNGLGWLEGFNEMMVRCGYEWT

GHPVTADGQIYTLHGKAGNTPASLVEVEVEVADSAPYEIRIRGLVKESTFKKADLQTLTELRYVPGSNSF

SLHDVLTNHADYPHDYQIIYHSNFGTPILEEGARFLAPMSSISPFNDYAKSGLKTWQTYQGPTKDFDEMV

FNIQPLADENHQTLAAVVNKAGDKGASIQFDTRQLPVLTLWKNTDTVKQGYVTGIEPGTSYAYPVTIERE

QKRVKQLQPGASAQFDLTYTLLHDSAQVAAVEQKIAKIQGDNKVAENETPIAKE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043951.1\_4864 [locus\_tag=BN49\_RS26345] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_046043951.1] [location=complement(5120186..5120713)] [gbkey=CDS]

MLTCESVRSTDSPHFAMLDALYARAFPWHEQRESEAKRQALSHPRYALEAWFDEGVFVGLSGCWQFAGYG

YIEHLAIDDTLRSRGYGKQLLAQILTRAPLTILEIDPLTTAIAHKRLRFYQSVGFHANPWAHHHPSYHQG

IADHELLVLSYPQPIDERQYQQFARDLGHEVMGRE

>lcl|NZ\_FO834906.1\_prot\_WP\_002886886.1\_4865 [gene=mpl] [locus\_tag=BN49\_RS26350] [protein=UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase] [protein\_id=WP\_002886886.1] [location=complement(5120782..5122155)] [gbkey=CDS]

MRIHILGICGTFMGGLAMLARSLGHEVTGSDANVYPPMSTLLENQGIDLIQGYDPSQLEPRPDLVIIGNA

MTRGNPCVEAVLENNIPYMSGPQWLHDFVLRDRWVLAVAGTHGKTTTAGMATWILEACGYKPGFVIGGVP

GNFDVSARLGDSPFFVIEADEYDCAFFDKRSKFVHYCPRTLILNNLEFDHADIFDDLKAIQKQFHHLVRI

VPGKGKIILPENDINLKQVMAMGCWSEQELVGEQGHWQAKKLNADASQWEVLLDGEKVGEVKWALVGEHN

MHNGLMAIAAARHVGVLPADAANALGSFINARRRLELRGEANGVTVYDDFAHHPTAILATLQALRGKVGG

TARILAVLEPRSNTMKMGVCKDDLAPSLGRADEVFLLQPQHIPWQVAEVAEACVQPAHWSADVDTLAEMV

VKTAHPGDHILVMSNGGFGGIHQKLLDKLAQKAAAAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002886827.1\_4866 [gene=fbp] [locus\_tag=BN49\_RS26355] [protein=class 1 fructose-bisphosphatase] [protein\_id=WP\_002886827.1] [location=5122331..5123329] [gbkey=CDS]

MKTLGEFIVEKQHEFSHATGELTALLSAIKLGAKIIHRDINKAGLVDILGASGAENVQGEVQQKLDLFAN

EKLKAALRARDIVAGIASEEEDEIVVFEGCEHAKYVVLMDPLDGSSNIDVNVSVGTIFSIYRRVTPVGTP

VTEEDFLQPGNKQVAAGYVVYGSSTMLVYTTGCGVHAFTYDPSLGVFCLCQERMRFPEKGNTYSINEGNY

IKFPQGVKKYIKYCQEEDKATQRPYTSRYIGSLVADFHRNLLKGGIYLYPSTASHPEGKLRLLYECNPMA

FLAEQAGGKASDGKERILDIIPESLHQRRSFFVGNNHMVEDVENFIKAFPDA

>lcl|NZ\_FO834906.1\_prot\_WP\_021312675.1\_4867 [gene=yjfF] [locus\_tag=BN49\_RS26360] [protein=sugar ABC transporter permease YjfF] [protein\_id=WP\_021312675.1] [location=complement(5123372..5124370)] [gbkey=CDS]

MIKRNLPLMITLAVFVLGYLYCLTQFPGFASTRVICNILTDNAFLGIIAVGMTFVILSGGIDLSVGSVIA

FTGVFLAKAIGFWGISPLAAFPLVLVMGCAFGAFMGLLIDALKIPAFIITLAGMFFLRGVSYLVSEESIP

INHPVYDTLSGLAWTIPGGGRLSAMGLLMLLVVVAGIFVAHRTRFGNQVYAIGGNATSANLMGISTRSAT

IRIYMLSTGLATLAGIVFSIYTQAGYALAGVGVELDAIASVVIGGTLLSGGVGTVLGTLFGVAIQGLIQT

YINFDGTLSSWWTKIAIGILLFIFIALQRGLTVLWENRQNAAVTRVSGAGSR

>lcl|NZ\_FO834906.1\_prot\_WP\_016531029.1\_4868 [locus\_tag=BN49\_RS26365] [protein=ABC transporter permease] [protein\_id=WP\_016531029.1] [location=complement(5124357..5125382)] [gbkey=CDS]

MMPRSLSQTGPEKRRFTWPKGTPQIIALLLVLLVDSLVAPHFYQVVLQDGRLFGSPIDILNRAAPVALLA

IGMTLVIATGGIDLSVGAVMAIAGATAASMTVAGHSLPVVLLAALAAGALAGLWNGILVAVLKIQPFVAT

LILMVAGRGVAQLITAGQIVTFDSPALAWLGSGSFLLFPTPVIVAAATLLLFWLFTRKTAPGMFIEAVGI

NIRAAKNAGVNTRIVVMLAYVLSGVCAAIAGIIVAADIRGADANNAGLWLELDAILAVVIGGASLMGGRF

NLLLSVVGALIIQGMNTGILLSGFPPELNQVVKAVVVLCVLIVQSPRFIGLLKGVRGHDKT

>lcl|NZ\_FO834906.1\_prot\_WP\_002886772.1\_4869 [locus\_tag=BN49\_RS26370] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_002886772.1] [location=complement(5125393..5126895)] [gbkey=CDS]

MSAEAHQEILRTEGLSKFFPGVKALDNVNFSLRRGEIMALLGENGAGKSTLIKALTGVYHADRGTIWLEG

QAISPKNTAHAQQLGIGTVYQEVNLLPNMSVADNLFIGREPRRFGLLRRKEMEARATALMASYGFSLDVR

EPLNRFSVAMQQIVAICRAIDLSAKVLILDEPTASLDTQEVEMLFTLMRQLRDNGVSLIFVTHFLDQVYA

VSDRITVLRNGSFVGCRETRELPQIELVKMMLGRELDHNALQRAGRTLLSDKPVAAFEGYGKKGTIAPFD

LQVRPGEIVGLAGLLGSGRTETAEVIFGIKTADSGKAWIKGKPQTLRSPHQASCLGIGFCPEDRKTDGII

AAASVRENIVLALQAQRGWLRPIPRREQNEIAERFIRQLGIRTPSAEQPIEFLSGGNQQKVLLSRWLLTK

PQFLILDEPTRGIDVGAHAEIIRLIETLCADGLALLVISSELEELVGYADRVIILRDRRQVAEIPLAELS

VPAIMNAIAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002886769.1\_4870 [locus\_tag=BN49\_RS26380] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_002886769.1] [location=complement(5127019..5127975)] [gbkey=CDS]

MWKRLLLVTAVSAAMSSMAIAAPLTVGFSQVGSESGWRAAETSVAKEEAAKRGITLKIADGQQKQENQIK

AVRSFIAQGVDAIFIAPVVATGWEPVLKEAKEAKIPVFLLDRSIDVKDKDLYMTTVTANNVLEGQLIGDW

LVKTVDGKPCNVVELQGTVGASVAIDRKKGFADAIAKASNIKIIRSQSGDFTRSKGKEVMESFIKAENNG

KNICMVFAHNDDMAIGAIQAIKEAGLKPGKDILTGSIDGVPDIYKAMIAGEANASVELTPNMAGPAFDAL

EKYKKDGTLPEKLTITKSTLYLPDTAKEELEKKKNMGY

>lcl|NZ\_FO834906.1\_prot\_WP\_002886766.1\_4871 [gene=ppa] [locus\_tag=BN49\_RS26385] [protein=inorganic diphosphatase] [protein\_id=WP\_002886766.1] [location=5128379..5128909] [gbkey=CDS]

MSLLNVPAGKDLPEDIYVVIEIPANADPIKYEVDKESGALFVDRFMSTAMFYPCNYGYINHTLSLDGDPV

DVLVPTPYPLQPGSVIRCRPVGVLKMTDESGEDAKLVAVPHTKLSKEYDHINDVNDLPELLKAQITHFFE

HYKDLEKGKWVKVDGWDNAEAAKAEIVASFERAKQK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043953.1\_4872 [locus\_tag=BN49\_RS26390] [protein=hypothetical protein] [protein\_id=WP\_046043953.1] [location=5128984..5130171] [gbkey=CDS]

MKSVRYFTLNFSGFTTAACEKQGYLRLIAGDHVFYTDKRYFNDPSLFDRLTINQPLHLGVRRLDNGSYWI

HWLSDGETLLEPSQRVKRWARPLLFISLLTLIVALIPLVMSTSEWGRFGFGIIAILAFIALLTGLCELLF

HRALKMHPAMRDLLAKMAQARRRDFSFCQPLPTTAQTLRQSAKPFTQALPERYAVRTGKISNIIFKKWFA

GNPTREYHGVGIQCDTAPLAFFWQNGFANFGLHPFFYRRQPPFLAIGDRIVVVYQRKDNDVQALYNVSDG

CAFLKNHPCYPGDRQMSLVYNLFYGMVLVMYLLILGMSLNNPYKPARGFGWLIQDSLDMLSLLLLSFGGI

LAVLELIGPTAWLLSHRVADWMKMRSAMRHYLQGAARHTALEEIM

>lcl|NZ\_FO834906.1\_prot\_WP\_002886724.1\_4873 [locus\_tag=BN49\_RS26395] [protein=gamma-glutamylcyclotransferase] [protein\_id=WP\_002886724.1] [location=complement(5130316..5130660)] [gbkey=CDS]

MRIFVYGSLRRKQGNSHWMTNAQWLGAHSVDDYQLYSLGHYPGAVPGEGTVHGEVYRIDASTLAELDALR

TKGGEYARHLIQTPYGSAWMYVYQRSVEGCTLIANGNWLDRDQY

>lcl|NZ\_FO834906.1\_prot\_WP\_046043954.1\_4874 [gene=tamB] [locus\_tag=BN49\_RS26400] [protein=autotransporter assembly complex protein TamB] [protein\_id=WP\_046043954.1] [location=complement(5130663..5134439)] [gbkey=CDS]

MSLWKKISLGVLIVLVLLLGTVGFLVGTTTGLHLVFKAADRWVPGLDIGKVTGGWRDLTLDNVRYEQPGV

AVTAGQFHLSVRLRCLWDSSLCVNDIALRDIYVAVDTKKMPPSAPVEEEDSGPLNFSTPYPITLSRVALH

NVNVKIDDTAVSVRDFSTGLNWQEKNLTLTPTSLQGLLIALPKVAKVAQEQVVEPKIDNPQPQEKPLGET

MTDLFSQPVLPAMTDVHLPLNLNIQAFRGEQLRLTGDTDITVYNLLLKVSSIDGQMKLDALDIDSDQGKV

SASGSAQLQDNWPVDITLAGTLNVDPMKGEKVQLKVGGEVRKTLKVGVDLSGPVAATLRADAQLAEVGLP

LNMELKSKQLAWPFSGEKQFQADDVQLKFSGKMTDYALAFSTAVKGQSLPPAKIALNAKGNERQINLDKL

TVNALEGKTELKALLDWQQAISWRGELTLDGINTAKEVPDWPSKLNGRIKTQGSLYGGSWQMSVPELKIT

GNVKQNKVDVAGSLQGNSYLQWKIPGLHLALGPNSADIKGELGVKDLNLDATIDAPHLDNALPGLGGTAK

GLVKVRGTVDAPQLLADITARALRWQELTIAQVNVKGDVKSTDQIGGNLDVRVDRISQPGVNISLVQLNA

KGTEKQHELRLRVQGDPVSGQLALAGSFDRQAERWKGSLSDTRFQTPVGPVALTRSIALDYRNLEQKISI

GPHCWTNPNAELCVPETIDAGASGRARVNLNRFDLAMLKPFMPEATQASGVFTGNADVSWDTTKEGLPQG

KVTLSGRNVKVTQVVNDAPLPVAFDTLNLSADLHNNRAELGWLIRLTNNGQLDGQVQVTDPQGRRNLGGN

VNISNFSLAMINPIFARGEKAEGRLNARLRLGGNVKSPQLFGQMQLSGVDIDGNFMPFDMQPSQLAMNFN

GTRSTLQGTVNTRQGQIALSGNADWTQIDNWRAQIAAKGSRVRITVPPMVRLDVSPDVVFTATPSLFNLD

GKVDVPWARIVVNEVPESAVGVSSDEVMLDKNLKPIKQQSASIPINSNLTIHVGNNVRLEAFGLKARLTG

DLKVAQDKQGLGLNGQINIPDGRFHAYGQDLIVRKGELLFSGPPDQPLLNIEAIRNPDATEDDVIAGVRV

TGSADQPKAEIFSDPVMSQQEALSYLLRGQGLSSGQSDSAAMTSMLIGMGVAQSGQVVGKIGETFGVSNL

ALDTEGVGDSSQVVVSGYVLPGLQVKYGVGIFDSLATLTLRYRLMPKLYVEAVSGIDQALDLLYQFEF

>lcl|NZ\_FO834906.1\_prot\_WP\_002886722.1\_4875 [gene=tamA] [locus\_tag=BN49\_RS26405] [protein=autotransporter assembly complex protein TamA] [protein\_id=WP\_002886722.1] [location=complement(5134436..5136169)] [gbkey=CDS]

MLKIRQLCVTSLLLVSGVASAANVRLQVEGLSGELEKNVRAQLSTIQSDEVTPDRRFRARVDDAIREGLK

ALGYYEPTIEFDLRPPPKRGRQVLIAKVTPGEPVRIGGTEVILRGGARTDSDYLALLKTRPAIGTVLNHG

DYDGFKSSLTRVALRKGYFDSEFLKSQLGVSLDRHQAFWDIDYDSGERYRFGHVTFSGSQIRDEYLQNLV

PFKEGDYYTSQDLAELNRRLAATGWFSSVVVAPDFAKSRKTKVLPLQGVVSPRKENTVETGVGYSTDVGP

RVKATWKKPWVNSYGHSLTSSVSLSAPEQQFDFTYKVPLLKSPLEQYYLMQGGFKRTDLNDTQADSTTLG

VSRFWEMSSGWQRAINLRWSLDHFTQANVTNTTMLIYPGVSVNRTRSRGGLMPTWGDSQRYSVDYSNTMW

GSDINFIVMQAQDVWIRTLYDRHRFVVRGNLGWIEADNFDKVPPDLRFFAGGDRSIRGYKYKSISPKDDD

GKLIGASKLATGSLEYQYNVSGKWWGAVFVDSGEAVSDIRESDFKTGAGVGVRWQSPVGPIKLDIARPIG

DKEEHGLQFYIGLGPEL

>lcl|NZ\_FO834906.1\_prot\_WP\_002886721.1\_4876 [gene=msrA] [locus\_tag=BN49\_RS26410] [protein=peptide-methionine (S)-S-oxide reductase MsrA] [protein\_id=WP\_002886721.1] [location=5136378..5137016] [gbkey=CDS]

MSLFDKTHLVAQADALPGRNTPMPVATLHAVNGHSMTNVPAGMEVALFAMGCFWGVERLFWQLPGVYSTA

AGYTGGYTPNPTYREVCSGQTGHAEAVRVVYDPQVISYEQLLQVFWENHDPAQGMRQGNDHGTQYRSAIY

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QA

>lcl|NZ\_FO834906.1\_prot\_WP\_002886718.1\_4877 [locus\_tag=BN49\_RS26415] [protein=hemolysin family protein] [protein\_id=WP\_002886718.1] [location=5137197..5138534] [gbkey=CDS]

MLNSILVILCLIAVSAFFSISEISLAASRKIKLKLLADEGNVNAQRVLKMQENPGTFFTVVQIGLNAVAI

LGGIVGDAAFSPAFHSLLSGYLSPELSEQLSFIISFTLVTSLFILFADLTPKRIGMIAPETVALRIINPM

RFCLLVFRPLVWLFNGMANMIFRIFKLPMVRKDDITSDDIYAVVEAGALAGVLRKQEHELIENVFELESR

TVPSSMTPRESVIWFDLHEDEQSLKNKVAEHPHSKFLVCNEDIDHIIGYVDSKDLLNRVLANQSLVLTGG

VQIRNTLIVPDTLTLSEALESFKTAGEDFAVIMNEYALVVGIITLNDVMTTLMGDLVGQGLEEQIVARDE

NSWLIDGGTPIDDVMRVLDIDEFPQSGNYETIGGFMMFMLRKIPKRTDAVKFSGYKFEVVDIDNYRIDQL

LVTRIDNKPTVLVPKQAETAESQNA

>lcl|NZ\_FO834906.1\_prot\_4878 [locus\_tag=BN49\_RS29675] [protein=helix-turn-helix domain-containing protein] [pseudo=true] [partial=5'] [location=<5138604..5138735] [gbkey=CDS]

TLPLNKIALSVGYSDPVYFTRLFRKHNGIPPGEYRKRYAEMKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002886707.1\_4879 [locus\_tag=BN49\_RS26420] [protein=DUF1107 domain-containing protein] [protein\_id=WP\_002886707.1] [location=complement(5138797..5139003)] [gbkey=CDS]

MKIFQRYNPLQVAKYVKILFRGRLYIKDVGAFEFDKGKILIPKVKDKLHLSVMSEVNRQVLRLQTEMA

>lcl|NZ\_FO834906.1\_prot\_WP\_002886706.1\_4880 [locus\_tag=BN49\_RS26425] [protein=YtfJ family protein] [protein\_id=WP\_002886706.1] [location=5139327..5139884] [gbkey=CDS]

MTLRSILAASLLLLPLLATAHNFVDGQRVAPVGVADRGELILDKDKFSYKNWNSAQLAGKVRVVQHIAGR

SSAKEKNANLIEAIKAAGFPHDRYQTTTIVNTDDAIPGTGMFVRNSIESNKKLFPWSQFIVDSNGLVRKA

WQLDEKSSAIVVLDKNGRVQWAKDGALTQQEVQQVIDLLHKLLNK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177677.1\_4881 [gene=cysQ] [locus\_tag=BN49\_RS26430] [protein=3'(2'),5'-bisphosphate nucleotidase CysQ] [protein\_id=WP\_004177677.1] [location=complement(5139874..5140617)] [gbkey=CDS]

MLEQVCQLARNAGDAIMEVYDGNQPINVASKKDDSPVTAADIAAHKVIVSGLQALDPDTPILSEEDPPAW

EVRQHWQRYWLVDPLDGTKEFIKRNGEFTVNIALIENGKPTLGVVYAPVMKVMYSAQNGKAWKEECGVRK

QIQVRDARPPLVVISRSHSNDPELQEYLEQLGEHQTTSIGSSLKFCLVAEGQAQLYPRFGPTSTWDTAAG

HAVAVAAGAHVHDWQGKTLDYTPRESFLNPGFRVSIY

>lcl|NZ\_FO834906.1\_prot\_WP\_015959297.1\_4882 [gene=cpdB] [locus\_tag=BN49\_RS26435] [protein=2',3'-cyclic-nucleotide 2'-phosphodiesterase] [protein\_id=WP\_015959297.1] [location=5140809..5142752] [gbkey=CDS]

MIKFSATLLATLIAASVNAATVDLRIMETTDLHSNMMDFDYYKDAATEKFGLVRTASLIEQARAEVKNSV

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NIIDAKTGKPMFTPYLIQDTRVVDSDGQIHTLRIGYIGFVPPQIMTWDKANLNGKVTVNDITETARKYIP

EMRAKGADVVVVVAHSGLSADPYQAMAENSVYYLSQVPGVDAIMFGHAHAVFPGKDFANIKGADIAKGTL

NGVPAVMPGMWGDHLGVVDLVLNNDSGKWQVTQSKAEARPIYDAVAKKSLAAEDGKLVSVLKADHDATRE

FVSKPIGKSADNMYSYLALVQDDPTVQVVNMAQKAYVEHYIQGDPDLAKLPVLSAAAPFKVGGRKNDPAS

FVEVEKGQLTFRNAADLYLYPNTLVVMKVSGKEVKEWLECSAGQFNQIDPASSKPQSLINWDGFRTYNFD

VIDGVNYQIDVTQPARYDGECQMIHPQAERIKHLTFNGKPVDPQATFLVATNNYRAYGGKFAGTGESHIA

FASPDENRSVLAAWIGAQSKKEGAIHPAADNNWRLAPIHSNTPLDIRFETSPGDKAAAFIKEKAQYPMRQ

VATDDIGFAIYQLDLSK

>lcl|NZ\_FO834906.1\_prot\_WP\_004152015.1\_4883 [locus\_tag=BN49\_RS26440] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004152015.1] [location=complement(5142807..5143178)] [gbkey=CDS]

MAEPTLSEKLRTGNLFAEQCPSRDVLKHVTSRWGVLILVALREGTHRFSDLRRKMGGVSEKMLAQSLQAL

EQDGFIDRVSYPVVPPHVEYSLTPLGLQVSEKVAALADWIEVNLPSVLANHGE

>lcl|NZ\_FO834906.1\_prot\_WP\_020864851.1\_4884 [locus\_tag=BN49\_RS26445] [protein=SDR family oxidoreductase] [protein\_id=WP\_020864851.1] [location=5143268..5144116] [gbkey=CDS]

MIALTGATGQLGHYVLQDLLNTVPASQIVAIVRNPAKAQALSQQGVVVRQADYSDEAALTAALQGVDKLL

LISSSEVGQRAVQHRNVINAAKAAGVKFIAYTSLLHADTSPLGLAAEHIETEQMLADSGIAYALLRNGWY

TENYLASAPPALEHGVFIGAAGEGKIASATRADYATAAARVIASEGHEGKIYELAGDNAWTLSDLAAELS

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>lcl|NZ\_FO834906.1\_prot\_WP\_020864850.1\_4885 [locus\_tag=BN49\_RS26450] [protein=AraC family transcriptional regulator] [protein\_id=WP\_020864850.1] [location=5144194..5145018] [gbkey=CDS]

MQGVPPQFSDEKDRARFRHLEQLPGVELYHAHISRYAFEPHTHEAFGIGVIEQGAERFRYRGSQHIAAAN

AIVTMNPDELHTGEAETADGWRYRMIYLEPDRLEAITGVRDWWFSEVVREDPLRSRQIGQLIYGLWHSDD

PLAQQGLLLDLIDTFRPLAHHASAQGEAGHRFDRVRDYLHDNYMRAITLDELAQVAALSPYHFQRQFKAH

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>lcl|NZ\_FO834906.1\_prot\_WP\_020864849.1\_4886 [locus\_tag=BN49\_RS26455] [protein=DMT family transporter] [protein\_id=WP\_020864849.1] [location=5145095..5146066] [gbkey=CDS]

MISGVLYALLAGLMWGLIFVGPLLVPEYPAMLQSMGRYLALGLIALPLAWLGRARLRQLSRNDWWTAVGL

TMMGNLIYYVCLASAIQRTGAPVSTMIIGTLPVVLPVFANLLYSQRDGKLPWRRLFPALICIAVGLICVN

VAELRQGLPNFSPWRYGSGIALALGSVVCWAWYALRNARWLRENPHQPPMMWATAQALVTLPVSLAGYLA

ACAWLHGQQAGFPLPFGPRPAVFITLMLAIAVLCSWVGALCWNIASQRLPTVILGPLIVFETLAGLLYTF

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>lcl|NZ\_FO834906.1\_prot\_WP\_020864848.1\_4887 [gene=ytfE] [locus\_tag=BN49\_RS26460] [protein=iron-sulfur cluster repair protein YtfE] [protein\_id=WP\_020864848.1] [location=5146149..5146811] [gbkey=CDS]

MAFRDQPLGELALTIPRASALFRQYDMDYCCGGKQTLARAASRKALDVAVIEAELAKLAEQPLSRDWRAA

PLPEIIDHIIVRYHERHREQLPELILQATKVERVHADKPNVPKGLTKYLTMLHQELSSHMMKEEQILFPM

IKQGMGAQAGGPISVMESEHDEAGELLEVIKHITHNVTPPPEACTTWKAMYNGINAMIDDLMEHISLENN

VLFPRALGGK

>lcl|NZ\_FO834906.1\_prot\_WP\_002886688.1\_4888 [gene=cycA] [locus\_tag=BN49\_RS26465] [protein=D-serine/D-alanine/glycine transporter] [protein\_id=WP\_002886688.1] [location=complement(5146876..5148279)] [gbkey=CDS]

MVDQVKVAAVEQEPTEQSLRRNLTNRHIQLIAIGGAIGTGLFMGSGKTISLAGPSIIFVYMIIGFMLFFV

MRAMGELLLSNLEYKSFSDFAADLLGPWAGYFTGWTYWFCWVVTGMADVVAITAYAQFWFPGLSDWVASL

AVILLLLGLNLATVKMFGEMEFWFAMIKIVAIVALIVVGLVMVMMHFKSPTGVEASFAHLWNDGGWFPKG

LSGFFAGFQIAVFAFVGIELVGTTAAETKDPEKSLPRAINSIPLRIIMFYVFALIVIMSVTPWSSVVPSK

SPFVELFVLVGLPAAASLINFVVLTSAASSANSGVFSTSRMLFGLAQDGQAPKMFAKLSKRAVPAKGLTF

SCMCLLGGVVMLMVNPSVIAAFTMITTVSAILFMFVWTIILCSYLAYRKNRPQLHEKSSYKMPLGKVMCW

VCMAFFVFVLVLLTLEDDTREALMVTPLWFVLLGAGWLFAGKKRLAK

>lcl|NZ\_FO834906.1\_prot\_WP\_002886687.1\_4889 [gene=fklB] [locus\_tag=BN49\_RS26470] [protein=FKBP-type peptidyl-prolyl cis-trans isomerase] [protein\_id=WP\_002886687.1] [location=complement(5148584..5149204)] [gbkey=CDS]

MATPTFDTIEAQASYGIGLQVGQQLSESGLQGLLPEALVAGIADALEGNQPQVPVEAVHRALREIHERAD

AVRRERFQAMAADGQKYLDENREKEGVNSTESGLQFRVLTQGEGPIPARTDRVRVHYTGKLIDGTVFDSS

VARGEPAEFPVTGVIGGWIEALTLMPVGSKWELTIPHNLAYGERGAGASIPPFSTLIFEVELLDII

>lcl|NZ\_FO834906.1\_prot\_WP\_004177687.1\_4890 [locus\_tag=BN49\_RS26475] [protein=hypothetical protein] [protein\_id=WP\_004177687.1] [location=5149423..5150097] [gbkey=CDS]

MPGRFELTSTLAKIWHAPDHFRLLDPLPPMHRRGIIAGFLLVIIGILLPSDDSQSPASTSREANLNLQSQ

SQPQAGGNQAVPLPPITNTPTVSDADQMAPVAPEPIQDEQPDQAQTQQPAATQPYQSSSQQSAPGIEQQW

RTYRIESGKTLAQLFRDHGLPATDVYAMAQVEGAGKPLSTLQSGQTVQIRQNANGVVTGLTIDTGNGQQV

LFTRQSNGSFVRAR

>lcl|NZ\_FO834906.1\_prot\_WP\_002886682.1\_4891 [gene=rplI] [locus\_tag=BN49\_RS26480] [protein=50S ribosomal protein L9] [protein\_id=WP\_002886682.1] [location=complement(5150206..5150655)] [gbkey=CDS]

MQVILLDKVANLGSLGDQVNVKAGYARNFLVPQGKAVPATKKNVEFFEARRAELEAKLADVLAAAEARAE

QINALESVTIASKAGDEGKLFGSIGTRDIADAVTAAGVKVAKSEVRLPNGVLRNVGEHEVNFQVHSEVFA

KVIINVVAE

>lcl|NZ\_FO834906.1\_prot\_WP\_000135199.1\_4892 [gene=rpsR] [locus\_tag=BN49\_RS26485] [protein=30S ribosomal protein S18] [protein\_id=WP\_000135199.1] [location=complement(5150697..5150924)] [gbkey=CDS]

MARYFRRRKFCRFTAEGVQEIDYKDIATLKNYITESGKIVPSRITGTRAKYQRQLARAIKRARYLSLLPY

TDRHQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002885722.1\_4893 [gene=priB] [locus\_tag=BN49\_RS26490] [protein=primosomal replication protein N] [protein\_id=WP\_002885722.1] [location=complement(5150929..5151243)] [gbkey=CDS]

MTNRLELSGIICRTPLRKVSPSGIPHCQFVLEHRSVQEEAGFHRQAWCQMPVIISGHENQAITHSITVGS

AVTVRGFISCHKAKNGLSKMVLHAEQIELIDSGD

>lcl|NZ\_FO834906.1\_prot\_WP\_002885691.1\_4894 [gene=rpsF] [locus\_tag=BN49\_RS26495] [protein=30S ribosomal protein S6] [protein\_id=WP\_002885691.1] [location=complement(5151249..5151644)] [gbkey=CDS]

MRHYEIVFMVHPDQSEQVPGMIERYTGAITAAAGTIHRLEDWGRRQLAYPINKLHKAHYVLMNVEAPQEA

IDELETNFRFNDAVIRSMVMRTKHAVTEASPMVKAKDERRERREDFANETADDSEAGDSEE

>lcl|NZ\_FO834906.1\_prot\_WP\_002885689.1\_4895 [locus\_tag=BN49\_RS26500] [protein=DUF1471 domain-containing protein] [protein\_id=WP\_002885689.1] [location=5151985..5152260] [gbkey=CDS]

MKLKIIAMMAALFFSANALAAIQITERQARNMDDVQSLGVIYINHNMATEHEAEQALSQMSDAQGAKYFQ

PILMHEPETNGPLRASAVIYR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529266.1\_4896 [locus\_tag=BN49\_RS26505] [protein=MFS transporter] [protein\_id=WP\_016529266.1] [location=5152410..5153603] [gbkey=CDS]

MVPRFATLGRIPKGVWVLGGVSLLMDVSSEMIHSLLPLFMATTLGASVIIIGLIEGLAEATALILKVFSG

AISDYVGKRKGLALLGYGLGALSKPLFAIAPTAGVVFSARMIDRVGKGIRGAPRDALVADVTPPEIRGAA

YGLRQALDTVGAFLGPLLAVLLMFIWANDFHAIFWVAVIPAVLSILLLGFGLQEPKSAIAHKRSNPLKRE

NLKKLSAAYWWVVAIGSIFTLARFSEAFLVLRAQQMEIPLYTIPLVMVAMNLVYSLTAYPFGKLSDSMSH

SKLLQWGLLVLILADIVLALSGHWSTLLIGVALWGIHMGMTQGLLAAMVAHTAPPELRGTAFGMFNLMSG

LALLLASTGAGVLWETFGAASTFYTGAIICVVTLIGMRVMPSAYRQD

>lcl|NZ\_FO834906.1\_prot\_WP\_004192457.1\_4897 [locus\_tag=BN49\_RS26510] [protein=L-ribulose-5-phosphate 4-epimerase] [protein\_id=WP\_004192457.1] [location=complement(5153667..5154353)] [gbkey=CDS]

MQQLKQQVFEANMDLPRYGLVTFTWGNVSAIDRQRGLVVIKPSGIAYESMTVDDMSVVDLQGHVVEGRWR

PSSDTATHLALYRRYPDLGGVVHTHSTHATAWAQAGLAIPALGTTHADYFFGDIPCTRALSAQEVDEAYE

LNTGQVIIETLGEANPLHTPGIVVYQHGPFAWGKDAHEAVHNAVVMEEVACMAWIARGINPQLQPIDSWL

MNKHFQRKHGPNAYYGQK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529265.1\_4898 [locus\_tag=BN49\_RS26515] [protein=L-ribulose-5-phosphate 3-epimerase] [protein\_id=WP\_016529265.1] [location=complement(5154353..5155207)] [gbkey=CDS]

MLAKSIPLGIYEKALPAGECWLERLKLAKALGFDFVEMSLDETDARLARLDWSPEQRLALVKAVAETGVR

VPSMCLSAHRRFPLGSEDDAVRHQGLEIMRKAIQLAQDVGIRVIQLAGYDVYYQQANDETRRRFRDGLKQ

SVEMASRAQVTLAMEIMDYPLMNSISKALGYAHYLNNPWFQLYPDIGNLSAWDNDVQMELKAGSGHIVAV

HVKDTKPGVFKNVPFGEGVVDFVRCFETLKQTGYCGPYLIEMWSETSADPLAEVAKARDWVKARMARAGL

MEAA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885684.1\_4899 [gene=ulaD] [locus\_tag=BN49\_RS26520] [protein=3-keto-L-gulonate-6-phosphate decarboxylase UlaD] [protein\_id=WP\_002885684.1] [location=complement(5155217..5155867)] [gbkey=CDS]

MSLPMLQVALDNQTLASAYETTRLIAEEVDIIEVGTILCVGEGVRAVRDLKALYPHKIVLADAKIADAGK

ILSRMCFEANADWVTVICCADINTAKGALDVAKEFNGDVQIELTGFWTWEQAQAWREAGIQQVVYHRSRD

AQAAGVAWSEADISAIKRLSDMGFKVTVTGGLALEDLPLFAGIPVHVFIAGRSIRDAASPVEAARQFKRS

IAQLWG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530756.1\_4900 [gene=ulaC] [locus\_tag=BN49\_RS26525] [protein=PTS ascorbate transporter subunit IIA] [protein\_id=WP\_016530756.1] [location=complement(5155881..5156348)] [gbkey=CDS]

MKLHESLAQNHSIRLQAEAETWQEAVKIGVDLLVAADVVEPRYYQVILDGVAQHGPYFVIAPGLAMPHGR

PEEGVKKTGFALVTLKKPLIFNHEDNDPVDILITMAAVDATTHQEVGIMQIVNLFDDEANFDRLRACRSE

QEVLDLIKNATAAAV

>lcl|NZ\_FO834906.1\_prot\_WP\_002885682.1\_4901 [gene=ulaB] [locus\_tag=BN49\_RS26530] [protein=PTS ascorbate transporter subunit IIB] [protein\_id=WP\_002885682.1] [location=complement(5156358..5156663)] [gbkey=CDS]

MTVRILAVCGNGQGSSMIMKMKVDQFLTQSNIDHTVNSCAVGEYKSELNGADIIIASTHIAGEITVSGNK

HVVGVRNMLSPADFGPKLLEVIKAHFPQDVK

>lcl|NZ\_FO834906.1\_prot\_WP\_016530755.1\_4902 [gene=ulaA] [locus\_tag=BN49\_RS26535] [protein=PTS ascorbate transporter subunit IIC] [protein\_id=WP\_016530755.1] [location=complement(5156676..5158070)] [gbkey=CDS]

MAILYNIFTVFFNQVMTNAPLLLGIVTCLGYILLRKSVSVIIKGTIKTIIGFMLLQAGSGILTSTFKPVV

AKMSEVYGINGAISDTYASMMATIDRMGEAYSWVGYAVLLALNICYVLLRRITGIRTIMLTGHIMFQQAG

LIAVSFFIFGYGMWTTIICTAVLVSLYWGITSNMMFKPTQLVTDGCGFSIGHQQQFASWIAYKVAPYLGK

KEESVEDLKLPGWLNIFHDNIVSTAIVMTIFFGAILLSFGIDVVQAMAGKTHWTVYILQTGFSFAVAIFI

ITQGVRMFVAELSEAFNGISQRLIPGAVLAIDCAAIYSFAPNAVVWGFMWGTIGQLIAVGILVGIGSSIL

IIPGFIPMFFSNATIGVFANHFGGWRAALKICLVMGMVEIFGCVWAVKLTGMSAWMGMADWSILAPPMMQ

GFASIGLAFMAVIILIALAYMFFAGRALRAEEDAEKQLAEASAQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004194176.1\_4903 [gene=ulaG] [locus\_tag=BN49\_RS26540] [protein=L-ascorbate 6-phosphate lactonase] [protein\_id=WP\_004194176.1] [location=5158433..5159497] [gbkey=CDS]

MSKVQTITRESWILNTFPEWGSWLNEEIEQEQVAPGTFAMWWLGCTGIWLKSEGGANVCVDFWCGTGKQS

HGNPLMKTGHQMQRMAGVKKLQPNLRTTPFVLDPFAIRQIDAVLATHDHNDHIDVNVAAAVMQNCPADVP

FIGPKTCVDLWIGWGVPKARCIVMKPGDVVKIKDIEIHALDAFDRTALITLPADQKAAGVLPDGMDQRAV

NYLFKTPGGNLYHSGDSHYSNYYAKHGNEHRIDVALGSYGENPRGITDKMTSADILRMAESLNAKVVIPF

HHDIWSNFQADPQEIRVLWEMKKDRLKYGFKPFIWQVGGKFTWPLDKDNFEYHYPRGFDDCFTIEPDLPF

KSFL

>lcl|NZ\_FO834906.1\_prot\_WP\_004177697.1\_4904 [gene=ulaR] [locus\_tag=BN49\_RS26545] [protein=HTH-type transcriptional regulator UlaR] [protein\_id=WP\_004177697.1] [location=5159605..5160360] [gbkey=CDS]

MTEAQRHQILLDLLAQTGFVTVEQVMSRLGISPATARRDINKLDESGKLKKVRNGAEAISEQRPRWTPMN

IHQAQNLDEKVRIARAASQLIAPGESIVINCGSTAFLLGRELCGKPVQIITNYLPLANYLIDQEHDSVII

MGGQYNRSHAITLSPHGSENSLYAGHWMFTSGKGLTAEGLYKTDMLTAMAEQKMLNVVGKLAVLVDSSKI

GERAGMLFSQAGQIDVVITGKQADAAILKQLEDQGVSVIRV

>lcl|NZ\_FO834906.1\_prot\_WP\_004178343.1\_4905 [gene=yjfP] [locus\_tag=BN49\_RS26550] [protein=esterase] [protein\_id=WP\_004178343.1] [location=complement(5160357..5161073)] [gbkey=CDS]

MIALEMRNLGGGEILHACPQESLDKPLPCIVFYHGFTSSKLVYSYFAVALAEAGFRVIMPDAPEHGARYQ

GDEAGRMQRFWPILQQNFREFPALREAIIAEGWLEGERLAVAGASMGGMTALGIMTHHPELNSVACLMGS

GYFRSLSQTLFPSPDFDVDSLNEWDVSHQLASLARRPLLLWHGDADDVVPPEETFRLEQALRQADLAARL

TCVWQKGVRHRITPEALATTVAFFQQHL

>lcl|NZ\_FO834906.1\_prot\_WP\_002885674.1\_4906 [gene=bsmA] [locus\_tag=BN49\_RS26555] [protein=biofilm peroxide resistance protein BsmA] [protein\_id=WP\_002885674.1] [location=5161283..5161591] [gbkey=CDS]

MVMRRFSPWLLAIVLSGCSALQGTPEAPPPATDHPQEIQRYQTAGLQKMATVSVLMYGSPMDVEAALKAK

AEAAKADYYVIIMIDDTMVPGQWYSQAILYRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002885673.1\_4907 [gene=yjfN] [locus\_tag=BN49\_RS26560] [protein=DUF1471 family protease activator YjfN] [protein\_id=WP\_002885673.1] [location=5161729..5162004] [gbkey=CDS]

MKRSFTLSSLLLTAATANTSAQSAEFASADCVTGLNEIGLISVTNLSGSQQDVEHAIARKADEQGASWYR

IIQMYEEQQPDSWRVQAILYA

>lcl|NZ\_FO834906.1\_prot\_WP\_071829963.1\_4908 [locus\_tag=BN49\_RS31230] [protein=isovaleryl-CoA dehydrogenase] [protein\_id=WP\_071829963.1] [location=complement(5161995..5163842)] [gbkey=CDS]

MHWQTHTVFNQPTPLNNSNLFLSDTALREAVVREGAGWDGDLLASIGQQLGTAESLELGRLANSNPPELL

RYDATGARLDDVRFHPSWHLLMQGLCANRVHNLAWQEDAREGAFVARAARFLLHAQVEAGTLCPITMTFA

ATPLLQHALPAPFRDWLSPLLSDRYDPHLAPGGQKRGLLIGMGMTEKQGGSDVLSNTTRAEKTAEGFYRL

VGHKWFFSVPQSDAHLVLAQAPAGLSCFFVPRLLPDGQRNGVRLERLKEKLGNRSNASSEVEFYEACGWL

VGHKWFFSVPQSDAHLVLAQAPAGLSCFFVPRLLPDGQRNGVRLERLKEKLGNRSNASSEVEFYEACGWL

VGDEGDGVRQILRMGGLTRFDCALGSHALMRRAFSVALYHALQRQAFGKNLVEQPMMRQLLGQMALRLEG

QTAFLFRLARAWDHRDDARESAWARLFTPAAKFAICKAGIPFVAEAMEVLGGIGYCEESELPRLYREMPV

NSIWEGSGNIMCLDVMRVLSKQPAAMELLAAECAEVKGQNRHLDRAWRQLQQLLKRPAEEQGREIARLVY

RLGAGAQMLRHASPPLAEAWCRMMLDTRGGIRLDALTLDDLLLRAMGRGRQAPQA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885669.1\_4909 [gene=rlmB] [locus\_tag=BN49\_RS26570] [protein=23S rRNA (guanosine(2251)-2'-O)-methyltransferase RlmB] [protein\_id=WP\_002885669.1] [location=complement(5163968..5164699)] [gbkey=CDS]

MSEMIYGIHAVQALLERAPERFQEVYILKGREDKRLLPLIHALEAQGVVIQLANRQFLDEKSEGAVHQGI

IARVKPGRQYQENDLPDLLAQLDQPFLLILDGVTDPHNLGACLRSADAAGVHAVIVPKDRSAQLNATAKK

VACGAAENVPLIRVTNLARTMRLLQEENVWIVGTAGEADHTLFQSKMTGPMALVMGAEGEGMRRLTREHC

DELISIPMAGSVSSLNVSVATGICLFEAVRQRS

>lcl|NZ\_FO834906.1\_prot\_WP\_016528905.1\_4910 [gene=rnr] [locus\_tag=BN49\_RS26575] [protein=ribonuclease R] [protein\_id=WP\_016528905.1] [location=complement(5164781..5167213)] [gbkey=CDS]

MSQDPFQEREAEKYANPIPSREFILEHLTKREKPASRDELAIELNIEGEEQTEALRRRLRAMERDGQLVF

TRRQCYALPERLDLLKGTVIGHRDGYGFLRVEGRKDDLYLSSEQMKTCIHGDQVLAQPLGADRKGRREAR

IVRVLVPKTSQIVGRYFTDAGVGFVVPDDSRLSFDILIPPEEIMGARMGYVVVVELTQRPTRRTKAVGKI

VEVLGDNMGTGMAVDMALRTHEIPYVWPPAVEKQVSGLKEQVPEEAKAGRVDLRSLPLVTIDGEDARDFD

DAVYCEKKRGGGWRLWVAIADVSYYVRPGTPLDAEARSRGTSVYFPSQVVPMLPEVLSNGLCSLNPQVDR

LCMVCEMTISSKGRLTGYKFYEAVMSSHARLTYTKVWHMLQGDQELREHYAPLVKHIEELHNLYKVLESA

REERGGISFESEEAKFIFNAERRIERIEQTQRNDAHKLIEECMILANISAARFVEKAQEPALFRIHDKPT

TEAITSFRTVLAELGLELPGGNKPEPRDYAELLTSIADRLDAEMLQTMLLRSMKQAVYDPENRGHFGLAL

QSYAHFTSPIRRYPDLSLHRAIKYLLAKEQGHKGNSTETGGWHYSMEEMLQLGQHCSMTERRADEATREV

SDWLKCDFMQDQVGNIFSGVIASVTGFGFFVRLNDLFIDGLVHVSSLDNDYYRFDQVGQRLIGESGGQTY

RLGDRVEVRVEAVNMDERKIDFTLISSERAPRNVGKTAREKAKKSTSGKPGGRRRQVGKQVNFEPDSAFR

KEKETARPKKEKKAKKPSAKTQKIAAATKAKRAAKKKIAE

>lcl|NZ\_FO834906.1\_prot\_WP\_002885667.1\_4911 [gene=nsrR] [locus\_tag=BN49\_RS26580] [protein=nitric oxide-sensing transcriptional repressor NsrR] [protein\_id=WP\_002885667.1] [location=complement(5167250..5167675)] [gbkey=CDS]

MQLTSFTDYGLRALIYMASLPEGRMTSISEVTEVYGVSRNHMVKIINQLSRMGYVTAVRGKNGGIRLGKP

AGQIRVGDVVRDLEPLSLVNCSSEFCHITPACRLKQALAEAAQSFLKELDNYTLADLVEKNQPLYKLLLV

E

>lcl|NZ\_FO834906.1\_prot\_WP\_002885665.1\_4912 [locus\_tag=BN49\_RS26585] [protein=adenylosuccinate synthase] [protein\_id=WP\_002885665.1] [location=complement(5167826..5169124)] [gbkey=CDS]

MGNNVVVLGTQWGDEGKGKIVDLLTERAKYVVRYQGGHNAGHTLVINGEKTVLHLIPSGILRENVTSIIG

NGVVLSPAALMKEMKGLEDRGIPVRERLLLSEACPLILDYHVALDVAREKARGAKAIGTTGRGIGPAYED

KVARRGLRVGDLFDKATFADKLKEVMEYHNFQLVNFYKAEAVDYQKVLDDVMAIADILTSMVVDVSDLLD

QARQRGDFVMFEGAQGTLLDIDHGTYPYVTSSNTTAGGVATGSGLGPRYVDYVLGIIKAYSTRVGAGPFP

TELFDETGEFLCKQGNEFGATTGRRRRTGWLDAVAVRRAVQINSLSGFCLTKLDVLDGLKEVKICVGYRM

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TETMILRDPFDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885664.1\_4913 [locus\_tag=BN49\_RS26590] [protein=DUF2065 domain-containing protein] [protein\_id=WP\_002885664.1] [location=complement(5169227..5169424)] [gbkey=CDS]

MNSTIWLALALVLVLEGLGPLLYPRAWRKMVASLSQLPDNLLRRFGGGLVVAGIVIYYMLRKSIG

>lcl|NZ\_FO834906.1\_prot\_WP\_004894787.1\_4914 [locus\_tag=BN49\_RS26600] [protein=hypothetical protein] [protein\_id=WP\_004894787.1] [location=5169647..5169937] [gbkey=CDS]

MRELTAFEIENVSGAGWLQDGLAALGSKVGAAAWTMGTDALSINLPLLGTLNLADLAPDLGKTLGESIGS

SIGGTIESTLASLPVIGGLLNKLLGN

>lcl|NZ\_FO834906.1\_prot\_WP\_004192484.1\_4915 [gene=hflC] [locus\_tag=BN49\_RS26605] [protein=protease modulator HflC] [protein\_id=WP\_004192484.1] [location=complement(5170020..5171024)] [gbkey=CDS]

MRKSVIAIIVIVLVVLYMSVFVVKEGERGITLRFGKVLRDDENKPLVYAPGLHFKIPFIESVKMLDARIQ

TMDNQADRFVTKEKKDLIVDSYIKWRISDFSRYYLATGGGDVSQAEVLLKRKFSDRLRSEIGRLDVKDIV

TDSRGRLTLEVRDALNSGSAGTEDEVSTPAADDAIAKAAERVEAETNGKVQVINPNSMAALGIEVVDVRI

KQINLPAEVSEAIYNRMRAEREAVARRHRSQGQEEAEKLRATADYEVTKTLAEAERQGRILRGEGDAESA

KLFADAFSQDPGFYSFIRSLRAYEKSFQSNQDVMVLSPDSDFFRYMRSPDSVRK

>lcl|NZ\_FO834906.1\_prot\_WP\_004146726.1\_4916 [gene=hflK] [locus\_tag=BN49\_RS26610] [protein=FtsH protease activity modulator HflK] [protein\_id=WP\_004146726.1] [location=complement(5171027..5172289)] [gbkey=CDS]

MAWNQPGNNGQDRDPWGSSKPGGNSEGNGNKGGREQGPPDLDDIFRKLSKKLGGLGGGKGGLGGGNSAQG

PRGPMGGRIVGIVAAAAVIIWAASGFYTIKEAERGVVTRFGKFSHLVEPGLNWKPTFIDNVQAVNVESVR

ELAASGVMLTSDENVVRVEMNVQYRVTDPERYLFSVTSADDSLRQATDSALRGVIGKYTMDRILTEGRTV

IRSDTQRELEETIRPYNMGITLLDVNFQTARPPEEVKAAFDDAIAARENEQQYIREAEAYTNEVQPRANG

QAQRILEEARAYKTQTVLEAQGEVARFAKILPEYKAAPEITRERLYIETMEKVLSHTRKVLVNDSKNGNL

MVLPLDQMLKGAAAPAAKSDSSDASDLLRLPPASSSSSASTSSTSSSTGGSIMDQRRANAQRNDYQRQGE

>lcl|NZ\_FO834906.1\_prot\_WP\_004146725.1\_4917 [gene=hflX] [locus\_tag=BN49\_RS26615] [protein=GTPase HflX] [protein\_id=WP\_004146725.1] [location=complement(5172355..5173635)] [gbkey=CDS]

MFDRYDAGEQAVLVHIYFSQDKDMEDLQEFETLASSAGVEAMQVITGSRKAPHPKYFVGEGKAVEIAEAV

KATGASVVLFDHALSPAQERNLERLCECRVIDRTGLILDIFAQRARTHEGKLQVELAQLRHMATRLVRGW

THLERQKGGIGLRGPGETQLETDRRLLRNRIMQILSRLEKVEKQREQGRRSRAKADIPTVSLVGYTNAGK

STLFNQITAAEVYAANQLFATLDPTLRRIDVPDVGETVLADTVGFIRHLPHDLVAAFKATLQETRQATLL

LHVIDAADVRVQENIDAVNTVLAEIEADEIPALLVMNKIDMLDDFEPRIDRDDENKPIRVWLSAQTGVGV

PLLFQALTERLSGEVAQHTLRLPPKEGRLRSRFYQLQAIEKEWMEDDGSVSLQVRMPIVDWRRLCKQEPT

LVDYVV

>lcl|NZ\_FO834906.1\_prot\_WP\_002885659.1\_4918 [gene=hfq] [locus\_tag=BN49\_RS26620] [protein=RNA chaperone Hfq] [protein\_id=WP\_002885659.1] [location=complement(5173711..5174019)] [gbkey=CDS]

MAKGQSLQDPFLNALRRERVPVSIYLVNGIKLQGQIESFDQFVILLKNTVSQMVYKHAISTVVPSRPVSH

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885652.1\_4919 [gene=miaA] [locus\_tag=BN49\_RS26625] [protein=tRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA] [protein\_id=WP\_002885652.1] [location=complement(5174112..5175062)] [gbkey=CDS]

MNDVTEASLPKAIFLMGPTASGKTALAIALRKVLPVELISVDSALIYRGMDIGTAKPDAAELSAAPHRLL

DILDPAEAYSAADFRRDALAAMADIVAAGRIPLLVGGTMLYFKALLEGLSPLPSADPEVRARIEQQAAEQ

GWNALHQQLQEIDPVAAARIHPNDPQRLSRALEVFFISGKTLTELTQTSGDALPYQVHQFAIAPASRELL

HQRIEQRFHQMLASGFEAEVRALFARGDLHTDMPSIRCVGYRQMWSYLNGEIPYDEMVYRGVCATRQLAK

RQVTWLRGWEGVHWLDSEQPEQALNKVLQVVGASQN

>lcl|NZ\_FO834906.1\_prot\_WP\_004152020.1\_4920 [gene=mutL] [locus\_tag=BN49\_RS26630] [protein=DNA mismatch repair endonuclease MutL] [protein\_id=WP\_004152020.1] [location=complement(5175055..5176914)] [gbkey=CDS]

MPIQVLPPQLANQIAAGEVVERPASVVKELVENSLDAGATRIDIDIERGGAKLIRIRDNGSGIKKDELAL

ALARHATSKIASLDDLEAIISLGFRGEALASISSVARLTLTSRTAEQQEAWQAYAEGRDQAVTVKPAAHP

VGTTLEVLDLFYNTPARRKFMRTEKTEFGHIDEVVRRIALARFDVTINLSHNGKVMRQYRAVAQDGQRER

RLGTICGAAFLEHALAIEWQHGDLTLRGWVADPLHTTPALAEIQYCYVNGRMMRDRLINHAIRQACEDKL

GADQQPAFVLYLEIDPHQVDVNVHPAKHEVRFHQSRLVHDFIYQGVLSVLQQQLDAPLAEKDDPPAPRPM

PENRIAAGGNQFARPAEAREPATRFSITPSREPAASSGKPGGASWPHAQPGYQKQQGALYRQLLDTPTAP

KPALQPPAAAELAGHSQSFGRVLTIVGGDCALLEREGGLALLSLTVAERWLRQAQLTPGAEAVCAQPLLI

PLRLKVTEGEKQALAAAQPALAQLGIDVHTDALHVTVRAVPLPLRQQNLQILIPELIGYLAQQNAFDVGN

IAQWMARNLTSEQTSWNMAQAIALLADVERLCPQLVRTPPGGLLQPVDLHSAMNALKDE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043957.1\_4921 [gene=amiB] [locus\_tag=BN49\_RS26635] [protein=N-acetylmuramoyl-L-alanine amidase AmiB] [protein\_id=WP\_046043957.1] [location=complement(5176925..5178190)] [gbkey=CDS]

MKYRITTWLAAALMLSSLHVTAASLSDIQVSNGDQQARITLSFVGEPEYSFTPQGKRLVALDIKQTGVLQ

GLPLQFSGSNLVKSIRAGTPQDTQTLRLLVDLTEDGKTRAVKQQNGANYTVVFTINADAPPPPPPPPVVV

KRADPPPVMTNNQTVTRPAARTVSADDKVIIAIDAGHGGQDPGAIGPNGTKEKNVTIAIARKLRALLNAD

PQFKPVLTRDGDYFISVMGRSDVARKQNANFLVSIHADAAPNRDATGASVWVLSNRRANSEMAGWLEQHE

KQSELLGGAGDVLANSQADPYLSQAVLDLQFGHSQRVGYDVATNVLSQLQRIGNLHKRRPEHASLGVLRS

PDIPSILVETGFISNNGEERLLGSDDYQEQIAEAIYNGLRNYFMQHPLQSAPRGEAAQTASAAAPGGMLI

N

>lcl|NZ\_FO834906.1\_prot\_WP\_016530982.1\_4922 [gene=tsaE] [locus\_tag=BN49\_RS26640] [protein=tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE] [protein\_id=WP\_016530982.1] [location=complement(5178207..5178668)] [gbkey=CDS]

MINRVIPLPDEQATLALGDRIAQACTGATVIYLYGDLGAGKTTFSRGFLQALGHRGNVKSPTYTLVEPYT

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SSRGESLLARLAF

>lcl|NZ\_FO834906.1\_prot\_WP\_171819485.1\_4923 [gene=nnr] [locus\_tag=BN49\_RS26645] [protein=bifunctional ADP-dependent NAD(P)H-hydrate dehydratase/NAD(P)H-hydrate epimerase] [protein\_id=WP\_171819485.1] [location=complement(5178661..5180172)] [gbkey=CDS]

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PRDPVAVLIHQANHHPAPVVALDIPSGLNAQTGATPGAVVQADHTLTFIALKPGLLTGKARDVVGQLHHH

ALGLERWLAGQSTPLTRFCAAHLADWLPPRRATSHKGDHGKLVIVGGDRGTAGAIRMCGEAALRSGAGLV

RVLTHPENVAPIVTVRPELMVDELTSQTLKAALEWADVVAIGPGLGQREWGRSALRTVESFNKPMVWDAD

ALNLLAFNPDKRHNRVLTPHPGEAARLLNVSVAEIESDRLLSAQRLVKRYGGVVVLKGAGTVVASESGAM

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RVVNPDVIDVDHD

>lcl|NZ\_FO834906.1\_prot\_WP\_004178333.1\_4924 [gene=queG] [locus\_tag=BN49\_RS26650] [protein=tRNA epoxyqueuosine(34) reductase QueG] [protein\_id=WP\_004178333.1] [location=5180186..5181325] [gbkey=CDS]

MSQPLDLVQLAQQIKQWGTELGFQQVGIADTDLSASEPKLQAWLDKQYHGEMEWMARHGMMRARPHELLP

GTLRVISVRMNYLPANAAFARTLKDPTLGYVSRYALGRDYHKLLRNRLKKLGEKIQEQCASLNFRPFVDS

APILERPIAEKAGLGWTGKHSLILSRDAGSFFFLGELLIDLPLPVDSPVAEECGRCVACMTICPTGAIVE

PYTVDARRCISYLTIELEGAIPEEFRPLIGNRIYGCDDCQLICPWNRFSQLTDEEDFSPRKALHAPPLVE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004186630.1\_4925 [locus\_tag=BN49\_RS26675] [protein=transporter substrate-binding domain-containing protein] [protein\_id=WP\_004186630.1] [location=5182258..5182989] [gbkey=CDS]

MRKVLTVLLLSTLAIGTASAETLHFGTTTANPPFVTANGKNQPVGFDIDLAHALCQQMQAQCQFTAQRFD

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YLRDKQKAVQAVPYDDVASALAALKAGQITGVMGDFATLDAWQRENPDYAIMDERATDPAYYGKQYAIAV

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885538.1\_4926 [gene=orn] [locus\_tag=BN49\_RS26680] [protein=oligoribonuclease] [protein\_id=WP\_002885538.1] [location=complement(5183033..5183578)] [gbkey=CDS]

MSANENNLIWIDLEMTGLDPERDRIIEIATLVTDANLNILAEGPTIAVHQSDAQLALMDEWNVRTHTGSG

LVDRVKASTVSEHDAELATIEFLKQWVPAGKSPICGNSIGQDRRFLFKYMPQLEAYFHYRYLDVSTLKEL

ARRWKPEILDGFKKQGTHQAMDDIRESVAELAYYREHFIKL

>lcl|NZ\_FO834906.1\_prot\_WP\_002885537.1\_4927 [gene=rsgA] [locus\_tag=BN49\_RS26685] [protein=small ribosomal subunit biogenesis GTPase RsgA] [protein\_id=WP\_002885537.1] [location=5183673..5184734] [gbkey=CDS]

MSKNKLSKGQQRRVKANHQRRLKTTAEKADYDDNLFGETSEGIVISRFGMHADVESADGSVHRCNIRRTI

RSLVTGDRVVWRPGKDAADGVSVKGIVEAVHDRASVLTRPDFYDGVKPIAANIDQIVVVSAILPELSLNI

IDRYLVACEAQDIEPLIVLNKIDLLDDDGLRFVNEQMDIYRNIGYRVLLVSSRTQDGLKPLEAALTDRIS

IFAGQSGVGKSSLLNALLGLSEDQILTNDVSDVSGLGQHTTTAARLYHFPHGGDVIDSPGVREFGLWHLE

AEQITNGFVEFHDYLGRCKYRDCKHDTDPGCALREAVENGKIAESRFENYHRILESMAQVQVKTRKNFSS

SDD

>lcl|NZ\_FO834906.1\_prot\_WP\_002885536.1\_4928 [gene=asd] [locus\_tag=BN49\_RS26690] [protein=archaetidylserine decarboxylase] [protein\_id=WP\_002885536.1] [location=5184895..5185857] [gbkey=CDS]

MLNDLKLSLQYILPKLWLTRLAGWGASKRAGWLTKLVIDLFVKYYKVDMKEAQKPDTAAYRTFNDFFVRP

LRDDVRPLNTDPNVLVMPADGVISQLGAIENDKILQAKGHDYSLEALLAGNYQMADLFRNGSFATTYLSP

RDYHRVHMPCNGILREMIYVPGDLFSVNHLTAQNVPNLFARNERVICLFDTEFGPMAQILVGATIVGSIE

TVWSGTVTPPREGIIKRWTWPAGDNEGSIALLKGQEMGRFKLGSTVINLFAPGQVKLVDTLQSLSVTKIG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004146716.1\_4929 [gene=mscM] [locus\_tag=BN49\_RS26695] [protein=miniconductance mechanosensitive channel MscM] [protein\_id=WP\_004146716.1] [location=5185881..5189210] [gbkey=CDS]

MRLIYTFLLALSLSFGAYAATAPDAKQITQELEQAKAAKPAQPETVEVLQSALNALEERKSSLERARQYQ

DVIDNFPKLFQSLRAQLNNLSEEPRQVPTGLTADALNQEILQVSSQLLESSRQAQQEQDRAREIADSLNQ

LPQQQTDARRQLNEVERRIGTQTGNNALAQAQNLALQAESARLKALVDELDLAQLSANNRQELSRARSEL

AQKQSEQLDAYLQALRNLQNSQRQREAEKALESTELLAENSENLPPDITAQFKVNRELSQALNQQAQRMD

LVASQQRQATNQTLQVRQALNTLREQSQWLGSSNLLGEALRAQVARLPERPRPQQLDTEMAQLRVQRLRF

EDLLSKQPQLRQIRQADGEPLTSEQNKILQAQLRTQNELLNSLLRGGDTLMLELTKLKVANGQLEDALKE

INEATHRYLFWTSDVSPIGFSWPLEIVQDLRRLISLDTISELGKASAMMLTSKETLLPLFAALLLVGFSI

SSRRHFTRFLERSSARVGKVTQDHFWLTLRTVFWSILVASPLPVLWMTLGYGLQSAWPFPLAVAIGDGVT

ATVPLLWVVMICATFARPNGLFIAHFGWPRSRVAKAMRYYLMSIGLIVPLIMALIMFDNLNDREFSASLG

RLCFLLICGALAVVTLSLKHAGIPLYLDKEGNGDNMVNRLLWNLMLGAPLVAMLAAAVGYLATAQALLAR

LETSVAIWFLLLVVYHIIRRWMLIQRRRLAFDRARHRRAEILAQRARGEDEPVHVSSPEGSVETEVSEVD

LDAISTQSLRLVRSLLMLIALLSVIVLWSEIHSAFGFLENISLWDVTSTVQGVESLEPITLGAVLIAILV

LIITTQLVRNLPALLELAILQHLDLTPGTGYAITTITKYLLMLVGGLVGFSMIGIEWSKLQWLVAALGVG

LGFGLQEIFANFISGLIILFEKPIRIGDTVTIRDLTGSVTRINTRATTISDWDRKEIIVPNKAFITEQFI

NWSLSDSVTRVVLTVPAPVDADTEEVTKILIAAAHRCSLVIDTPAPEAFLVDLQQGIQIFELRIFAAEMG

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>lcl|NZ\_FO834906.1\_prot\_WP\_042942921.1\_4930 [gene=yjeM] [locus\_tag=BN49\_RS26700] [protein=glutamate/gamma-aminobutyrate family transporter YjeM] [protein\_id=WP\_042942921.1] [location=complement(5189248..5190750)] [gbkey=CDS]

MHQQLKKMSLIGLILMIFTSVFGFANSPSAFYLMGYSAIPFYLFSALFFFIPFALMMAEMGSAYRREEGG

IYSWMNHSVGPRFAFIGTFMWFASYVVWMVSTAAKIWVPLSTFLFGADKTQTWALGSLTPTQTVGILAAC

WMVVVTFIAVKGINKIAKITAVGGIAVMGLNLVLLLVSGAILLLNGGHFAQPLNFTLSPNPGYQSGMAML

SFVVFAIFAYGGIEAVGGLVDKTDKPEKNFAKGIIIAAIVISIGYSLAIVLWGVSANWQQVLGARSTNLG

NITYVLMTSLGATLGQALHLTPAASALTGVWFARITGLSMFLAYTGAFFTLSYSPLKAIIQGTPKALWPS

VMTRLNVNGMPAAAMWLQCLLVGVFIVLVSFGGDSASAFYNKLTLMANVSMTLPYLFLTIAFPFFKAKTH

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MASGALVMES

>lcl|NZ\_FO834906.1\_prot\_WP\_016532552.1\_4931 [gene=epmA] [locus\_tag=BN49\_RS26705] [protein=elongation factor P--(R)-beta-lysine ligase] [protein\_id=WP\_016532552.1] [location=complement(5190933..5191910)] [gbkey=CDS]

MSETATWQPSAPIPNLLKRAAVMAEIRRFFTDRGVLEVETPCMSQATVTDIHLFPFETRFVGPGHSQGLN

LYLMTSPEYHMKRLLAAGCGPVFQLCRSFRNEEMGRHHNPEFTMLEWYRPCYDMYRLINEVDDLLQQVLE

CQPAESLSYQQAFQRHLEIDPLSADKAQLREVAAKLDLSNIADTEEDRDTLLQLLFTMGVEPHIGKDRPT

FIYHFPATQASLAQISPEDHRVAERFEVYYKGIELANGFHELTDAHEQRLRFEQDNRKRAARGLPQQPID

NNLLAALEAGLPDCSGVALGVDRVVMLALGAESIGEVIAFTVDCA

>lcl|NZ\_FO834906.1\_prot\_WP\_032412622.1\_4932 [gene=frdA] [locus\_tag=BN49\_RS26710] [protein=fumarate reductase (quinol) flavoprotein subunit] [protein\_id=WP\_032412622.1] [location=5192186..5193976] [gbkey=CDS]

MQTFQADLAVIGAGGAGLRAAIAAAQANPNAKIALISKVYPMRSHTVAAEGGSAAVAQDHDSFEYHFHDT

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FQTSLQFPQIQRFDEHFVLDLLVDDGQARGLVAMNMMEGTLVQIRANAVVLATGGAGRVYRYNTNGGIVT

GDGMGMALGHGVPLRDMEFVQYHPTGLPGSGILMTEGCRGEGGILVNKNGYRYLQDYGMGPETPLGEPKN

KYMELGPRDKVSQAFWHEWRKGNTIPTPRGDVVYLDLRHLGEKKLLERLPFICELAKAYVGVDPVKEPIP

VRPTAHYTMGGIETDQQCETRIKGLFAVGECSSVGLHGANRLGSNSLAELVVFGRLAGEQAMQRAAQAGE

ANGAALDAQAADVEQRLKDLVNQEGNENWARIRDEMGLSMEEGCGIYRTPELMQKTIDKLAELQERFKRV

RITDNSSVFNTDLLYTIELGHGLNVAECMAHSAIARKESRGAHQRLDEGCTERDDVNFLKHTLAFREADG

TTRLEYGDVKITTLPPAKRVYGAEADAAEKKETTHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177729.1\_4933 [gene=frdB] [locus\_tag=BN49\_RS26715] [protein=fumarate reductase iron-sulfur protein] [protein\_id=WP\_004177729.1] [location=5193969..5194703] [gbkey=CDS]

MAEMKNLKVEVVRYNPEVDTAPHSAFYDVPYDEQTSLLDALGYIKDNLAPDLSYRWSCRMAICGSCGMMV

NKVPKLACKTFLRDYTKGIKVEALANFPIERDLVVDMTHFIESLEAIKPYIIGNNRTPDQGPNKQTPAQM

AKYHQFSGCINCGLCYAACPQFGLNPEFIGPAAITLAHRYNEDSRDHGKKERMAQLNGQNGVWTCTFVGY

CSEVCPKHVDPAAAIQQGKVESSKDFLIATLKPR

>lcl|NZ\_FO834906.1\_prot\_WP\_002885530.1\_4934 [gene=frdC] [locus\_tag=BN49\_RS26720] [protein=fumarate reductase subunit FrdC] [protein\_id=WP\_002885530.1] [location=5194714..5195109] [gbkey=CDS]

MTTKRKPYVRPMTSTWWKKLPFYRFYMVREGTAVPTVWFSIVLIYGLFALKHGAESWAGYIGFLQNPVVV

ILNLITLAAALLHTKTWFELAPKAANVIIKGEKMGPEPVIKGLWVVTAVVTVVILFVALFW

>lcl|NZ\_FO834906.1\_prot\_WP\_002885526.1\_4935 [gene=frdD] [locus\_tag=BN49\_RS26725] [protein=fumarate reductase subunit FrdD] [protein\_id=WP\_002885526.1] [location=5195120..5195479] [gbkey=CDS]

MINPNPKRSDEPVFWGLFGAGGMWGAIVAPVMVLLVGILLPLGLAPADAFSYERVLAFAQSFIGRAFIFL

MIVLPLWCGLHRIHHAMHDLKIHVPNGKWVFYGLAAILSVITLVGVLFI

>lcl|NZ\_FO834906.1\_prot\_WP\_002885523.1\_4936 [locus\_tag=BN49\_RS26730] [protein=lipocalin family protein] [protein\_id=WP\_002885523.1] [location=5195593..5196126] [gbkey=CDS]

MRILPIITAIAVSFLSVACSTPAPPPGVTVVSPFDVQRYLGTWYEIARFDHPFESGLEKVTIAWHPRDDG

GLDVVNKGYNPDRGMWQKTDGVAYFTGEPSRAALKISFFGPFYGSYNVIALDKEYRYALVCGPDRDYLWL

LARAPTIAPEVRQQMLDIATRQGFDVGKLVWVNQRYD

>lcl|NZ\_FO834906.1\_prot\_WP\_002885521.1\_4937 [gene=sugE] [locus\_tag=BN49\_RS26735] [protein=quaternary ammonium compound efflux SMR transporter SugE] [protein\_id=WP\_002885521.1] [location=complement(5196123..5196440)] [gbkey=CDS]

MSWIVLFIAGLLEVVWAVGLKYTHGFSRLVPSVITIVAMVASMALLSWAMKTLPVGTAYAVWTGIGAVGA

AVTGIVLLGESASAMRIASLVCIVIGIIGLKISAH

>lcl|NZ\_FO834906.1\_prot\_WP\_002885518.1\_4938 [gene=ecnB] [locus\_tag=BN49\_RS26740] [protein=lipoprotein toxin entericidin B] [protein\_id=WP\_002885518.1] [location=complement(5196584..5196730)] [gbkey=CDS]

MVKKTIAAFFTVLVLSSALTACNTTRGVGEDISDGGNAISGAATKAQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002885511.1\_4939 [locus\_tag=BN49\_RS26745] [protein=entericidin A/B family lipoprotein] [protein\_id=WP\_002885511.1] [location=complement(5196890..5197021)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885506.1\_4940 [gene=efp] [locus\_tag=BN49\_RS26750] [protein=elongation factor P] [protein\_id=WP\_002885506.1] [location=complement(5197095..5197661)] [gbkey=CDS]

MATYYSNDFRAGLKIMLDGEPYAVEASEFVKPGKGQAFARVKLRRLLTGTRVEKTFKSTDSAEGADVVDM

NLTYLYNDGEFWHFMNNETFEQLSADAKAIGDNAKWLLDQAECIVTLWNGQPIAVTPPNFVELEIIETDP

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885500.1\_4941 [gene=epmB] [locus\_tag=BN49\_RS26755] [protein=EF-P beta-lysylation protein EpmB] [protein\_id=WP\_002885500.1] [location=5197703..5198731] [gbkey=CDS]

MAHIVTLNTPSREDWITQLANVVTSPDELLRLLNVDADEKLLAGREARRLFPLRVPRAFIARMEKGNPND

PLLRQVLTAEEEFIVAPGYSTDPLEEQHSVVPGLLHKYRNRALLLVKGGCAVNCRYCFRRHFPYAENQGT

RRNWQTAMDYIAAHPQLDEIIFSGGDPLMAKDHELDWLMTQLEAIPHVKRLRIHSRLPIVIPARITETLA

SRFQRSSLQVILVNHVNHANEIDGEFRAAMAMLRQAGVTLLNQSVLLRGVNDNAQTLADLSNALFDAGVM

PYYLHVLDRVQGAAHFMVSDDEAREIMRELLTLISGYMVPKLAREIGGEPSKTPLDLGLKQR

>lcl|NZ\_FO834906.1\_prot\_WP\_009309349.1\_4942 [locus\_tag=BN49\_RS26760] [protein=winged helix-turn-helix domain-containing protein] [protein\_id=WP\_009309349.1] [location=complement(5198892..5199467)] [gbkey=CDS]

MTFNSYIINDEVIFNMDVNELQPVAGKDHEAITLNTPTARCLQLLLESNGNIISRDEFLSAVWKERGVVV

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>lcl|NZ\_FO834906.1\_prot\_WP\_016529869.1\_4943 [locus\_tag=BN49\_RS26765] [protein=HlyD family secretion protein] [protein\_id=WP\_016529869.1] [location=5199846..5201132] [gbkey=CDS]

MARKLYRKEAIEYKKLHWKGKALLLAGMPAWLIVTLSSCFLIALISTLILCTFTQRIDVRGEVITLPHSV

NVFAPQQGFVLNQYVKVGDIVKKGQKLYEIDISRNTTNGNVSLAQTAVINEKIINAESIITKLIRNKDET

LNALDTQLNTIKKSLSETTSMLANTQAGLNKMHQNLSSYDKYLKEGLITKDQYNYQHSLYFQQQSAYQSL

VSQKMQLESQITQFTSDKVTKAADFDNQISNQQNQINDYKNQLVESDAKGNVIIKATTDGRIESLAVTKG

QMVDNGSSLAQIKPTGNVEYYLILWLPNNSIPYVKPGDTINIRYDAFPADKFGQFPGEVISISSMPASRQ

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SVSGPINE

>lcl|NZ\_FO834906.1\_prot\_WP\_016529870.1\_4944 [locus\_tag=BN49\_RS26770] [protein=peptidase domain-containing ABC transporter] [protein\_id=WP\_016529870.1] [location=5201125..5203245] [gbkey=CDS]

MNNKLFETIIAKLNFSLIKKTPVILQSESAECGIASLAMICGHYGLDIDLFNFRQRFGSPSQGASLLHLS

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VALELWPDQNFQQEKAKARLRLLDLMRNIVGLKSALIKIFAFSVVIEAIGLLLPIGTQLVTDHVIMAHDQ

SLLSVICIGLVFFTLFRTFVSMLRAWTSLTLNTLTNIQWKTTLFDHLTSLPLSFFEKRHLGDIQSRFTSL

DTIRSTFTNSIVSGIIDSIMTIGLLIMLTLYGGWLVWVVVGFTLCYAIMRLATYRFYRRVAEEQVIKGAR

SSSHFIESLYGISTIKALNLKERRSQHWLNINIDACNAGIKQTRFDMMFSGINTFISSIDQVAILWLGAI

MVIDNNMTLGMFMAFNSYRGQFSQRASNLIDLFMQLRMLSLHNERLSEIVFSEPEKELPARRVFDENSGV

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GLNNYRLGTACVLQEDRLFSGSISDNISGFEDNADEELIVECARRSNIHDEIMKMPMGYETMIGELGLGI

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YGKQAS

>lcl|NZ\_FO834906.1\_prot\_WP\_009309355.1\_4945 [locus\_tag=BN49\_RS26775] [protein=YjeJ family protein] [protein\_id=WP\_009309355.1] [location=5203272..5204132] [gbkey=CDS]

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RQAFLHADAEDFLNLIDSTTDFVMLYAVQVMEDTRFNYEYFEHELWKQNLFSHHLAVLYCYETENGKKIL

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QAKLEF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529871.1\_4946 [locus\_tag=BN49\_RS26780] [protein=DUF4156 domain-containing protein] [protein\_id=WP\_016529871.1] [location=complement(5204176..5204529)] [gbkey=CDS]

MQVKYFAVIIGASLLLAGCSSSSDLTAGGEAVRFVQDKPGAECQLLGTATGKQSNWLSGQNGDEGGSMRG

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>lcl|NZ\_FO834906.1\_prot\_WP\_009309357.1\_4947 [locus\_tag=BN49\_RS26785] [protein=fimbrial protein] [protein\_id=WP\_009309357.1] [location=5205177..5205719] [gbkey=CDS]

MNKRIIAALIAASGLVAFNASANDGTVNFIGDITDGACTVDVQNTGSSTGQVTLGSVPKSAFSGVGSTAG

NGSGLAAITISLSGCPTTKTDAYVTFDGDYYNGLNDYLKLTGYGNTGVAKGVAIQLMDSNNNHLKLGEKS

AAIPLTAGAANVAFKATYAQVESTVDAGTANGVATLLVTY

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MIDVLGPEKRRRRTTQEKIAIVQQSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

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DEPMTGRTAAAAVTRMIRMCFAVYTMLSESCPHMVIVGYGRCFADKTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPKPDGLTAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_WP\_009309358.1\_4949 [locus\_tag=BN49\_RS26800] [protein=molecular chaperone] [protein\_id=WP\_009309358.1] [location=5207106..5207786] [gbkey=CDS]

MRILNSLLSIILLFSTSLACYAGVQVGTTRIIYAEGKKEASVSLDNLDSTPYLIKSWIENNNNAGTHFLV

TPPLFRLEGKQKNVVRIFKLDGVLPADRESLFFFNTTSIPASTTDADRNTLQIAVRTRLKLIFRPKGLSD

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IINDMGGQSDLYQSSL

>lcl|NZ\_FO834906.1\_prot\_WP\_046043965.1\_4950 [locus\_tag=BN49\_RS26805] [protein=fimbrial biogenesis outer membrane usher protein] [protein\_id=WP\_046043965.1] [location=5207836..5210409] [gbkey=CDS]

MIKKFKLSPCCLALISIGVLAISSELYAREFFNPAFLTDLNGSDVSPDLSAFEVANSQAPGKYRVDIIIN

GTVVDTKDVDFFSTAEQKASYLNEAGEELKLYPCLSTEELSGYGIKVKAISSLKTNANGCVIISSIPEAS

VDFNFNLQKLELSVPQAAVSSTVRGYVSPDEFDNGINAFYLNYRYNGTSSYARDNGSSDQENHSVNLLPG

LNIGPWRIKNYTTWNKDSYDNDSNGKWDTIYTYAERNIISLKSLLTLGESTSDADIFDSVPYRGAQLNSD

DYMDAESIQGYAPVVRGIAKSNAKVIIKQSGYVIYQSFVPPGAFEITDLYSTGGNGDLNVTIEEADGTQQ

NFVVAYASLPVLRREGSLKYSITSGQYRSSDGSVDYTPFSQATASYGLPHNTTLYGGFQAASKYQSVAIG

VGNNLGVLGAVSLDVTQAWSTKQDQDKISGQSVRIRYSKNLNDIGTNIAIAGYRYSTSGFNTLSDVLETY

RDDYKYYYNDRVKNRTEITVSQSLGDKLGYFNIGGVMEDYWNQRRRNNSLNVGYSNSWSGITYNLNYSHS

RSSTDYEGYGRNYSTDNIFSFNVNIPLDIWMPNTWVTYGLNTSDPDSTSNSVGLSGLALADNNLSWNLQQ

QYDNRDFSSGNAGVDYKGSYGEIYGSYNYDHDWQRLNYGINGGVIVHRNGITAGQSFSDTSALVKAPGVT

GTRVIGNTGVKTDYRGYAIVPNITMYRRNDVVLDTETMPEDVDLDTTTATVVPTRGAIVLAQYTGKKGIR

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>lcl|NZ\_FO834906.1\_prot\_WP\_009309362.1\_4951 [locus\_tag=BN49\_RS29690] [protein=fimbrial protein] [protein\_id=WP\_009309362.1] [location=5210428..5211387] [gbkey=CDS]

MYKIMVAIITTFIGIYSSQCLADASGCIVLDGKTYTLNLSSIAIDPDAEVGATLYTARLDTEGPKITCPL

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ISFIKTGTVGKGTTNYGLAAQFNVDNWVVAKISIKAKISWITKSCVTDPSLRIQNIQLGNHLASSFTSVG

STSTDTKFSVKLNCQKDANAVYVSFDPTTGSTGKGILNVDTSNSDAATGIAVEILNAKDRSPLVFSSETK

YHTNMESSIEIPLVAHYKRIGTVKSGTANAAMTFTINQY

>lcl|NZ\_FO834906.1\_prot\_WP\_009309364.1\_4952 [locus\_tag=BN49\_RS26810] [protein=hypothetical protein] [protein\_id=WP\_009309364.1] [location=5211631..5211993] [gbkey=CDS]

MKELSVIEMESIAGAYSWDFSSLGSALTSIVSNGVEAVASAVTLGSILASYGSSIGGTHGSDNGGIFGVG

TIGMAVGGLWGLIAGGIIGAITGALLGWDDSMQLTMDGYKGLIDGTTGIF

>lcl|NZ\_FO834906.1\_prot\_WP\_009309366.1\_4953 [locus\_tag=BN49\_RS26815] [protein=hypothetical protein] [protein\_id=WP\_009309366.1] [location=5212024..5212386] [gbkey=CDS]

MKELSVIEMESISGAYSWDFSSLGSAISSIASNGVEAVASALLLGAITAGGGSIVGGSHGSDNGGIFGVG

TIGMMIGGLYGLIVGAINGAAAGFFLGWDQSKQIAIDSLEGIFNGTPGIY

>lcl|NZ\_FO834906.1\_prot\_4954 [locus\_tag=BN49\_RS31560] [protein=transposase] [pseudo=true] [partial=5'] [location=<5212747..5212943] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885441.1\_4955 [gene=groL] [locus\_tag=BN49\_RS26820] [protein=chaperonin GroEL] [protein\_id=WP\_002885441.1] [location=complement(5213064..5214710)] [gbkey=CDS]

MAAKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGAPTITKDGVSVAREIELEDKFENMG

AQMVKEVASKANDAAGDGTTTATVLAQAIVNEGLKAVAAGMNPMDLKRGIDKAVLAAVEELKALSVPCSD

SKAIAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDGTGLEDELDVVEGMQFDRGYLSPYFINKPDT

GAVELESPFILLADKKISNIREMLPVLEAVAKAGKPLVIIAEDVEGEALATLVVNTMRGIVKVAAVKAPG

FGDRRKAMLQDIATLTGGTVISEEIGMELEKATLEDLGQAKRVVINKDTTTIIDGVGEESAIQGRVAQIR

KQIEEATSDYDREKLQERVAKLAGGVAVIKVGAATEVEMKEKKARVDDALHATRAAVEEGVVAGGGVALV

RVAAKLAGLTGQNEDQNVGIKVALRAMEAPLRQIVSNAGEEPSVVANNVKAGDGNYGYNAATEEYGNMID

FGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKGDAPDLGAAGGMGGMGGMGGMM

>lcl|NZ\_FO834906.1\_prot\_WP\_004152420.1\_4956 [locus\_tag=BN49\_RS26825] [protein=co-chaperone GroES] [protein\_id=WP\_004152420.1] [location=complement(5214748..5215041)] [gbkey=CDS]

MSIRPLHDRVIVKRKEVETKSAGGIVLTGSAAAKSTRGEIIAVGKGRILENGTVQPLDVKVGDIVIFNDG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004146698.1\_4957 [gene=yjeH] [locus\_tag=BN49\_RS26835] [protein=L-methionine/branched-chain amino acid transporter] [protein\_id=WP\_004146698.1] [location=5215272..5216522] [gbkey=CDS]

MSGLKQELGLGQGVGLLSTSLLGTGVFAVPALAALVAGDNSLWAWPLLILLVFPIAIVFALLGRHFPSAG

GVAHFVDMAFGPRLASVTGWLFLSVIPVGLPAALHIATGFGQALFGWHDAQLLLAELGTLAIVWWVGSRG

ASSSANLQTLVAVLIVALIVVVWWRGGISPAQIPFPAPAEIDRGQLFLALSVMFWCFVGLEAFAHLASEF

KHPERDFPRALMIGLLLAGSVYWACTVLVLHFHAFGEEMAAAASLPNIVVRLFGVEALWVACVIGYLACF

ASLNIYIQSFARLVWSQAQHKPHSYLARLSPRQIPRNALNAVLGSCVVSTLGIYLLDINLDALIVYANGI

FIMIYLLCMLAGCRLLRGRYRLLAVVGSILCLLLLAMVGWKSLYALVMLAGLWLFLPRRKLATGSV

>lcl|NZ\_FO834906.1\_prot\_WP\_002885425.1\_4958 [gene=fxsA] [locus\_tag=BN49\_RS26840] [protein=membrane protein FxsA] [protein\_id=WP\_002885425.1] [location=complement(5216573..5217049)] [gbkey=CDS]

MRWIPFIAFFLYVYIEISIFIQVAHVLGVFMTLILVIFSSVVGMSLVRNQGFKNFLLMQQKMAAGESPAA

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QRKDEQRDRLDHKDDRRD

>lcl|NZ\_FO834906.1\_prot\_WP\_016530408.1\_4959 [gene=aspA] [locus\_tag=BN49\_RS26850] [protein=aspartate ammonia-lyase] [protein\_id=WP\_016530408.1] [location=5217387..5218823] [gbkey=CDS]

MLNNIRIEEDLLGTREVPADAYYGVHTLRAIENFYISNSKISDIPEFVRGMVMVKKAAALANKELQTIHK

SAANAIIAACDEVLNNGKCMDQFPVDVFQGGAGTSVNMNTNEVLANIGLELMGHQKGEYQYLNPNDHVNK

CQSTNDAYPTGFRIAVYASILKLIDAIKQLGEGFQAKAVEFQDILKMGRTQLQDAVPMPLGQEFHAFNVL

LNEETKSILRTAELLLEVNLGATAIGTRLNTPDGYQQLAVQKLAEVSNLPVVPAEDLIEATSDCGAYVMV

HSSLKRLAVKLSKICNDLRLLSSGPRAGLNEINLPELQAGSSIMPAKVNPVVPEVVNQVCFKVIGNDTTV

TMASEAGQLQLNVMEPVIGQAMFESIHILTNACYNLLEKCVNGITANKAVCEGYVYNSIGIVTYLNPFIG

HHNGDIVGKICAETGKSVREVVLERGLLTAAELDDIFSAQNLMHPAYKAKRYTDESEQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002885423.1\_4960 [locus\_tag=BN49\_RS26855] [protein=anaerobic C4-dicarboxylate transporter] [protein\_id=WP\_002885423.1] [location=5218939..5220240] [gbkey=CDS]

MFGAELVIVLLAIYLGARLGGIGIGFAGGLGVLVLTLIFQIKPGAIPFDVIEIIMAVIAAIAAMQVAGGM

DYLVSLAERMLRRHPKYITFLAPLVTWFMTVLAGTGHTAFSTLPVITEVAKEQGIRPSRPLSIAVVASQI

AITASPISAAVVFFAGILEPLGVSYLTLLAICIPVTLLAVMLTAIVCNFLGCELKDDPVYQERLAKGEVR

LRGSQVFELQPHAKRSVLLFLIGIVAVMFYATAISDTVGLIKNPVLPRNEAIVVFMLTIATLISITCKID

TGEVLNASTFKSGMSACVCVLGVAWLGDTFVKAHISDIQAVAGDLLHNYPWLLAVVLFFAATLLYSQAAT

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CVILGFIFGGIML

>lcl|NZ\_FO834906.1\_prot\_WP\_002885422.1\_4961 [gene=cutA] [locus\_tag=BN49\_RS26860] [protein=divalent cation tolerance protein CutA] [protein\_id=WP\_002885422.1] [location=5220365..5220688] [gbkey=CDS]

MTTPDAVVVLCTAPDEATAQDLAAKALAEKVAACATLLPGATSLYYWEGKLEQEYEVQMLLKTDLAHQQA

LLDCLKSHHPYQTPELLVLPVTHGDNDYLSWLTASLR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529183.1\_4962 [locus\_tag=BN49\_RS26865] [protein=protein-disulfide reductase DsbD] [protein\_id=WP\_016529183.1] [location=5220664..5222460] [gbkey=CDS]

MAYRIITLILLLCSTSATAGLFDAPGRSNFVPADQAFAFDFQQQQHDVNLSWQIKDGYYLYRQQLTFSAA

GATIDEPALPAGEWHEDEFYGKSETFRQRLTVPVTVKEADKEATLTVTWQGCADAGFCYPPETKVIPLSA

VRAASNDAQPTAAAPVLSLNHRPAFNPPLPVEPRPMEENAVPQAPAMAPPADVPARLPFTALWALLIGIG

IAFTPCVLPMYPLISGIVLGGKQRLSTARALLLAFIYVQGMALTYTALGLVVAAAGLQFQAALQHPYVLV

GLSAVFILLALSMFGLFTLQLPSSLQTRLTLLSNKRQGGSPGGVFAMGAIAGLICSPCTTAPLSAILLYI

AQSGNLWLGSGTLYLYALGMGLPLILVTVFGNRLLPKSGPWMSHVKTAFGFVILALPVFLLERIFGDQWG

LRLWSMLGVAFFSWAFITSLGATRPWMRLVQIILLAAALVSARPLQDWAFGAPAVEQQAHLAFTRVSSVA

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885410.1\_4963 [locus\_tag=BN49\_RS26870] [protein=transcriptional regulator] [protein\_id=WP\_002885410.1] [location=5222481..5223071] [gbkey=CDS]

MEENTVLREDVLAEAIKILEIEGIANTSLEMVAERVSCPTSDLKRFWPDREALLYDALRYLSQQVDAWRR

QLLLDETLSAEQKLLARYAALTTCVSNQRYPGCLFIAACTFYPDPQHPIHQLAEQQKQASLAYTHELLTQ

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>lcl|NZ\_FO834906.1\_prot\_WP\_046043968.1\_4964 [locus\_tag=BN49\_RS26875] [protein=DUF1176 domain-containing protein] [protein\_id=WP\_046043968.1] [location=5223139..5225226] [gbkey=CDS]

MRAFFWAAWLGLCSTPLLAAPLQGFSFAQKDWELACDNTGACRAAGYGVRMGEVSVLLTRNAGSEQHLTA

TVTFAQIEHDIPADSTASLLIDDRDFGALDALDDSHFRLDSDQTTALLQALTNQRKIEFTLNGQHLPLSS

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PLLNQRCDDWQNQAIPAADRQITLTALDKTHSLAQALCWRAPYNDGYTLWLVDNAQLSKPRLLTTEASSY

ADGAIVFLHKERGMADCVTGETRVWDGKTFTPSLKYSTGMCREITPGGTWMLPTFVSQVIPRQQKEADNL

ALRTLYNAVLKAQKSDPELSLNKVAEQFPLTGHITDFTLTYADDTLITTSKPSPDISDDEWQAFLRSSIS

ADSENGKVSFTLIDLDGDGKRDLIIDSYVGGTGLFSYTGVLKRGDDDFAAVNGSDSDNGDDFDAGVPGAL

FSINGRGANQWNHWVKINGQVYALWYNGQFGEDNLYLLRPFSTTSQTPAVTVRYRYTLNSIRSPEKDQPL

TPSLSDGDKADLLRSLEVMQGSLLKDRPASDNDAPICPIPPGTSADEADNYYSGVAVNYIYETVAYIPVW

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>lcl|NZ\_FO834906.1\_prot\_WP\_009484465.1\_4965 [locus\_tag=BN49\_RS26890] [protein=PAAR domain-containing protein] [protein\_id=WP\_009484465.1] [location=5226534..5227010] [gbkey=CDS]

MSQQYTNELTTDVLERLRQPPFTDEFLSELEPQSRQSLVAEMESMLQRPVLHIFRGATIGSLTRHGGVIR

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REGDALPDGFLTVPGDKH

>lcl|NZ\_FO834906.1\_prot\_WP\_016532176.1\_4966 [locus\_tag=BN49\_RS26895] [protein=PAAR domain-containing protein] [protein\_id=WP\_016532176.1] [location=5227010..5228245] [gbkey=CDS]

MALEGYFLFQGDRTVCGGKIITGAEDTEFFGRSQARESDKVTCGKHPGIYRICGGMGDMYEVGGVNRQLA

GSIESYSSCPCRAKFIPQDLDNTYEYNCNAGLAAEREREASRKKLNEAKAKGPQPMPLPALIYATQRAMD

DYGAKDMHHGDLSEEALKERFGLTDVSAKVNPYTLTLVPPAPASSYGVFYPGSLTGSTPVVVSREESVRL

MFDEFRGLAKVFSFHGPYKNIITEMINHMQGNSGTPYSSPLLDRALKEQILNDHSSDSSLLGIKRALDDA

VSYEYGFLPLGKKDDLFDGKGNFKEVNKAVLPKFDRQIDKTNGLVITVHDTWSTHITLESLEVTGDSYRA

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>lcl|NZ\_FO834906.1\_prot\_WP\_009484467.1\_4967 [locus\_tag=BN49\_RS26900] [protein=DUF943 family protein] [protein\_id=WP\_009484467.1] [location=5228238..5228645] [gbkey=CDS]

MNKRLIAGVVAAAVGGYLLWQYLSPVEIVAVHDGNTILVRHFPYLKSRQIAWWEANKAVIQAKYGIPHEG

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>lcl|NZ\_FO834906.1\_prot\_WP\_004153693.1\_4968 [locus\_tag=BN49\_RS26905] [protein=PerC family transcriptional regulator] [protein\_id=WP\_004153693.1] [location=complement(5228981..5229271)] [gbkey=CDS]

MRIRDSIAERLEACGLYRRAASRWIEVMQRCLDDEDREWIRHHRNQCLKKAQRPPAPKEEFADLHQAAKE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004146686.1\_4969 [locus\_tag=BN49\_RS31235] [protein=hypothetical protein] [protein\_id=WP\_004146686.1] [location=5229466..5229588] [gbkey=CDS]

MPSSIPPGIDGCTYQYLFNLLDFRQQIPCDNIHSLYSEAS

>lcl|NZ\_FO834906.1\_prot\_WP\_002885396.1\_4970 [locus\_tag=BN49\_RS26915] [protein=LuxR C-terminal-related transcriptional regulator] [protein\_id=WP\_002885396.1] [location=complement(5229583..5230149)] [gbkey=CDS]

MILVTQDYYLFQGVKNFFPDIIQLDSSGKAILDNEVDEVSLLVDSRSPLCHYDYLVLAAAKSRKRICCIV

LDMRHREEHLLSLKSFLNMSLSPADMATLFGLFLEMNSKRLTKEWFDDLRLSLSEQLMLRLLMAGMTMEE

VAVNLNTSLKSLYRKRTALYERLGLDNFNEACLFIFRNKLLEQTERSL

>lcl|NZ\_FO834906.1\_prot\_WP\_171819486.1\_4971 [gene=pgaA] [locus\_tag=BN49\_RS26920] [protein=poly-beta-1,6 N-acetyl-D-glucosamine export porin PgaA] [protein\_id=WP\_171819486.1] [location=5230783..5233230] [gbkey=CDS]

MERSPYSNTLLFNRNTKLSLSIGLLLLFPALVQGADSLYDQQILQARQGQYAPFLSYLQQYQLRHALTPS

QVADWLQVALWAGQDDEVVKVWRRYQVYMPLPARGTAAAAQALRNQKQWQTSLTLWQQALSQAPGSDDYR

IGYIKTLADARKDGEALSEARRLVAEQASVAHLQTLSYVYLRLGKSWDQLLVDTQILDRDPQNKTALASL

MATLTRNRIDSPALGLANSVELTPAEKRNLQLNAAAELVRLADTPSREEKARYALARTALTQYDAMIAAW

HPDPQAAPDIIRARIDRLGALYASAEYAQVIREYQSLIAQQQTVPDWAIGWVISSFIALKQIEPALTLIH

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ATNDLPQAEARMQRLAATAPGNQGLQIDYAALLQERGLPRAAERQLKAAESLEPASLQLERQQAWVALDL

QEWRQMDLLTDDVVARSPRDLNTQRLARAREIHHLSELRLSVGKGLHSDNPVSGTHDLSFETAIYSPPLA

DSWRLFGGHRFAEGNFEEGKGSRRQLFAGIEWRPRDYWGELELSSVNFHGENKPGVRLSAAHDVSDRWQL

GGELERISQQTPLRALRNGVSANRGEGWLRWSPNERREYRFSAAASRFTDRNRRQEYTLSGKERLWQTPW

LTLDLQPGLSASANSRTDTAYYSPARDLAATAALAVDHTLYQRYDTVWSQQLLAGGGSYWQKNHAAGAIT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530069.1\_4972 [gene=pgaB] [locus\_tag=BN49\_RS26925] [protein=poly-beta-1,6-N-acetyl-D-glucosamine N-deacetylase PgaB] [protein\_id=WP\_016530069.1] [location=5233239..5235254] [gbkey=CDS]

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GSWVDTPAGQPVNFGGLMTPRERFATWEMVRELSRSPLVEIGAHTWASHYGLPANPQGSREPAAANRGWD

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VKDLDNIPRLLIAGNPSLKAFASAVTQIQEADPVRVMHVDLDYVYDPNPVQQAKNIDKLVQRVYDMKISH

VFLQAFSDPQGDGTVKSLYFPNRWLPMRADLFNFVSWQLQTRGNVKVYAWMPVLAFDLASDLPRVQHWDP

QTGKALLARQPYVRLSPWDPRVRQQITDIYEDLARHASFSGILFHDDAVLTDFEDVSPEAVAAWRQTGMA

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LAAYDWTVPMAMPLMESVPIDASQAWLTRLVQAVARHPGALKKTIFELQARDWNRRQQNAIPDQQLADWM

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MTDRIIALCILCLVFGLPLGVAAVFTGELILDFVFFWPLFMSVLWITGGLYFWFQLERHWPWGEDTPPPT

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SSIIGLIKRTQRIYGRVFTVSGVIAAFRRQALADVGYWSPDMITEDIDISWKLQLRHWDIFFEPRALCWI

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177775.1\_4974 [gene=pgaD] [locus\_tag=BN49\_RS26935] [protein=poly-beta-1,6-N-acetyl-D-glucosamine biosynthesis protein PgaD] [protein\_id=WP\_004177775.1] [location=5236575..5237024] [gbkey=CDS]

MNENTLILTEHRVLPRLVDAGLTLLAWLGFLFFLYANLLMQFIAPPSPRWESLMDSLNTALVYLLIAALN

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PPQEESDDA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885391.1\_4975 [locus\_tag=BN49\_RS26940] [protein=DsbA family protein] [protein\_id=WP\_002885391.1] [location=complement(5237070..5237855)] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_020802083.1\_4976 [locus\_tag=BN49\_RS26950] [protein=TerC family protein] [protein\_id=WP\_020802083.1] [location=5238081..5238764] [gbkey=CDS]

MYAFLQQWDMAVIMLQIVAIDLLLGGDNAVVIAMACRKLPPQKRTKAIIIGTVGAILARVLLLAIALYLL

SLPWLKIVGALLLLWIGIKLVRNEEEESEVSSSGSLWRTAITITVADVIMSLDNVLAVAAAGKGHIALVA

LGVAISIPVIVAGSKLVLVLLTRFPAVVLLGGMLIGWIAGSMLVSDPTIRRLFPSAGEGTARLAGTVGAL

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>lcl|NZ\_FO834906.1\_prot\_WP\_020802082.1\_4977 [locus\_tag=BN49\_RS31240] [protein=hypothetical protein] [protein\_id=WP\_020802082.1] [location=complement(5238721..5238834)] [gbkey=CDS]

MRPDGEEKWRKLDAVGVDGAVDKVSLSPAAVGGGAIR

>lcl|NZ\_FO834906.1\_prot\_WP\_002885338.1\_4978 [gene=cbpA] [locus\_tag=BN49\_RS26960] [protein=curved DNA-binding protein] [protein\_id=WP\_002885338.1] [location=5238910..5239827] [gbkey=CDS]

MELKDYYAILGVQPTDDLKTIKTAYRRLARKYHPDVSKENDAEAKFKDLAEAWEVLKDEQRRAEYDQLWQ

HRNDPGFGRQRQTHEQSYSQQDFDDIFSSMFGQQAHQRRRQHAARGHDLEIEVAVFLEETLAEQTRTISY

NLPVYNVFGMIESETPKTLNVKIPAGVVDGQRIRLKGQGTPGENGGPNGDLWLVIHIAPHPLFDIVGHNL

EIVLPLAPWEAALGAKVTVPTLKESILLTVPPGSQAGQRLRIKGKGLVSKTHTGDLFAVIKIVMPPKPDE

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885324.1\_4979 [gene=cbpM] [locus\_tag=BN49\_RS26965] [protein=chaperone modulator CbpM] [protein\_id=WP\_002885324.1] [location=5239827..5240132] [gbkey=CDS]

MATVTVTFTITELCLRTGVSEEELTEIVGLGMIEPHQPQADTWLFDDSAVTIVHRAVRLRNELELDWPGI

AVALTLLDENARLTRENRLLQQRLARFLAHG

>lcl|NZ\_FO834906.1\_prot\_WP\_016528813.1\_4980 [locus\_tag=BN49\_RS26970] [protein=chromosome partitioning protein ParB] [protein\_id=WP\_016528813.1] [location=complement(5240382..5240753)] [gbkey=CDS]

MTLDRRKVLIYLRPDISASERFADAKIEAHHRGDRGDMSRTALLAGLALGEVDSRLPSMLAALLAEDTKP

ETLRKMLASFLEIQPASPAPAAAAAAAPAKAPEPPAPVSESVSARNLAGSLPD

>lcl|NZ\_FO834906.1\_prot\_WP\_016528812.1\_4981 [locus\_tag=BN49\_RS26975] [protein=plasmid stability protein StbA] [protein\_id=WP\_016528812.1] [location=complement(5240763..5241719)] [gbkey=CDS]

MRIFIDDGSTNIKMLWEQDGETFTHISPNSFKRGWSATFGSGKPFNYTVDDEKYSFDLITPDALPTNNID

WQYSPLNSIAVHHALLTSGLEPQDVEIVVTLPLTEFYDEDAQYRFDNIERKKKSLLREVKLNKGVVFNIT

KVTVRPESIPAGISLCDELKPSHSVLIIDLGGTTLDISMVAGQMTSVSRIYGDPKLGVSLVTDAVKLALA

RANTDTSSYNVDQIIINRHDEEYLTDNINDPDAVTEVKKVINNSIERLTTRVLTAIDSFKGYSHAIVIGG

GAPLVADAIRERMGLREDRFVVAEEPQFALVRGLKIIG

>lcl|NZ\_FO834906.1\_prot\_WP\_042940285.1\_4982 [locus\_tag=BN49\_RS31245] [protein=hypothetical protein] [protein\_id=WP\_042940285.1] [location=complement(5241867..5241989)] [gbkey=CDS]

MRKPLTKERRDALFLSKKQCLKKTERENFSSLFYLNYFSF

>lcl|NZ\_FO834906.1\_prot\_WP\_019724884.1\_4983 [gene=melB] [locus\_tag=BN49\_RS26985] [protein=melibiose:sodium transporter MelB] [protein\_id=WP\_019724884.1] [location=complement(5241995..5243410)] [gbkey=CDS]

MSISMTTKLSYGFGAFGKDFAIGIVYMYLMYYYTDIVGLSVGVVGTLFLVARILDAIADPIMGWIVNCTR

SRWGKFKPWILIGTITNSVVLYMLFSAHHFSGGALLAWVWLTYLLWGFTYTIMDVPFWSLVPTITLDKRE

REQLVPYPRFFASLAGFVTAGVTLPFVNAVGGADRGFGFQMFTLVLIAFFVVSTLVTLRNVHEVYSSDSG

VSEDSSHLSLRQMVALIYKNDQLACLLGMALAYNTAANIIAGFAIYYFTYVIGSAEMFPYYMSYAGAANL

LTLILFPRLVKGLSRRILWAGASIMPVLGCGVLLLMALGGVYNIALISLAGVLLNIGTALFWVLQVIMVA

DTVDYGEYTMNIRCESIAYSVQTLVVKAGSAFAAWFIAIVLGIIGYVPNVVQSSHTLLGMQAIMIALPTL

FFALTLFLYFRYYKLNGDMLRRIQIHLLDKYRRVPENDVEPERPIVVPNQV

>lcl|NZ\_FO834906.1\_prot\_WP\_042940283.1\_4984 [locus\_tag=BN49\_RS26990] [protein=alpha-glucosidase/alpha-galactosidase] [protein\_id=WP\_042940283.1] [location=complement(5243503..5244855)] [gbkey=CDS]

MSAPKITFIGAGSTVFVKNILGDVFQRPALKSAHIALMDIDETRLEESHIVVRKLMDSVGANGEISCHRD

RKTALQGADFVVVAFQIGGYEPCTVTDFAVCKRHGLEQTIADTLGPGGIMRALRTIPHLWAICDDMTEVC

PDATMLNYVNPMAMNTWAMYARYPHIKQVGLCHSVQGTAEELARDLDLDPADLRYRCAGINHMAFYLSLE

KKLADGSYVSIYPDLLQAYADGRAPNPNLHGNPRCENIVRYEMLKKLGYFVTESSEHFAEYTPWFIKPGR

DDLLARYKVPLDEYPKRCVEQLANWHQELESYKRGERIEVKPSREYASTIMNAIWTGEPSVVYGNVRNDN

LIDNLPQGCCVEVACLVDANGIQPTKVGALPAHLAALMQTNINVQTLLTEAILTENRDYVYYATMMDPHT

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>lcl|NZ\_FO834906.1\_prot\_WP\_016528809.1\_4985 [gene=melR] [locus\_tag=BN49\_RS26995] [protein=transcriptional regulator MelR] [protein\_id=WP\_016528809.1] [location=5245095..5246033] [gbkey=CDS]

MEHRFTSLPPDPFMCSSDEKQSRSPLALYSEYQRMDIELRPPHAMPTSHWHGQVEVNVPFDGDVEYLINN

EVVRIEKGYITLFWACTPHQLTRPGDCQQMAIFNLPMHLFLSWPLDRELINHVTHGMVIKSLAAQQLSAF

EVRRWQQELSHENEQIRQLAIDEIALMLKRLSLAGWQPILVNKTSRTHKNSVSRHAQFYVSQMLEFIAAH

YDQALTVNAVAEHVKLNPNYAMGVFQRVMQQTMKQYITAMRINHVRALLSDTDKTILDIALTAGFRSSSR

FYSTFTRYVGMPPHQYRKLSQQRRHGLALPKA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885227.1\_4986 [gene=proP] [locus\_tag=BN49\_RS27000] [protein=glycine betaine/L-proline transporter ProP] [protein\_id=WP\_002885227.1] [location=complement(5246083..5247585)] [gbkey=CDS]

MLKRKKIKPITLKDVTIIDDGKLKKAITAASLGNAMEWFDFGVYGFVAYALGKVFFPDANPSVQMIAALG

TFSVPFLIRPLGGLFFGMLGDKYGRQKILAITIVIMSISTFCIGLIPSYATIGIWAPILLLLCKMAQGFS

VGGEYTGASIFVAEYSPDRKRGFMGSWLDFGSIAGFVMGAGVVVLISSVVGEQNFLDWGWRIPFFLALPL

GIIGLYLRHALEETPAFQQHVDTMEQGDREGLQDGPKVSFKEIATKHWRSLLTCIGLVISTNVTYYMLLT

YMPSYLSHNLHYSEDHGVLIIIAIMVGMLFVQPVIGMLSDRFGRRPFILIGSVALFALSIPAFIMINSNV

TSLIFAGLLLLAVVLNCFIGVMASSLPAMFPTHIRFSALASAFNISVLIAGLTPTLAAWLVETTQNLMMP

AYYLMVIAVVGMATGLSMKETANRPLKGATPAASDIQEAKEILGEHYDNIEQKIEDIDQEIADLQAKRSR

LVQQHPRIND

>lcl|NZ\_FO834906.1\_prot\_WP\_004177783.1\_4987 [locus\_tag=BN49\_RS27010] [protein=zinc ribbon domain-containing protein YjdM] [protein\_id=WP\_004177783.1] [location=5248130..5248465] [gbkey=CDS]

MQLPHCPKCDSTYTYEDSGMYICPECAHEWNPAEATEESDILIVKDANGNLLADGDSVTVVKDLKVKGSS

SMLKIGTKVKNIRLVEGDHNIDCKIDGFGPMKLKSEFVKKN

>lcl|NZ\_FO834906.1\_prot\_WP\_002885221.1\_4988 [gene=yjdN] [locus\_tag=BN49\_RS27015] [protein=VOC family metalloprotein YjdN] [protein\_id=WP\_002885221.1] [location=5248694..5249128] [gbkey=CDS]

MSLSPYLAFAGNCAEAIAFYQQTLGAELMFKMTFGEMPPPAQEASDGCPSGQKMADDAIAHASLRINNGE

LMLSDSAFGPDVHYAGFTLVLDPSDVAEGQRWFDALAVGGRIEMAWQETFWAHGFGKVVDRFGVPWMINV

VKQG

>lcl|NZ\_FO834906.1\_prot\_WP\_004177785.1\_4989 [gene=phnF] [locus\_tag=BN49\_RS27020] [protein=phosphonate metabolism transcriptional regulator PhnF] [protein\_id=WP\_004177785.1] [location=5249284..5250009] [gbkey=CDS]

MHLSRHPTSYPTRYQEIAARLEQELRHHYRCGDYLPAEQQLATRFDVNRHTLRRAIDQLVERGWVQRRQG

VGVLVLMRPIDYPLNAQARFSQNLLEQGSDPTSEKLLSVLRPASAHVAEAFGINEGENVIHLRTLRRVNG

VALCLIDHYFADLRFWPVLQTFSHGSLHDLLRDRLDVELTRVRTKISARRAQAKESKLLEIPNMAPLLCV

RTLNSREGESLTAEYSVSLTRADMIEFTMEH

>lcl|NZ\_FO834906.1\_prot\_WP\_002885214.1\_4990 [gene=phnG] [locus\_tag=BN49\_RS27025] [protein=phosphonate C-P lyase system protein PhnG] [protein\_id=WP\_002885214.1] [location=5250010..5250462] [gbkey=CDS]

MHFDTATRQRWMSVLAHSEPQDLLARMQSLQLAPEYELIRTPETGLVQLQARMGGIGDRFFAGDATLTRA

AVRLADGTLGYSWILGRDRPHAERCAAIDALLQSPRHFHTLMETLITPLEALRSARIEARRAEVNASRVD

FFTLVRGDNV

>lcl|NZ\_FO834906.1\_prot\_WP\_002885207.1\_4991 [gene=phnH] [locus\_tag=BN49\_RS27030] [protein=phosphonate C-P lyase system protein PhnH] [protein\_id=WP\_002885207.1] [location=5250459..5251043] [gbkey=CDS]

MTLQPAFTLAVQDAQHSFRRLLKAMSEPGVIVSLQQLQHGWQPLNVASTSLLLTLADHETPVWLASALRN

DLVGQNLRFHTGAPLVDQPQQAVFAVANDGISAEQLNVLSAGTVTAPETGVTLIVQLASLSGGRMLRLTG

AGIAEERMIAPQLPDCIIDELTERPHPFPLGIDLILTCGERLLAIPRTTHVEVC

>lcl|NZ\_FO834906.1\_prot\_WP\_004177786.1\_4992 [locus\_tag=BN49\_RS27035] [protein=carbon-phosphorus lyase complex subunit PhnI] [protein\_id=WP\_004177786.1] [location=5251044..5252108] [gbkey=CDS]

MYVAVKGGEKAIRAAHALQEQKRRGDGRLPELSVEQIGDQLSLAVDRVMTEGGIADRELAALALKQASGD

NVEAIFLLRAYRTTLPRLAVSEPINTAEMRLERRISAVYKDIPGGQLLGPTYDYTHRLLDFTLLANGEAP

SVQQADGEAEPTPHVFSLLTQQGLAKTEEDRGTPPDDITRTPPVYPCSRSSRLQQLMRGDEGYLLALAYS

TQRGYGRNHPFAGEIRSGYVQVEIVPEELGFSVNIGELLLTECEMVNGFVAPQEEPPHFTRGYGLTFGMS

ERKAMAMALVDRALQAPDYDEEIAGPAQDEEFVLAHADNVEAAGFVSHLKLPHYVDFQAELALLKRLQRE

NERG

>lcl|NZ\_FO834906.1\_prot\_WP\_002885202.1\_4993 [locus\_tag=BN49\_RS27040] [protein=alpha-D-ribose 1-methylphosphonate 5-phosphate C-P-lyase PhnJ] [protein\_id=WP\_002885202.1] [location=5252101..5252949] [gbkey=CDS]

MANPLTGYNFAYLDEQTKRMIRRAILKAVAIPGYQVPFGGREMPMPYGWGTGGIQLTASVIGENDVLKVI

DQGADDTTNAVSIRQFFKRVTGVATTERTEDATLIQTRHRIPETPLVEDQILIYQVPIPEPLRFIEPRET

ETRTMHALEEYGVMQVKLYEDIARFGHIATTYAYPVKVNGRYVMDPSPIPKFDNPKMHMMPALQLFGAGR

EKRIYAVPPYTPVESLDFDDHPFTVQEWDEPCAICGSRHSYLDEVVLDDSGQRMFVCSDTDYCRQQSEGQ

KK

>lcl|NZ\_FO834906.1\_prot\_WP\_004178305.1\_4994 [gene=phnK] [locus\_tag=BN49\_RS27045] [protein=phosphonate C-P lyase system protein PhnK] [protein\_id=WP\_004178305.1] [location=5252946..5253704] [gbkey=CDS]

MNQPLLAVNNLTHLYAPDKGFRDVSFELWPGEVLGIVGESGSGKTTLLKAISARLTPQQGEVLYQQRSLY

AMSEAERRRLLRTEWGVVHQHPMDGLRRQVSAGGNIGERLMATGARHYGNIRATAEKWLQEVEIPPSRID

DLPTTFSGGMQQRLQIARNLVTQPKLVFMDEPTGGLDVSVQARLLDLLRGLAVELNLAVVIVTHDLGVAR

LLANRLLVMKQGQVVESGLTDRVLDDPHHPYTQLLVSSVLQN

>lcl|NZ\_FO834906.1\_prot\_WP\_016528808.1\_4995 [gene=phnL] [locus\_tag=BN49\_RS27050] [protein=phosphonate C-P lyase system protein PhnL] [protein\_id=WP\_016528808.1] [location=5253812..5254492] [gbkey=CDS]

MIRVENVHKTFVLHQQHGVRLPVLADASLTVNAGECVVLHGHSGSGKSTLLRSLYANYLPDSGHIHIRHG

DEWVDLVTATPRKVLEVRKITIGWVSQFLRVIPRISALEVVMQPLLDLGTPREASAAKAAQLLTRLNVPE

RLWHLAPSTFSGGEQQRVNIARGFAVDYPILLLDEPTASLDGKNSAAVVNLIHDAKARGAAIVGIFHDEE

VRRQVADRLHSMGMTA

>lcl|NZ\_FO834906.1\_prot\_WP\_009484481.1\_4996 [gene=phnM] [locus\_tag=BN49\_RS27055] [protein=alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase] [protein\_id=WP\_009484481.1] [location=5254489..5255625] [gbkey=CDS]

MIINNVKLVLDDEVVHGSLEVQDGRILAFAESQSRLPQALDGEGGWLLPGLIELHTDNLDKFFTPRPKVD

WPAHSAMSSHDAMMVASGITTVLDAVAIGDVRDGGDRLENLEKMVNAVEETQKRGLNRAEHRLHLRCELP

HHTTLPLFEKLIDRESVSMVSLMDHSPGQRQYADRSKYRDYYQGKYHLTHDEMDRFEAEQMALAATWSQP

NRQTIAAMCRARRIALASHDDATEAHVAESHQLGSVIAEFPTTLAAAQASRQHGMHVLMGAPNIVRGGSH

SGNVAAHQLASHGLLDILSSDYYPASLLDAAFRIADAEDNAFTLPQAIRLVSQHPAQALGLDDRGVIAEG

KRADLVLAHRRGEHIQIDHVWRQGKRVF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151727.1\_4997 [gene=phnN] [locus\_tag=BN49\_RS27060] [protein=ribose 1,5-bisphosphokinase] [protein\_id=WP\_004151727.1] [location=5255625..5256188] [gbkey=CDS]

MPGKLIWLVGPSGSGKDSLLAALRQREHPQLLVAHRYITRPFNAGSENHIALSEHEFFTRAEQHLFALSW

HANNTYYGIGVEIDLWLHAGFDVVANGSRAHLALARERYGEVLVPICLAVSPPVLRQRLEQRGRENALEI

AQRLERAARYKPDNCLTLNNDGSLRQSVDEFFRLLRSHAAREADQLV

>lcl|NZ\_FO834906.1\_prot\_WP\_046043972.1\_4998 [gene=phnP] [locus\_tag=BN49\_RS27065] [protein=phosphonate metabolism protein PhnP] [protein\_id=WP\_046043972.1] [location=5256204..5256962] [gbkey=CDS]

MSLTLRLTGTGGAQLVPVFGCDCAACRRARREESHRRRPCSGVVTFNSAVTLLDAGRPDLMEHHPAGSFQ

QVLLTHYHLDHVQGLFPLRWGVGASIPVYGPPDDAGCDDLLKHPGLLDFNHTVTPFVMFNLQGLRVTPLP

LNHSKLTFGYLLESAHSRLAWLSDTAGLPDKTLKFLLNNRPQAMIIDCSHEPRAQTPRNHNDLNTVRSLN

QVIGCPRVILTHISHQFDVWMMDNPLPTGFEAGYDGMEIALD

>lcl|NZ\_FO834906.1\_prot\_WP\_004151729.1\_4999 [locus\_tag=BN49\_RS27070] [protein=membrane protein] [protein\_id=WP\_004151729.1] [location=complement(5256984..5257337)] [gbkey=CDS]

MKRYATALLFCTLSLTSLAARADIIDDAIGNIQQAINDAYNPGSSRSDDDDRYDDDGRYDDGRYQGSRQQ

SRDSQRQYDERQRQLDERRRQLDERQRQLDRDRRQLESDQRRLDDSY

>lcl|NZ\_FO834906.1\_prot\_WP\_016530513.1\_5000 [locus\_tag=BN49\_RS27075] [protein=ATP-binding protein] [protein\_id=WP\_016530513.1] [location=complement(5257408..5259693)] [gbkey=CDS]

MTARRHPFFTSARGRLLSFNLLMGVVTLLVSGVAVFGFHHASQLQEQVQRQTLNDMRGSMDLARDTANVA

TAAVRLSQVVGALEYKSEAERLLATQQALKHSLAQLAAAPLAQQEQARVANIIRRSNALQQSVAEMLERG

QRRHLQRNALLSSLYQNQSNLRHLADLNDRGGDKAIDPRRLAEMDRLIVAAIHTVTPRSIVLQLDQLRGA

LPTRSADPALAFVLPDVNRELATLAPLSAQLEESDLTISWYMYHIKALVALLNEDINQYVTRVAEASEQR

AAQSHRELRSISMFILLSALLALAITGCAGWYIYRNLGSNLTAISRAMSRLAQGEPNVSVPALQRRDELG

ELARAFNVFARNMASLEHTTRLLKEKTNQMEIDRIKRQELEEALLHSQKMKAVGQLTGGLAHDFNNLLAV

IIGSLELVEPDARDAPRLSRALKAAERGALLTQRLLAFSRKQALHPQAVAMAPLLENLSELMRHSLPATL

SLKIEAQSPAWPAWIDVGQLENALINLVMNARDAMAGRDGVIKIRTWNQRVTRSSGQRQDMVALEVIDHG

SGMSQAVKARVFEPFFTTKATGSGSGLGLSMVYGFVRQSGGRVALESAPGQGTTVRLQLPRALTEVEKEV

APAVDEPPPAGERLALVLEDEEDVRQTLCEQLHQLGWLTLETASGEEALQLLEASPDIALLISDLMLPGA

LSGADVIHTARRRFPALPVLLISGQDLRPAQNPALPEVEWLRKPFTRAQLAQALSAAYARI

>lcl|NZ\_FO834906.1\_prot\_WP\_004210021.1\_5001 [locus\_tag=BN49\_RS27080] [protein=sugar ABC transporter ATP-binding protein] [protein\_id=WP\_004210021.1] [location=5259873..5261393] [gbkey=CDS]

MTATPVLEMRHIAKAFGKFYALKGVDLTVWPGEIHALMGENGAGKSTLMKILAGAYTATSGEILIDGKPQ

TIRGPKDALAAGITLIYQEMQLAPNLTVAENIFLGSELARGGLVQRKAMLSQAQAVIDRLGAQFKASDRV

MTLTIAEQQQVEIARALHRQSRILVMDEPTAALSSRETQRLFELILRLRDEGMAIIYISHRMAEVYELSD

RVSVLRDGQYVGSLVRDKLNAPELVRMMVGRPLSDLFNKERDIPRGQPRLRVEDLTDGGKVKPSSLVVHA

GEIVGLAGLVGAGRSELAQLIFGVRKATAGVIEIDGEPVVIHSPREAIDLGIGFLTENRKEQGLFLELAA

QENITMATLERDATWGMLNRRKAQTISDDAIQLLNIRVPHAQVRAGGLSGGNQQKLLISRWVAIGPRILI

LDEPTRGVDVGAKSEIYRIMNDMARQGVAILMISSELPEVVGMSDRVYVMREGVIAGELQAGDISQESIM

TLATGVTDSHLKAGQL

>lcl|NZ\_FO834906.1\_prot\_WP\_002885172.1\_5002 [locus\_tag=BN49\_RS27085] [protein=ribose ABC transporter permease] [protein\_id=WP\_002885172.1] [location=5261390..5262388] [gbkey=CDS]

MSIPKETSAPVAKSASAKKMLMGDLMQTVGILPILILIVAVFGFIAPNFFTESNLLNITRQASINIVLAA

GMTFIILTGGIDLSVGSILGTTAVAAMVVSLIPAFALLSIPAALMLGLLLGLFNGALVAFAGLPPFIVTL

GTYTALRGAAYLLADGTTVINSDISFEWIGNDYLGPVPWLVVIALAVIAVCWFILRRTTLGVHIYAVGGN

MQAARLTGIKVWLVLLFVYGMSGLLSGLGGVMSASRLYSANGNLGVGYELDAIAAVILGGTSFVGGIGTI

TGTLVGALIIATLNNGMTLMGVSYFWQLVIKGAVIIIAVLIDKYRTRHHQSA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885156.1\_5003 [locus\_tag=BN49\_RS27090] [protein=ABC transporter substrate-binding protein] [protein\_id=WP\_002885156.1] [location=5262419..5263360] [gbkey=CDS]

MRLKPIVTALCAGALLAASPFASAKELKAIGVTVGDLANPFFVQITKGAELEARKLAGDNVKVTLVSSGY

DLGQQVAQIDNFIAAKVDMIILNAADSKGIGPAVKRAKEAGIVVVAVDVAAEGADATITSDNTQAGELAC

KYISDRLNNKGNVVIINGPPVSAVQNRVEGCETEFKKHPDIKILSANQNAKGSREGGLEVMTSLLAANPK

IDGVFAINDPTAIGADLAAKQAQRSEFFIVGVDGSPDGEEALKRKNSLFVATPAQDPQVMAAKAVEIGYD

ILQGKPAPTAPVLIPVTMIDKNNVSSYKGWTVK

>lcl|NZ\_FO834906.1\_prot\_WP\_004221949.1\_5004 [locus\_tag=BN49\_RS27095] [protein=carbohydrate kinase family protein] [protein\_id=WP\_004221949.1] [location=5263435..5264442] [gbkey=CDS]

MERKGIIAAGNMLVDHVHQIGQWPERGWLVEIVHSERATGGAPLNVLLTLAKMHAGLPLQAVGLIGEDND

GDYITAMLDQYHINRQLVQRTSSAPTSMTQVMTDAEGQRTFFHSPGANRLLDLPAFEPLDAPLKIFHLGY

LLLLESLDRPDEVYGTRSARLLAQMRERGYEVSLDLVSRKGDPRYRPLVLPALKHLDYLTINELEASEFS

GLEIRLPNGEPHVANIARAASALLDAGVRQRVVIHCPEGAWGVSRTEAGRWVPSWRLPPEEIIGSVGAGD

AFCAGLLYGSHERWPLTASLQLAHACARASLQAVNAIDGAKTLPELQAFIQLQNV

>lcl|NZ\_FO834906.1\_prot\_WP\_004146663.1\_5005 [locus\_tag=BN49\_RS27100] [protein=nucleotidyl transferase AbiEii/AbiGii toxin family protein] [protein\_id=WP\_004146663.1] [location=complement(5264567..5265484)] [gbkey=CDS]

MDIQAPYYRQVALLMQVLPYVAVEREFALKGGTAINLFIRDFPRLSVDIDLAWVPLESRAIALPHIRDAL

ARIAANLQQQAGMSAVLQANRSDEMRVIVTTDSAQIKIEVSPVARGTLYPPQEREVVGAVEDVFGYASLP

VVSLPDLYGGKLCAALDRQHPRDFYDVKLLLDAQELDRPIFNGFIAYLLSHNRPLAEVLNPRWKDIAEPF

YREFSGMTFETIALEELTAVPNRMIAALKSCFTQQDVDFLLSFKRGEPDWRLAPEMRIQDLPAVQWKLRN

IHQMPAIKRAESLDKLEKVLAEWRS

>lcl|NZ\_FO834906.1\_prot\_WP\_016531766.1\_5006 [locus\_tag=BN49\_RS27105] [protein=type IV toxin-antitoxin system AbiEi family antitoxin] [protein\_id=WP\_016531766.1] [location=complement(5265490..5266248)] [gbkey=CDS]

MATKLNWLLQNSAPGDVILQSWLSQHAISPSLAFKYAQSGWLKKRGNGVYARAGREPEWNDALACLQNQL

AAPVYVAGLSSLVWQGRSHYLQLKQNQCWLSVENKALLPKWFRGFPGVEWIVISGKKLPVLDDRYRVTLD

IKGKKLIGSAPELAAYELLSAVPGTLSFNHAAELFQGLVNLNPRKVEYLLSVSQSVQAKRLYLFFASFYE

HGWLKRIDSQKIDLGAGKRQIVENGKFNAQYQITVPERFQKE

>lcl|NZ\_FO834906.1\_prot\_WP\_004177810.1\_5007 [locus\_tag=BN49\_RS27110] [protein=response regulator transcription factor] [protein\_id=WP\_004177810.1] [location=complement(5266334..5267062)] [gbkey=CDS]

MKPVILVVDDDRAMGELLSDVLGAHAFEVLVSQTGNDALATVAQRADIALVLLDMILPDTYGLQVLQQLQ

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WRLDTTRCELYNPQQQAIPLTQGEYGLLLALAQNARRVLNREQLLALTHNESTEVFDRTIDVLIMRLRRK

IELNPHQPTLIKTLRGLGYVFSADVTHSEKAA

>lcl|NZ\_FO834906.1\_prot\_WP\_012737173.1\_5008 [locus\_tag=BN49\_RS27125] [protein=formate dehydrogenase H subunit alpha, selenocysteine-containing] [transl\_except=(pos:418..420,aa:Sec)] [protein\_id=WP\_012737173.1] [location=5267335..5269482] [gbkey=CDS]

MKKVVTVCPYCASGCKINLVVDNGKIVRAEAAQGKTNQGTLCLKGYYGWDFINDTQILTPRLKTPMIRRQ

RGGKLEAVSWDEALDYVATRLSAIKAKYGPDAIQTTGSSRGTGNETNYVMQKFARAVIGTNNVDCCARVU

HGPSVAGLHQSVGNGAMSNAITEIDNTDLVFIFGYNPADSHPIVANHVINAKRNGAKIIVCDPRKIETAR

IADMHIALKNGSNIALLNAIGHVIIEEDLYDKSFVASRSEGFEEYRKIVEGYTPESVEEITGVSAQEIRA

CARMYASAKSAAILWGMGVTQFYQGVETVRSLTSLAILTGNLGKPSVGVNPVRGQNNVQGACDMGALPDT

YPGYQYVKFPENREKFAKAWGVESLPAHTGYRISELPHRAAHGEVRAAYIMGEDPLQTDAELSAVRKAFD

DLELVIVQDIFMTKTASAADVILPSTSWGEHEGVYTAADRGFQRFFKAVEPKWDLKTDWQIISEIATRMG

YPMHYNNTQEIWDELRHLCPDFYGATYEKMGELGYVMWPCRDESDADQGTSYLFKEKFDTPNGLAQFFTC

DWVAPIDKLTDEYPMVLSTVREVGHYSCRSMTGNCAALAALADEPGYAQINTADAERLGIEDEELVWVNS

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EYNKLKSRLRESAMG

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MKYLFLFLLVFTSGAAVATEPGSQYQQQAEAGDRRAQYYLADTWVSSGDYQKAEYWAQKAAAQGDGDALA

LLAQLKIRNPQQADYPQARQLAEKAVEAGSKSGEIVLARVLVNRQAGATDVAHAITLLQDAARDSESDAA

VDAQMLLGLIYASGVHGPEDDVKASEYFKGSSSLSRTGYAEYWAGMMFQQGEKGFIEPNKQKALHWLNVS

CLEGFDTGCEEFDRISKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004146659.1\_5010 [gene=gltP] [locus\_tag=BN49\_RS27135] [protein=glutamate/aspartate:proton symporter GltP] [protein\_id=WP\_004146659.1] [location=complement(5270435..5271748)] [gbkey=CDS]

MKKTKKVSLAWQILLALVLGILLGSYLHYHAESRDWLISNLLTPAGDIFIHLIKMIVVPIVISTLVVGIA

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MGTILSLVPTNIVASMAKGDMLPIIFFSVLFGLGLSSLPATHREPLVTVFRSISETMFKVTHMVMRYAPV

GVFALISVTVATFGFASLWPLAKLVLLVYFAILFFALVVLGIVARLCGLSIWILIRILKDELILAYSTAS

SESVLPRIIEKMEAYGAPASITSFVVPTGYSFNLDGSTLYQSIAAIFIAQLYGIDLSIWQEITLVLTLMV

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>lcl|NZ\_FO834906.1\_prot\_5011 [locus\_tag=BN49\_RS27140] [protein=hypothetical protein] [pseudo=true] [location=complement(5271860..5272059)] [gbkey=CDS]

MIKLGEISSNETLKRNNYANEFIETEAVKFFYYKYLCNITGGNSLLYA\*KQRKALFLKACAACRAN

>lcl|NZ\_FO834906.1\_prot\_WP\_002885145.1\_5012 [gene=acs] [locus\_tag=BN49\_RS27145] [protein=acetate--CoA ligase] [protein\_id=WP\_002885145.1] [location=5272160..5274118] [gbkey=CDS]

MSQIHKHPIPANIAERCLINPDQYKAQYQQSITDPDTFWGEQGKILDWMRPYTRVKNTSFAPGNISIKWY

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MVPEAAVAMLACARIGAIHSVIFGGFSPEAVAGRIIDSSSRLVITADEGLRAGRAIPLKKNVDDALKNPN

VKSIEHVVVLKRTGGNIDWQEGRDLWWSDLIANASAEHRPVEMNAEDPLFILYTSGSTGKPKGVLHTTGG

YLVYAATTFKYVFDYHPGDIYWCTADVGWVTGHSYLLYGPLACGATTLMFEGVPNWPTPARMCQVVDKHK

VSILYTAPTAIRALMAEGDKAIEGTDRSSLRILGSVGEPINPEAWEWYWKKIGNEKCPVMDTWWQTETGG

FMITPLPGAIELKAGSATRPFFGVQPVLVDNEGLPLDGATEGNLAIADSWPGQARTLFGDHERFEQTYFS

TFKNMYFSGDGARRDEDGYYWITGRVDDVLNVSGHRLGTAEIESALVSHPKIAEAAVVGIPHNIKGQAIY

AYVTLNHGEEPTPELYAEVRNWVRKEIGPLATPDVLHWTDSLPKTRSGKIMRRILRKIAAGDTSNLGDTS

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177812.1\_5013 [locus\_tag=BN49\_RS27155] [protein=DUF485 domain-containing protein] [protein\_id=WP\_004177812.1] [location=5274302..5274613] [gbkey=CDS]

MNEQLCQRIENSAHFRELVASRQRFAAILSVIMLVIYVGFILLIAFAPGWLGTPLHAGTSVTRGIPLGIG

VIVISFILTGIYVWRANGEFDRLTKSVLNEVKA

>lcl|NZ\_FO834906.1\_prot\_WP\_042941673.1\_5014 [gene=actP] [locus\_tag=BN49\_RS27160] [protein=cation/acetate symporter ActP] [protein\_id=WP\_042941673.1] [location=5274613..5276265] [gbkey=CDS]

MKRVLTALAATLLPLGAHAADAITGAVQRQPTNWQAIVMFLIFVALTLYITYWASKRVRSRSDYYTAGGN

ITGFQNGLAIAGDFMSAASFLGISALVYTSGYDGLIYSLGFLVGWPIILFLIAERLRNLGRYTFADVASY

RLKQGPIRTLSACGSLVVVALYLIAQMVGAGKLIQLLFGLNYHVAVVLVGVLMVLYVLFGGMLATTWVQI

IKAVLLLCGASFMAFMVMKHVGFSFNNLFTEAMAVHPKGAAIMSPGGLVKDPISALSLGLGLMFGTAGLP

HILMRFFTVSDAKEARKSVFYATGFMGYFYILTFIIGFGAIMLVGANPAFKDAAEQLIGGNNMAAVHLAD

AVGGNLFLGFISAVAFATILAVVAGLTLAGASAVSHDLYANVFRKGATERQELKVSKITVLILGVVAILL

GILFENQNIAFMVGLAFSIAASCNFPIILLSMYWSKLTTRGAMVGGWLGLLTAVILMILGPTIWVQILGH

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885139.1\_5015 [locus\_tag=BN49\_RS27165] [protein=type 1 fimbrial protein] [protein\_id=WP\_002885139.1] [location=complement(5276312..5277409)] [gbkey=CDS]

MKKLILLLILALCPVYSWAACTGTNYGDVSMTNLPEKILVNAGSYTAGTVLYDSGKITRSQTELLNCEGS

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LFDSFASTHYTPAYQLQLVATGGAIASKSQLSFSDPVATVSAKDKKGTIAISQLHISGTTSIQLIPMGCI

VGSNNLSFSMGSINASEFNTATKVGSARQSLSLSCEPGTNVSMRVAAASASGDNPDNTVMALTAEQNAAT

GVGVQLNLNGKALPLNTDISLYTSSRATVTNSGADASYSYFTNPDSPGGAAAMQTLALSTNYYRTGSAVT

AGTANATGVITFTYN

>lcl|NZ\_FO834906.1\_prot\_WP\_004151734.1\_5016 [locus\_tag=BN49\_RS27170] [protein=fimbrial protein] [protein\_id=WP\_004151734.1] [location=complement(5277429..5277977)] [gbkey=CDS]

MNMRDGSTRGLLVAILLLSLPALAYEGSSTVNFNVTGTIEAPSCEVAVEPSNSIDLGTVSSQTFSGHAGA

SGASVPVKLVFSSCSADASAVTIAFSGTSFDSTHASIYKNFQTGSNGASGVGLQLQSMADQQPLGPGDQY

LYTFGDDADIHTFNMVARMFSPYGQVRSGMVGFTATFDVAYK

>lcl|NZ\_FO834906.1\_prot\_WP\_032105257.1\_5017 [locus\_tag=BN49\_RS27175] [protein=fimbrial biogenesis outer membrane usher protein] [protein\_id=WP\_032105257.1] [location=complement(5278013..5280592)] [gbkey=CDS]

MIMVCQGRNIPLSFSSVELLFSTKSICVAIILCLSTLPSRAEAGEYFNPNLLEVAESPAASVDLSYFSQD

GIPPGTYHLDVYINDKYVSSDSLTFQEISHDAGATASPCLSAEYLNSWLINTTAYPQLFEAGETCARLSA

IPGMTFSVSLAQQRIDFTVPQAAMLNRPRDYIPESQWQQGINAGLLNYSVTGQRNAPRHNGATIDSQFVS

LQPGLNLGPWRLRNYSTYSHSDNNSRWESVYSYLARDIHTLRSQLVVGNTYTSSGIFDSLSFTGLQLSSD

KEMLPDSLHGFAPTIRGIARTTAEVSVYQNGYSIYKTTVAPGAFEINDLYATGSAGDLYVNIKESDGSEQ

NFVVPFASLAILQREGQLDYALSSGRTRSGSSDDKEYNFIQSSLAYGATSNITLYTGFQQAEDKYTNLLL

GAGFNLGTIGALSFDGSQSWADVKTSDTASSTSKEQGQSYRVRFSKSFLQTGTSFSVAGYRYSTSGYYSF

QDFVDNSSTQRDCCTQSGRTKGRFDASLSQTLFGYGSLSLSLVNETYWDSSRMESVGVGYSGSIGKASYF

INYSYNRNVQRTDDSSNNRPSSDTVVSLTLSIPLGETLSANYTLNHGRHNDTTHSVGLNGSAFEDRSLNW

SVLEGYNTQDKSTSGNLSVNYQGSKGDVAGGYGYDRYSNHYNYSLRGGMVAHAGGLTLSRFLGESSALVE

TPGVSDVTVRGQTNVTTDAAGYAVVPYVRPYHRNSLALDEQEIPGAEVDNVARTVVPTRNAIVKVKYDTR

IGYKAMLTLRTRNGVVPFGALVTLDNDHGSASRSNIVGDEGQVYLTGLQKKGQLLARWGEKSSEQCTVHY

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151735.1\_5018 [locus\_tag=BN49\_RS27180] [protein=fimbrial assembly chaperone] [protein\_id=WP\_004151735.1] [location=complement(5280546..5281235)] [gbkey=CDS]

MRYPFFAIGLLLSSSFAQASVVVGGTRLVFDGTKNNAVITVENKDQNSNIVQSWLSVVDAASPAKDAFII

TPPLFRLKAGEKGFVRVVRSGKKLPDDRESMFWLNIKGIPATEYVPDKNVVQFAINSKIKLIYRPAALKG

NTPESYAEKLQWGKERTSVTVKNNSPLYMNFSQVSLNGKNISGAWFAAPFSTLKIPVQSSLSATGKKEIT

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>lcl|NZ\_FO834906.1\_prot\_WP\_004192602.1\_5019 [locus\_tag=BN49\_RS27185] [protein=fimbrial protein] [protein\_id=WP\_004192602.1] [location=complement(5281296..5281853)] [gbkey=CDS]

MDMGINMKMSKKFLAGALIFSACSALSTVAQADNTITFNGIVSDTTCTATIDGGVTAIDMGTTSVADLKA

YTFGAAKNFSFSLADCPTAEEGGNSIARVTFGGVSDTANSDYFKNQATDEPATGVAVALFDEAGNVMKNN

EEGSDVDISSGAATIPFTVKMVKSGDADPTKGTVQTTVTYNVTYH

>lcl|NZ\_FO834906.1\_prot\_WP\_002885088.1\_5020 [locus\_tag=BN49\_RS27195] [protein=LrgB family protein] [protein\_id=WP\_002885088.1] [location=complement(5282364..5283053)] [gbkey=CDS]

MSDAVLSILCLVATLVLYYANKKLYRRFHKLPLMPLVFTPILLVLILVVGHISYQSYMGETHWLLWLLGP

ATIAFAVPVYENVAVIKRHWMSLSAGVVTAVVVAVTSSVWLARGFMLSDEIQRSLAVRSVTTPFALAAAK

PLGGQPDLVALFVVITGVFGMAVGDMLFLRLAIREGMAKGAGFGAASHGAGTARSYELGQQEGVVASLVM

MLSGVVVVLAAPVVRWLLF

>lcl|NZ\_FO834906.1\_prot\_WP\_002885086.1\_5021 [locus\_tag=BN49\_RS27200] [protein=CidA/LrgA family protein] [protein\_id=WP\_002885086.1] [location=complement(5283050..5283457)] [gbkey=CDS]

MAFAPARVAPAVAQRLQIPVQVLLYVGLFIFAQYLVNRWQVPLPANLVGMVMLLLLIVCRVIPVSWVRAG

ARWLLAEMLLFFVPAVVAVVNYAQLLMVDGWRIFLVIALSTLMVLGATAWVVDKVYRYEVGRLKK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177821.1\_5022 [locus\_tag=BN49\_RS27205] [protein=LysR family transcriptional regulator] [protein\_id=WP\_004177821.1] [location=5283563..5284444] [gbkey=CDS]

MDIRTLRYFVEVVRQQSFTRAAEKLFVTQPTISKMLKNLEDELNCTLLIRDGRKLLLTDTGRVVFERGQA

ILGEFSQLESELSDINHLHKGVLRLGIPPMVGMLMAEPISRFRQRYPGVELKIAEFGGLTVQQAVSNGEL

DMAMTALPVEEDSSLTILPLFNHPLCVLTPRTAEWEGKTSLSPAELASHPLVIYNEEFALSQQLMRLFAE

HDVKPRIAVRSGQWDFLAAMVQAGIGVAILPEPICQRLDRQNFCWIPLQSELRWELGMIWREGVYMSRSA

EAWLACSKAFWLE

>lcl|NZ\_FO834906.1\_prot\_WP\_002885082.1\_5023 [locus\_tag=BN49\_RS27210] [protein=Na+/H+ antiporter] [protein\_id=WP\_002885082.1] [location=complement(5284606..5286252)] [gbkey=CDS]

MEIFFTILIMTLVVSLSGVVTRVLPFQVPLPLMQIAIGALLAWPTFGLHVEFDPELFLVLFIPPLLFADG

WKTPTREFIEHGREILGLALALVVVTVVGIGFLIYWIVPGIPLIPAFALAAVLSPTDAVALSGIVGEGRI

PKKIMGILQGEALMNDASGLVSLKFAVAVAMGTMVFTVGGATVEFLKVAIGGVLAGFVVSWSYGRSMRFL

SRWGGDEPATQIVLLFLLPFASYLIAEHIGVSGILAAVAAGMTITRSGVMRTAPLAMRLRANSTWAMLEF

VFNGMVFLLLGLQLPDILSSSLVAAEADPNVETWMLFTDIILIYAALMLVRFGWLWSMRKLSQRFLKKKP

MEFGSWTTRELLISSVAGVRGAITLAGVLSIPLLLPDGNVFPARYELIFLAAGVILFSLFVGVIALPILL

RHIESSDNVQQRKEERLARAATADVAIVAIQKMEERLAADTKENIDTQLLTEVSSRVIGNLRRRADGRND

VETSMLEESLERRFRLAALRSERGELYHLRATRQISNETLQKLLHDLDLLEALLIEDQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530150.1\_5024 [locus\_tag=BN49\_RS27215] [protein=NCS2 family permease] [protein\_id=WP\_016530150.1] [location=complement(5286400..5287749)] [gbkey=CDS]

MSTPSARTGGSLDAWFKISARGSTVRQEVVAGLTTFLAMVYSVIVVPGMLGKAGFPPAAVFVSTCLVAGV

GSLAMGLWANLPMAIGCAISLTAFTAFSLVLGQQISIPVALGAVFLMGVLFTVISATGIRSWILRNLPQG

VAHGTGIGIGLFLLLIAANGVGLVIKNPLDGLPVALGNFDSFPVVMSLIGLAVIIGLEKMKVPGGILLTI

IGVSIVGLIFDPNVHFSGIFAMPSLSDGQGNSLIGSLDIVGALNPVVLPSVLALVMTAVFDATGTIRAVA

GQANLLDKDGQIINGGKALTTDSLSSVFSGLVGAAPAAVYIESAAGTAAGGKTGLTAVTVGVLFLLILFL

SPLSYLVPAYATAPALMYVGLLMLSNVAKIDFNDFVDAMAGLITAVFIVLTCNIVTGIMIGFATLVIGRL

VSGEWRKLNLGTVIIAVALVVFYAGGWAI

>lcl|NZ\_FO834906.1\_prot\_WP\_002885078.1\_5025 [locus\_tag=BN49\_RS27220] [protein=glutathione S-transferase] [protein\_id=WP\_002885078.1] [location=complement(5288138..5288806)] [gbkey=CDS]

MLTVHHLNQSRSQRVLWALEELQLPYQIVRYQREKTMLAPAALKKIHPLGKSPVLEDNGYVLAESGAILE

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IERGGPFTLPGA

>lcl|NZ\_FO834906.1\_prot\_WP\_002885077.1\_5026 [gene=soxR] [locus\_tag=BN49\_RS27225] [protein=redox-sensitive transcriptional activator SoxR] [protein\_id=WP\_002885077.1] [location=complement(5289066..5289524)] [gbkey=CDS]

MEKKSPRIKMLLTPGEVAKRTGVAVSALHFYESKGLIHSQRNAGNQRRYRRDVLRAVAIIKIAQRIGIPL

ATIGDAFGVLPEGHNLSAKEWKMLSSQWREELDRRIHTLTALRDQLDGCIGCGCLSRRDCPLRNPGDKLG

EEGTGARLLEDE

>lcl|NZ\_FO834906.1\_prot\_WP\_004151738.1\_5027 [gene=soxS] [locus\_tag=BN49\_RS27230] [protein=superoxide response transcriptional regulator SoxS] [protein\_id=WP\_004151738.1] [location=5289609..5289938] [gbkey=CDS]

MSHQDIIQTLIEWIDEHIDQPLNIDIVARKSGYSKWYLQRMFRTVMHQTLGDYIRQRRLLLAAEALRTTQ

RPIFDIAMDLGYVSQQTFSRVFRREFDRTPSDYRHQISA

>lcl|NZ\_FO834906.1\_prot\_WP\_004177824.1\_5028 [locus\_tag=BN49\_RS27235] [protein=EAL domain-containing protein] [protein\_id=WP\_004177824.1] [location=complement(5289923..5291527)] [gbkey=CDS]

MGDSAPHKALRLIGTGLVILLPVVLALWFAQLRAKAETIDQLHSFSQLALQKTEMVIREADQARAKASQY

RGELCSADHQRYLLHIVRGLLYVEDLIYANGQRFICSTSVHQQTGWRMPAANYTKKPDVAIYYYRDTPFY

PGFAMNYMQKGPYVVVVNPFSYSSVIASDRDLAYGVFDTKTNLFFSVSNNVEPAELHALIREGDTFFNQN

GRVYTIARSAIRPIAVIMSTSRASYYHNFCDQASLTLPLGIICSILLVLVWSRTRRQYHSPRNMLQRALS

CRQLRLHYQPIIDIKNNRCVGAEALLRWPGFDGPVMNPAEFIPLAENEGMIAQVTDYVVDELFYEMGEFL

ASHPQLYIAINLSASDFHSARLISQISEKAHSYAVCIGQIKIEVTERGFIDVPKTTPVIQAFREAGYEIA

IDDFGTGYSNLHNLHALNVDILKIDKTFVDTLTTNNTSHLIAEHIIEMARGLRLKTIAEGVETPEQVSWL

YKRGVQYCQGWLFAKAMPAREFMQWLANAPAPANVPQPPRHAEI

>lcl|NZ\_FO834906.1\_prot\_WP\_004177826.1\_5029 [locus\_tag=BN49\_RS27240] [protein=YjcB family protein] [protein\_id=WP\_004177826.1] [location=5292034..5292315] [gbkey=CDS]

MASITTSVVLLRWPLVSAVLMFLASSLNIQLRKSDYAGLAVICSCLGLAAACWFATGLLGITLLDMAKIW

GNIKDVMIEVMSQTPPEWPMMMT

>lcl|NZ\_FO834906.1\_prot\_WP\_004186517.1\_5030 [locus\_tag=BN49\_RS27245] [protein=ABC transporter permease subunit] [protein\_id=WP\_004186517.1] [location=complement(5292362..5293219)] [gbkey=CDS]

MKALALVSTPAWWVKGRRKVRASPVLQTLLLLFMLLAMFGPLLNLLIWTVAESWYFPHSLPSRWGLKYWY

QVFNPYSDVSSSLLTSVLIALLSVGVCLLISVPAGYALSRRKMPLRMLFMLLFLIPQAFPNLTVYMNVAR

LFYQWGLNGSIAGVVLVHSVHGLMYSVWICVAAFSAIDPLLARASRNLGAGPVYTFWHIVLPQAAPGIVA

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AKLGK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177833.1\_5031 [locus\_tag=BN49\_RS27250] [protein=ABC transporter permease subunit] [protein\_id=WP\_004177833.1] [location=complement(5293216..5294049)] [gbkey=CDS]

MSSSLKYLLLVAPAALMIAILFLYPLGFSLVSAFTAPGQPFTLDHFRKVYALYASDVLFSLLIVLISVAL

LALLAITLSAVIALSPCRPVVRLLGFLYRLPLFIPFIVVAQMMRTFLAKNGLMNNALVAADLVTPLETLS

WLGWKGIVITFVWKQLAFATLLICGAMAALESSQILAARNLGASRPRILFDIMLPQVLPTIGVALVLSTV

TMMSVLSVPLMIGVGTPTMLTVDMAFRVNSYGDYAVANALGVVSLAICGALSWFYLRHSLQQKGGES

>lcl|NZ\_FO834906.1\_prot\_WP\_004177835.1\_5032 [locus\_tag=BN49\_RS27255] [protein=extracellular solute-binding protein] [protein\_id=WP\_004177835.1] [location=complement(5294110..5295249)] [gbkey=CDS]

MLTKTKAAIVTTLFLSLGAQADTILNVATAGDQNMVDYVKTWLGPKFEAAHPGVKVRVIGTGPGDAGSNK

ISEKLTAQQESGAQQWDIDVAVVHQKAGGEQVAKGLLQKYRQDIQTGGMVSSPSATQALGVNVDGYVMPM

FLSQTAIAWNSDLVTTPPASYDELVAWTQKHPQAFGYNGIKNGMSGVSFVVGWIYAYGTDAQRLSAGPYD

KSVEKGWQQAYEKLKAFNKNVTFTPGNAGTLDMLSRGEIAMGPVWVDMFYSWKDQGKLPPSIKLALLAPG

MPGQPMYYVIPAKAANPQLARDFIALATSPEVQAQGIVKQFNWYPGIDAGQVKPKLDAATWQKLFAEISP

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>lcl|NZ\_FO834906.1\_prot\_WP\_042941291.1\_5033 [locus\_tag=BN49\_RS27260] [protein=ABC transporter ATP-binding protein] [protein\_id=WP\_042941291.1] [location=complement(5295279..5296310)] [gbkey=CDS]

MSYLQISGLKISYGDKVVLHNIDLAVEQGEMIALLGPSGCGKTTLLNALCGFIPVQSGEVAIASRTITHL

APEQRNITMVFQSYALWPHLTVARNIGYGLKLRKWRGADIARRVAELLRIVNLEGLGEVKVTELSGGQRQ

RVALARALAIEPQVLVLDEPLSNLDAKVRLNVRHEIKSLQKRLGFTSLIVTHDQQEALVMADRIAVLNQG

RIEQTGTPEEIYQRPATPFVADFMGADNKIISGELSAAAISGLSAAQQGDNVIYFRSADAALAELTQPAS

QEGLALEGVVEQSAFLGNLYRHSVRCHDRLLLADAAQCWPTKSRVRLHVPTPALHIFPLPLSQ

>lcl|NZ\_FO834906.1\_prot\_WP\_171819497.1\_5034 [locus\_tag=BN49\_RS27265] [protein=ribonuclease Z] [protein\_id=WP\_171819497.1] [location=5296485..5297243] [gbkey=CDS]

MLGCGSAFSCTQNTSALRVIDADNKQWLIDCGPTVPRALWQRGGEVNDIDAIYFTHVHPDHCTGLTALLN

HWKSYSRQKPVIIYCQPAQQPVLMQLAALANWPQADLGFTIDWQECREAWTWQDWQIRTAPTQHELSNRA

IRITIAGQTLFYSGDGRPTADSIALMAGAGLAFQECASVAALDDDASHGDFPSCLMLFRTLQLPAMGLYH

CEDTSLSALKQACQPWPGLFVSRDGLTLTLPRPTPTDETYLL

>lcl|NZ\_FO834906.1\_prot\_WP\_002885046.1\_5035 [locus\_tag=BN49\_RS27270] [protein=LacI family transcriptional regulator] [protein\_id=WP\_002885046.1] [location=5297240..5298253] [gbkey=CDS]

MNPRKPSVTAQDVARRAGVSRAVVSRALSNNGSISPDARARVLRAAEELGYQVNFLAQGLNRQRSHLIGV

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QQHIPVVGINRQPTIPGVDYVCSDNAAGAELAADQLLRSGCQRFGWLNHHPSTWAGRMRGEAFGRALQTR

GVDVERHLAILACQQEGYAGGLQAAALADEALEGIFCANAQLACGFLDGMRQRGREAPADFQLIGFDNTP

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177841.1\_5036 [locus\_tag=BN49\_RS27275] [protein=inositol monophosphatase] [protein\_id=WP\_004177841.1] [location=5298264..5299025] [gbkey=CDS]

MTEAQRESLCALIRQAGAHAQALRDAGLQVDKKARQDFVSQADLAVEQEIKGWLQAHFPEEGFLGEESGF

EGDDQTVWVLDPVDGTTNFILGMDYWCISLARVCQGELSLGIIYAPDRDEFFFAARGEGAYLNGRRLTLR

EPEPDAVVIGMGRSSRAPASDYARAIDTLLDAGLEYRRFGAGALMLAHVAAGQLHAYYEAHMNSWDALAG

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>lcl|NZ\_FO834906.1\_prot\_WP\_002885039.1\_5037 [gene=iraM] [locus\_tag=BN49\_RS27280] [protein=anti-adapter protein IraM] [protein\_id=WP\_002885039.1] [location=complement(5299064..5299417)] [gbkey=CDS]

MKWTILNTLICPQSGIAFSAISSLRFLKFIMWYEADVILLPGESIRLYSSRVLINDQYHSLKIYNITVYD

EAQWEKLRERPSCPYHAGGERSDSCFYQSFCTIKRCPNNIPRSEPWR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529080.1\_5038 [gene=bamA] [locus\_tag=BN49\_RS27285] [protein=outer membrane protein assembly factor BamA] [protein\_id=WP\_016529080.1] [location=complement(5299969..5302392)] [gbkey=CDS]

MLKKTHIISGLLITPLTLYAATSYQVDDIRFEGLQRVTVGAALLSMPLHAGDAVTPEDVSEAVRALYASG

NFENVQILRDGKTLVVQVKERPTIASVSFSGNKAVKDDALKENLTASGISAGSALDRNSLSEIEKGLQDF

YYSAGKYSAQVHAVVTPLPRNRVDLTFVFQEGISAKIAQINIIGNQAFREETLLDQLQLRDNVPWWNVVA

DKKYQKQKLEADLETLRSFYLDRGYARFAIESTQVSMTPDKKSLYITIALNEGERYRVDRTQVMGDLAQH

GPEIEALAQPLAGAWYSGAQVTTVENEIKKHFGKYGYAWPQVTSTPEIDDAHHRVVLHIQVNAGRRYSVR

QIRFSGNDTSRDAVLRREMRQMEGAWLNNEKVDQGKVRLDRTGFFENVEQQIVPVNGTADQVDVVYKVKE

RNTGSFNVGLGFGTDSGVSYQLGVTQDNWLGTGNSVSFNGTRNSYQSYLELGATNPWFTVDGISLGGKIF

YNSYDASDADAGSYNQQSYGLGSTLGFPISENNSLNLGLDYVHNRLTNMDPELTTWRYLSSRGIEPSVVT

KDGDSGAKYSANDYFVSLGWGYNDLDRGFFPRAGNKSSLSGKVTLPGSDNSYYKLSFDTAQYLPLSENKR

WVWMERLRAGYAGGLDGKSVPFYDNFYAGGSSSVRGFSSNTIGPKAAYYRCNGSESSYSACPLDASSDAV

GGNAMAVLNSEFIIPTPFVNDKYADSLRTSLFVDAGTVWSTSWHNTAQTLAAGIPDYGDPSHIRLSAGIA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004192625.1\_5039 [locus\_tag=BN49\_RS27290] [protein=potassium:proton antiporter] [protein\_id=WP\_004192625.1] [location=5302414..5302644] [gbkey=CDS]

MSNSSVLLALSLFVQDASLKYATENNLSEAQNYMQLWRQNGEKMDVKASLKIYLMMELFLKRMVLMANTS

TIFRFA

>lcl|NZ\_FO834906.1\_prot\_WP\_016529079.1\_5040 [locus\_tag=BN49\_RS27300] [protein=tannase/feruloyl esterase family alpha/beta hydrolase] [protein\_id=WP\_016529079.1] [location=5303018..5304778] [gbkey=CDS]

MTRLLKTILPIILCALFGLSFASPTQAVASLPIVLPALTCDALSATDFSAAVGAKVTINHTEMQTSAQGS

WCKVSATIAPEIGVQIALPTQRWSQRFLQVGCGGLCGSINLSLSNASGCLPAMNGEFVVAATDMGHHGSM

MDASWAEDPQKRIDFAWRANHLTAVLAKAVMQTLYRQPPKYAYFMGCSDGGREALMEAQRFPQDFDGISA

GAPAAFFQFQNSFFHGWNVAANQRPDGTAILLKNRLPLIHQAVLAHCPTLSGVQDGILQSPYACQFSESW

LPRCPADARDRSTCLTQEEIEVVKKLYRGAYDSHGAQFVAGGLPLGSELRWPVPETPTGHSMSEMMVLPA

LQSVLLPGEKQKIQSMRDFPLNQQNFDAVAQLAPLYNAANTNLHAYQQRGGKLILWHGLADDSVSPAFSI

AYYRGVEAEMGHAATDTFLRLFLLPGVAHCGNGEGYDQIDLLTPLMRWTEEGIAPQEIMAGKRATAAADL

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>lcl|NZ\_FO834906.1\_prot\_WP\_004177844.1\_5041 [locus\_tag=BN49\_RS27305] [protein=helix-turn-helix transcriptional regulator] [protein\_id=WP\_004177844.1] [location=5304812..5305180] [gbkey=CDS]

MGLAAIMRSKTLQQSVLSDLLLWIDNNLDKKLTVDDLSDISGYSPWHLFRLFRHYFDRSPMEYIRQQRMS

LCRRLLLTTPGYRIVDICMMVGYDDLSAFNRTFKKYHALTPTQYRYQITRQK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529078.1\_5042 [locus\_tag=BN49\_RS27310] [protein=TonB-dependent siderophore receptor] [protein\_id=WP\_016529078.1] [location=complement(5305444..5307702)] [gbkey=CDS]

MKYTSHFPLGIVIPLLACSVPLQAAENMTEQSTPDESAATAENHEETMVITAARQNLQAPGVSTITAEEI

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SRGDTSWVPAEMIDHIDVIRGPAAARYGNGAMGGVVNIVTKPTTPEWHGSWNTYMNAPQHRKEGATKRTN

FSLNGPLSDSVSFNLWGNLSKTQADAQDINAGHEAERTGSYAGSYPAGREGVVNKDIHSKLRWEFAPMQA

LEFEAGYSRQGNLYAGDTQNTNTSTLVKSMYGKETNRLYRQTYGVTWTGGWDNGVTSNSYAQYEHTRNSR

MDEGLAGGTEGIFSSSEFSDIDLADVLLHSEVNIPFTLGVDQNLTLGTEWNQQRMKDGVSTTQALSYGTI

DGVSATGRSPYSSAEIFSLFTEDNMALTDSTMLTPALRFDHHSIVGNNWSPSLNLSQVLTDDWTLKLGIA

RAYKAPNLYQLNPNYILYSNGQGCYASSSACYLMGNSDLKAETSVNKEIGLEYKHDGYQAGITWFRNDYH

NKIESGYAAVGTASNGTTNIYQWENVPKALVEGLEGTLNLPVGEAVNWSNNLTWMLQSKNKTTGDRLSVI

PQFTLNSTLSWQVREDLSLQSTFTWYGRQKPKRFNYKGEAVSGSELNEVSPYSIVGLSATWDVNKNLSFT

SGIDNLFDIRHYRAGNAQTTGNATTGAYLYGAGAETYNESGRTFFMSVNTHF

>lcl|NZ\_FO834906.1\_prot\_WP\_016529076.1\_5043 [locus\_tag=BN49\_RS27325] [protein=lytic transglycosylase F] [protein\_id=WP\_016529076.1] [location=5308291..5309871] [gbkey=CDS]

MNAYSLSRLFIAWLTCLATLLFAPLLPAVEAEKAPPAAAEDNTLSIHIDDMLRPWRGDLPGMIDRRTIRV

LTTYSKTFFFIDKGTQRGATHDIFIALENDLNKQLAKNKKLKQRHLKLHIVFVPVSRDNLFIALNEGKGD

IAAANLTITPSREAQVDFAQPLYSNVKELLISGPASPKVDSLEQLSGQTVFVRRSSSYYDSLQALNARFA

GESRPPVILEAAPEALEDEDLLEMLNAGLIPLIVVDQHKALFWKQVFPKIQVHDNVVLRDGGDIAWAVRK

DSPQLLTVLNNFVKKNRQGTTLGNTLLLRYLKNAKYVKNAAASKERRKFLAMVDVFRKYGDRYDVDWLLM

AAQGYQESRLNQSVRSHVGAIGVMQVMPSTGKELKVGDIKQLDPNIHAGVKYMRWMMDRYYADEPMTRLD

KALFTFASYNAGPARITRLRTMTKQRGFDPNVWFGNVENMAAEKIGAETVTYVSNIYKYYIAYRLIVDDM

ARKQKATAVPRQEPVAQPAKPQPSVATAATAQVPVI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151744.1\_5044 [gene=ssb1] [locus\_tag=BN49\_RS27330] [protein=single-stranded DNA-binding protein SSB1] [protein\_id=WP\_004151744.1] [location=complement(5309996..5310520)] [gbkey=CDS]

MASRGVNKVILVGNLGQDPEVRYMPSGGAVANFTLATSESWRDKQTGEMKEQTEWHRVVLFGKLAEVAGE

YLRKGSQVYIEGQLRTRKWTDQSGQDKYTTEVVVNVGGTMQMLGGRQGGGAPAGGGQQQGGWGQPQQPQG

GNQFSGGAQSRPQQQAPAAPSNEPPMDFDDDIPF

>lcl|NZ\_FO834906.1\_prot\_WP\_004146620.1\_5045 [gene=uvrA] [locus\_tag=BN49\_RS27335] [protein=excinuclease ABC subunit UvrA] [protein\_id=WP\_004146620.1] [location=5310772..5313597] [gbkey=CDS]

MDKIEVRGARTHNLKNINLVIPRDKLIVVTGLSGSGKSSLAFDTLYAEGQRRYVESLSAYARQFLSLMEK

PDVDHIEGLSPAISIEQKSTSHNPRSTVGTITEIHDYLRLLYARVGEPRCPDHDVPLAAQTVSQMVDNVL

AQPEGLRLMLLAPIIKERKGEHTKTLENLASQGYIRARIDGEVCDLSDPPKLELQKKHTIEVVIDRFKVR

DDLAQRLAESFETALELSGGTAIVANMDDEKAEELLFSANFACPICGYSMRELEPRLFSFNNPAGACPTC

DGLGVQQYFDPDRVVQNPELSLAGGAIRGWDRRNFYYFQMLKSLAEHYKFDVEAPWGTLSANVQKVVLYG

SGKESIEFKYMNDRGDTSVRRHPFEGVLHNMERRYKETESSAVREELAKFISNRPCASCDGTRLRREARH

VFVENTPLPTISDMSIGHAMDFFNNLKLSGQRAKIAEKVLKEIGDRLKFLVNVGLNYLTLSRSAETLSGG

EAQRIRLASQIGAGLVGVMYVLDEPSIGLHQRDNERLLGTLIHLRNLGNTVIVVEHDEDAIRAADHVIDI

GPGAGVHGGQVVAEGPLEAIMAVPESLTGQFMSGKRKIEVPKQRVPANPEKVLKLTGARGNNLKDVTLTL

PVGLFTCITGVSGSGKSTLINDTLFPIAQRQLNGATIAEPAPYRDIQGLEHFDKVIDIDQSPIGRTPRSN

PATYTGVFTPVRELFAGVPESRSRGYTPGRFSFNVRGGRCEACQGDGVIKVEMHFLPDIYVPCDQCKGKR

YNRETLEIKYKGKTIHEVLDMTIEEAREFFDAVPALARKLQTLMDVGLTYIRLGQSATTLSGGEAQRVKL

ARELSKRGTGQTLYILDEPTTGLHFADIQQLLEVLHQLRDQGNTIVVIEHNLDVIKTADWIVDLGPEGGS

GGGEILVSGTPETVAECEASHTARFLKPMLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002884953.1\_5046 [locus\_tag=BN49\_RS27340] [protein=MmcQ/YjbR family DNA-binding protein] [protein\_id=WP\_002884953.1] [location=complement(5313598..5313954)] [gbkey=CDS]

MTISELLQYCMAKPGAEQSVHSDWKATQIKVSDVLFAMVKEVEDQRPAVALKASPELAELLRQQHRDVRP

SQHLNKAHWSTVYLDGSLPDSQIYYLVDASYQQAVKMLPEPVRQQLTR

>lcl|NZ\_FO834906.1\_prot\_WP\_002884951.1\_5047 [locus\_tag=BN49\_RS27345] [protein=secondary thiamine-phosphate synthase enzyme YjbQ] [protein\_id=WP\_002884951.1] [location=complement(5313958..5314374)] [gbkey=CDS]

MWYQQTLTLGPKSRGFHLVTDEILGQIRGLSGVKVGLLHLLLQHTSASLTLNENCDPTVRYDMEQYFLNA

VPDNAPYEHDYEGPDDMPSHIKSSMLGVSLMLPVEDGRVRLGTWQGIWLGEHRIHGGSRRIVATLMGE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530115.1\_5048 [gene=aphA] [locus\_tag=BN49\_RS27350] [protein=acid phosphatase AphA] [protein\_id=WP\_016530115.1] [location=complement(5314505..5315218)] [gbkey=CDS]

MRKLTLALAAASLLFTLNSAVVARASTPQPLWVGTNVAQLAEQAPIHWVSVAQIENSLLGRPPMAVGFDI

DDTVLFSSPGFWRGQKTFSPGSEDYLKNPQFWEKMNNGWDEFSMPKEVARQLIAMHVKRGDSIWFVTGRS

QTKTETVSKTLQDDFLIPAANMNPVIFAGDKPGQNTKTQWLQAKQIKVFYGDSDNDITAAREAGARGIRV

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530114.1\_5049 [gene=tyrB] [locus\_tag=BN49\_RS27355] [protein=aromatic amino acid transaminase] [protein\_id=WP\_016530114.1] [location=complement(5315409..5316602)] [gbkey=CDS]

MFQQVDAYAGDPILSLMERFKEDPRSDKVNLSIGLYYNDDGIIPQLQAVAEAEARLNAEPHGASLYLPME

GLSGYRQAIAPLLFGAEHTALKQNRIASIQTVGGSGALKVGADFLKRYFPESHVWVSDPTWENHIAIFEG

AGFEVSTYPWFDKATNGVRFEDLLATLQTLPARDIVLLHPCCHNPTGADLTPAQWDRVVEVLKARQLIPF

LDIAYQGFGGGLEEDAYAIRAIASAGMPMLVSNSFSKIFSLYGERVGGLSVVCEDSETAGRVLGQLKATV

RRNYSSPPSFGAQVVATVLNDAALKATWQAEVDAMRAHILTMRQALVDALQQVAPGSKVDYLLKQRGMFS

YTGFSAAQVDRLRDEFGVYLIASGRMCVAGLNSRNVQQVAKAFAAVM

>lcl|NZ\_FO834906.1\_prot\_WP\_016530113.1\_5050 [gene=alr] [locus\_tag=BN49\_RS27360] [protein=alanine racemase] [protein\_id=WP\_016530113.1] [location=complement(5316780..5317859)] [gbkey=CDS]

MQAATVVINRRALRHNLQRLRELAPASKLVAVVKANAYGHGLLETARTLTDADAFGVARLEEALRLRAGG

IAQPILLLEGFFAAEDLAVIAAQRLHTAVHSPEQLAALEQADLPEPVTVWMKLDTGMHRLGVRPEEAEAF

YQRLSQCKNVRQPVNVVSHFARADEPTCGATERQLDIFTTFTEGKPGLRSIAASGGILLWPQSHYDWVRP

GIILYGVSPLDDRSTGKDFGCQPVMTLTSSLIAVREHKAGEPVGYGGTWISERNTRLGVVAMGYGDGYPR

AAPSGTPVLVNGREVPIVGRVAMDMICVDLGPQAQDKAGDAVVLWGEGLPVERIAEITKVSAYELITRLT

SRVAMKYFD

>lcl|NZ\_FO834906.1\_prot\_WP\_002884942.1\_5051 [gene=dnaB] [locus\_tag=BN49\_RS27365] [protein=replicative DNA helicase] [protein\_id=WP\_002884942.1] [location=complement(5317891..5319306)] [gbkey=CDS]

MAGNKPFNKPQTETRERDPQLAGLKVPPHSIEAEQSVLGGLMLDNERWDDVAERVVADDFYTRPHRHIFT

EMARLQESGSPIDLITLAESLERQGQLDSVGGFAYLAELSKNTPSAANISAYADIVRERAVVREMISVAN

EIAEAGFDPQGRTSEDLLDLAESRVFKIAESRANKDEGPKNIADVLDATVARIEQLFQQPHDGVTGVNTG

YDDLNKKTAGLQPSDLIIVAARPSMGKTTFAMNLVENAAMLQDKPVLIFSLEMPSEQIMMRSLASLSRVD

QTRIRTGQLDDEDWARISGTMGILLEKRNIYIDDSSGLTPTEVRSRARRIAREHGGIGLIMIDYLQLMRV

PSLSDNRTLEIAEISRSLKALAKELQVPVVALSQLNRSLEQRADKRPVNSDLRESGSIEQDADLIMFIYR

DEVYHENSDLKGIAEIIIGKQRNGPIGTVRLTFNGQWSRFDNYAGPQYDDE

>lcl|NZ\_FO834906.1\_prot\_WP\_002884941.1\_5052 [locus\_tag=BN49\_RS27370] [protein=quinone oxidoreductase] [protein\_id=WP\_002884941.1] [location=5319476..5320459] [gbkey=CDS]

MATRIEFSKHGGPEVLQAVEFTPRDPAEHEIQVENKAIGINYIDTYVRSGLYPPPSLPSGLGTEAAGIVS

KVGHGVTHIKVGDRVVYAQSALGAYSTVHNVLADKAAVLPDAISFEQAAASFLKGLTVWYLLRKTYEIKP

DEMFLFHAAAGGVGLIACQWAKALGAKLIGTVGSAQKAQRAKEAGAWQVINYREESIVERLKALTDGKKV

AVVYDSVGKDTWEASLDCLQRRGLMVSFGNSSGPVTGVNLGILNQKGSLYVTRPSLQGYITNREELEEAC

SELFSLIASGVIKVDVAESQIYPLSEARRAHEVLESRVTQGSSLLLP

>lcl|NZ\_FO834906.1\_prot\_WP\_004894969.1\_5053 [gene=pspG] [locus\_tag=BN49\_RS27375] [protein=envelope stress response protein PspG] [protein\_id=WP\_004894969.1] [location=complement(5320642..5320884)] [gbkey=CDS]

MLELLFVIGFFVMLLVTGVSLLGIIAAIVVATALMFVGGLFALMIKLLPWLLLAVAVVWIIRALKSPNGN

AFRDNNRWRY

>lcl|NZ\_FO834906.1\_prot\_WP\_002884937.1\_5054 [gene=dusA] [locus\_tag=BN49\_RS27380] [protein=tRNA dihydrouridine(20/20a) synthase DusA] [protein\_id=WP\_002884937.1] [location=complement(5321024..5322022)] [gbkey=CDS]

MMPESTSPVFPAHRFSIAPMLDWTDRHCRYFLRLLSRHTLLYTEMVTTGAIIHGKGDYLAYSEEEHPVAL

QLGGSDPQALAQCAKLAEARGYDEINLNVGCPSDRVQNGMFGACLMGNAPLVADCIKAMRDVVSIPVTVK

TRIGIDDQDSYEFLCDFIETVSGKGECEMFIIHARKAWLSGLSPKENREIPPLDYPRVWQLKRDFPHLTM

AINGGIKSLDEARVQLEHMDGVMVGREAYQNPGILASVDREIFGVAGADADPVAVVRAMYPYIERELSKG

TYLGHITRHMLGLFQGIPGARQWRRYLSENAHKAGADIAVLEHALKLVADKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002884935.1\_5055 [locus\_tag=BN49\_RS27385] [protein=cupin domain-containing protein] [protein\_id=WP\_002884935.1] [location=complement(5322123..5322611)] [gbkey=CDS]

MKRPDCIRHWRELEGPDDATYPDSPERFSIGAPLGRGLRLNRLGIHHERLPPGRRTSYPHAESDEEEFIY

VLEGYPEVWINGYLWKLEPGDSVGFPAGTGICHTFLNNTEQEVRLLVVGEANKKYNRIYYPLNPGYAATR

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>lcl|NZ\_FO834906.1\_prot\_WP\_016530110.1\_5056 [gene=zur] [locus\_tag=BN49\_RS27395] [protein=zinc uptake transcriptional repressor Zur] [protein\_id=WP\_016530110.1] [location=5322861..5323376] [gbkey=CDS]

MDKTPSQEMLAHAERLCAQRGVRLTPQRLEVLRLMSLQQGAISAYDLLDLLREKEPQAKPPTVYRALEFL

LEQGFVHKVESTNSYVLCHLFDQPTHSSAMFICDRCGVVKEEAAEGVEDIMHTLAARMGFALRHNVIEAH

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151747.1\_5057 [locus\_tag=BN49\_RS27400] [protein=CsbD family protein] [protein\_id=WP\_004151747.1] [location=complement(5323472..5323681)] [gbkey=CDS]

MNKDEIGGNWKQFKGKAKEQWGKLTDDDMTVIEGKRDQLVGKIQERYGYEKDQAEKEVSDWEHKNDYRW

>lcl|NZ\_FO834906.1\_prot\_WP\_004219133.1\_5058 [locus\_tag=BN49\_RS31250] [protein=hypothetical protein] [protein\_id=WP\_004219133.1] [location=5323747..5323896] [gbkey=CDS]

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151748.1\_5059 [gene=dinF] [locus\_tag=BN49\_RS27410] [protein=MATE family efflux transporter DinF] [protein\_id=WP\_004151748.1] [location=complement(5323916..5325232)] [gbkey=CDS]

MLLNAADKALWRLALPMIFSNITVPLLGLVDTAVIGHLDSPVYLGGVAVGATATSFLFMLLLFLRMSTTG

LTAQAWGAKDPQRLARALVQPLALALGAGVLIILLRLPLIDLALHIVGGSEAVLEQARRFLEIRWLSAPA

SLANLVLLGWLLGVQYARAPVILLVVGNLLNIVLDLWLVMGLRMNVQGAALATVTAEYATLIIGLLMAKR

VLTLRGVSLAMLKNAWRGDLRRLLALNRDIMLRSLLLQLCFGALTVFGARLGSDIVAVNAVLMTMLTFTA

YALDGFAYAVEAHSGQAYGARDGSQLLEVWRAACRQSGMVALAFALIYSLAGQYIIALLTSLPSLQQLAD

RYLIWQTILPVVGVWCYLLDGMFIGATRGAEMRNSMAVAAAGFAVTLLTLPVLGNHGLWLALAVFLALRG

LSLALIWRRHWRRGTWFS

>lcl|NZ\_FO834906.1\_prot\_WP\_002884822.1\_5060 [gene=lexA] [locus\_tag=BN49\_RS27415] [protein=transcriptional repressor LexA] [protein\_id=WP\_002884822.1] [location=complement(5325302..5325910)] [gbkey=CDS]

MKALTTRQQEVFDLIRDHISQTGMPPTRAEIAQRLGFRSPNAAEEHLKALARKGAIEIVSGASRGIRLLT

EEEQGLPLIGRVAAGEPLLAQQHIEGHYQVDPSMFKPNADFLLRVSGMSMKDIGILDGDLLAVHKTQDVR

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>lcl|NZ\_FO834906.1\_prot\_WP\_002884819.1\_5061 [locus\_tag=BN49\_RS27420] [protein=diacylglycerol kinase] [protein\_id=WP\_002884819.1] [location=complement(5326033..5326401)] [gbkey=CDS]

MANNTTGLTRIIKAAGYSWKGFRAAWINEAAFRQEGVAAIVAVAVACWLDVDAITRVLLIGSVLLVMIVE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004178269.1\_5062 [gene=plsB] [locus\_tag=BN49\_RS27425] [protein=glycerol-3-phosphate 1-O-acyltransferase PlsB] [protein\_id=WP\_004178269.1] [location=5326530..5328953] [gbkey=CDS]

MSGWQRIYYKLLNLPLQVLVKSKSIPAEPAQELGLDTSRPVMYVLPYNSKADLLTLRAQCLAHDLPDPLE

PLEIDGALLPRYVFIHGGPRVFTYYTPKEESIKLFHDYLDLHRNHPDLDVQMVPVSVMFGRSPGREKGEV

NPPLRMLNGIQKFFAVSWLGRDSFVRFSPSVSLRRMADEHGTDKIIAQKLARVARMHFARQRLAAVGPRL

PARQDLFNKLLASKAIARAVEDEARSKKISHEKAQQNAIALMEEIAANFSYEMIRLTDRILGFTWNRLYQ

GINVHNAERVRQLAHDGHEIVYVPCHRSHMDYLLLSYVLYHQGLVPPHIAAGINLNFWPAGPIFRRLGAF

FIRRTFKGNKLYSTVFREYLGELFSRGYSVEYFVEGGRSRTGRLLDPKTGTLSMTIQAMLRGGTRPITLV

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DPIEAVRPSWLTPTVNSIAADLMVRINNAGAANAMNLCCTALLASRQRSLTREQLTQQLECYLALLRNVP

YSPDATAPSASASELIDHALQMNKFEVEKDTIGDIIILPREQAVLMTYYRNNIAHMLVMPSLLAALVTQH

RHLSRAEVLRHVETLYPFLKAELFLRWEKAELAGVVDALIAEMLRQELIVVDGDVMSLNPSHSRSLQLLA

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>lcl|NZ\_FO834906.1\_prot\_WP\_009309455.1\_5063 [gene=ubiA] [locus\_tag=BN49\_RS27430] [protein=4-hydroxybenzoate octaprenyltransferase] [protein\_id=WP\_009309455.1] [location=complement(5329002..5329868)] [gbkey=CDS]

MEWSLSQNKLLAFHRLMRTDKPIGALLLLWPTLWALWVASPGVPPLWILAVFVAGVWLMRAAGCVVNDYA

DRKFDGYVKRTARRPLPSGDVTEKEARTLFIVLVLLSFLLVLTLNTMTILLSVAALALAWVYPFMKRYTH

LPQVVLGAAFGWSIPMAFSAVSESLPLSCWLMFLANILWAVAYDTQYAMVDRDDDVKIGIKSTAILFGEN

DRLIIGILQVAVLALMGAVGWLNGLGWEYYWSLFVAAGLFGWQQKLIFNRDRDNCFKAFMNNNYVGLVLF

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>lcl|NZ\_FO834906.1\_prot\_WP\_002884807.1\_5064 [gene=ubiC] [locus\_tag=BN49\_RS27435] [protein=chorismate lyase] [protein\_id=WP\_002884807.1] [location=complement(5329881..5330378)] [gbkey=CDS]

MSHPALTRLRALRYFAVMPSLPPPLSDWLLLEDSMTQRFEQQGKQVTVTLVNEGYIGRDALTDEAALLPD

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151749.1\_5065 [gene=malM] [locus\_tag=BN49\_RS27440] [protein=maltose operon protein MalM] [protein\_id=WP\_004151749.1] [location=complement(5330566..5331489)] [gbkey=CDS]

MKMKKTLVALCLSAGMLACVPGMSLADVNFVPQNTSAAPAIPASALQQLIWTPADQSKTQSVDLTTGGQR

LDVPGIVGPVAAWSVPANIGELTLTLDSELNKHKQIFAPNVLILDQNMTPAAFFPSNYFTYQQPGVMTAD

RLGGVMRLTPALGQQKLYVLVFTTEKDLQQTTTLLDPAKAYAKGAGNAAPDIPDPIAKHTTDGVLKLKVK

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>lcl|NZ\_FO834906.1\_prot\_WP\_002884747.1\_5066 [locus\_tag=BN49\_RS27445] [protein=maltoporin] [protein\_id=WP\_002884747.1] [location=complement(5331604..5332893)] [gbkey=CDS]

MMITLRKLPLAVAVAAGVMSAQALAVDFHGYARSGIGWTGSGGEQQCFKATGAQSKYRLGNECETYAELK

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DFYYWDISGPGAGLENVDLGFGKLSLAATRNSESGGSYTFSSDDTKKYAAKTANDVFDIRLAGLETNPGG

VLELGVDYGRANPQDDYRLEDGASKDGWMWTGEHTQSIWGGFNKFVVQYATDAMTSWNSGHSQGTSIDNN

GSMIRVLDHGAMDFNDDWGLMYVAMYQDVDLDSKNGSTWYTVGVRPMYKWTPIMSTQLEIGYDNVKSQRT

SENNNQYKITLAQQWQAGNSVWSRPAIRIFATYAKWDENWGYSNTSGLQTKDSSGSGAFTSSRGDDSEVT

FGAQMEVWW

>lcl|NZ\_FO834906.1\_prot\_WP\_002884743.1\_5067 [gene=malK] [locus\_tag=BN49\_RS27450] [protein=maltose/maltodextrin ABC transporter ATP-binding protein MalK] [protein\_id=WP\_002884743.1] [location=complement(5332977..5334086)] [gbkey=CDS]

MASVQLRNVTKAWGDVVVSKDINLDIHEGEFVVFVGPSGCGKSTLLRMIAGLETITSGDLFIGDTRMNEI

PPAERGVGMVFQSYALYPHLSVAENMSFGLKLAGAKKDLINQRVTQVAEVLQLAHLLERKPKALSGGQRQ

RVAIGRTLVAEPSVFLLDEPLSNLDAALRVQMRIEISRLHKRLGRTMIYVTHDQVEAMTLADKIVVLDAG

RVAQVGKPLELYHYPADRFVAGFIGSPKMNFLPVKVTATAIDQVQVELPNRQQIWLPVDSANVQAGANMS

LGIRPEHLLPSDIADVTLEGEVQVVEQLGHETQIHIQIPAIRQNLVYRQNDVVLVEEGATFAIGLPPERC

HLFREDGTACRRLHKEPGV

>lcl|NZ\_FO834906.1\_prot\_WP\_002884740.1\_5068 [gene=malE] [locus\_tag=BN49\_RS27455] [protein=maltose/maltodextrin ABC transporter substrate-binding protein MalE] [protein\_id=WP\_002884740.1] [location=5334457..5335647] [gbkey=CDS]

MKIKTGARILALSALTTMMFSASALAKIEEGKLVIWINGDKGYNGLAEVGKKFEKDTGIKVSVEHPDKLE

EKFPQVAATGDGPDIIFWAHDRFGGYAQSGLLAEITPDKAFQDKLYPFTWDAVRYNGKLIAYPIAVEALS

LIYNKDLVPNPPKTWEEIPALDKELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKFENGKYDVKDVGVD

SAGAKAGLTFLVDLIKNKHMNADTDYSIAEAAFNKGETAMTINGPWAWSNIDKSKVNYGVTLLPTFKGKP

SKPFVGVLSAGINAASPNKELAKEFLENYLMTDQGLEAVNNDKPLGAVALKSFQEKLEKDPRIAATMANA

QKGEIMPNIPQMSAFWYAVRTAVINAASGRQTVDAALKDAQSRITK

>lcl|NZ\_FO834906.1\_prot\_WP\_002884726.1\_5069 [gene=malF] [locus\_tag=BN49\_RS27460] [protein=maltose ABC transporter permease MalF] [protein\_id=WP\_002884726.1] [location=5335765..5337309] [gbkey=CDS]

MDAVKKRHWWQSPQLTWSVIGLLCLLVGYLVVLMYAQGEYLFAIMTLILSSVGLYIFANRKAYAWRYVYP

GLAGMGLFVLFPLICTIAIAFTNYSSTNQLTFERAQQVLMDRSFQAGKAYNFTLIPAGDEWKLALTDGES

GKNYLSDAFKFGGEQKLALKETDALPEGERANLRVITQNRTALNQLTAVLPDDSKVIMSSLRQFSGTQPL

YTLGEDGVLTNNQTHVKYRPNNDVGFYQSINADGSWGNEKLSPGYTVTIGWDNFTRVFHDEGIQKPFFAI

FVWTVVFSVLTVVLTVAVGMILACLVQWEALKGKAIYRVLLILPYAVPSFISILIFKGLFNQSFGEINMM

LSTLFGIKPAWFSDPTTARTMIIIVNTWLGYPYMMILCMGLLKAIPDDLYEASAMDGAGPFQNFFKITFP

LLIKPLTPLMIASFAFNFNNFVLIQLLTNGGPDRLGTTTPAGYTDLLVSYTYRIAFEGGGGQDFGLAAAI

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>lcl|NZ\_FO834906.1\_prot\_WP\_002884725.1\_5070 [gene=malG] [locus\_tag=BN49\_RS27465] [protein=maltose ABC transporter permease MalG] [protein\_id=WP\_002884725.1] [location=5337324..5338214] [gbkey=CDS]

MAMVQPKSQKLRLFTTHLLLLIFIAAIMFPLLMVIAISLREGNFATGSLIPDTISWEHWRLALGFSVEHA

DGRVTPPPFPVLLWLWNSIKVAGITAIGIVALSTTCAYAFARMRFPGKATLLKGMLIFQMFPAVLSLVAL

YALFDRLGQYIPFVGLNTHGGVIFAYMGGIALHVWTIKGYFETIDGSLEEAAALDGATPWQAFRLVLLPL

SVPILAVVFILSFIAAITEVPVASLLLRDVNSYTLAVGMQQYLNPQNYLWGDFAAAAVLSAIPITVVFLL

AQRWLVNGLTAGGVKG

>lcl|NZ\_FO834906.1\_prot\_WP\_002884721.1\_5071 [gene=psiE] [locus\_tag=BN49\_RS27470] [protein=phosphate-starvation-inducible protein PsiE] [protein\_id=WP\_002884721.1] [location=complement(5338406..5338816)] [gbkey=CDS]

MPSVYRPLVNFVAKAMQAVLNLALLCLGIILVVFLGKETLHLAHVLFTPEPVSKYKLVEGLVVYFLYFEF

IALIVKYFESGFHFPLRYFVYIGITAIVRLIIVDHESPLAVLIYSAAILILVITLWLCNSNRLKRE

>lcl|NZ\_FO834906.1\_prot\_WP\_016530300.1\_5072 [locus\_tag=BN49\_RS27475] [protein=L-serine ammonia-lyase, iron-sulfur-dependent, subunit alpha] [protein\_id=WP\_016530300.1] [location=5339190..5340467] [gbkey=CDS]

MNTDNASLYVKWLKQEVAPALGCTEPVAISFAAAYAAQYLDQPCTKISGFISANLYKNAMGVTIPGTTVC

GVPLAAAIGAFGGDPQKGLKTLEDITPRHVEMAQKLIANNAVDIAVEETPDFIHLDLTLSAGENCCRVVV

KGTHTNVVELYINGQPQPLSEKQNTSIQRETLPTFSLQQAYDFINRVDLNDIRFILDAARLNSALAAEGK

TKKYGLNINGTFSDAVKNGLMSNDLLSKVIINTVAASDARMGGAPVVAMSNFGSGNQGITATMPVVVVAE

HLGVDEETLARALSLSHLTAISIHSRYTRLSALCAASTAAMGAAAGMAWLFTRDINTINTAIINMVSDIT

GMICDGASNSCAMKVSSVVSSAFKAVLMAMQNSCAGANDGIVCADVEQTINNLCRLVIKPMTLTDKEIIS

IMVAK

>lcl|NZ\_FO834906.1\_prot\_WP\_004177854.1\_5073 [locus\_tag=BN49\_RS27480] [protein=AzlC family ABC transporter permease] [protein\_id=WP\_004177854.1] [location=5340551..5341291] [gbkey=CDS]

MNKKVIFRGASAIMPLCIGDFPFSFIVGALSVSAGMSVWQSTAWSAIVIAGSAQMLALNMLKTGATLGVI

IFTTLIINLRHVLYSASISGTVREASFFKKCFMSYALTDEVYATTVKEMEGNKKEKYLFYGSAMITFWAI

WVLADFLGALVGASFPHIEKYGLDFAMVAAFIAIVVPQIKSQACTVAAVVAAVSGVLLVVLPYSLGIVVA

SVLGVLAGLCVDLAEERKQMAKTESDMPLVEAMENE

>lcl|NZ\_FO834906.1\_prot\_WP\_004177855.1\_5074 [locus\_tag=BN49\_RS27485] [protein=AzlD domain-containing protein] [protein\_id=WP\_004177855.1] [location=5341284..5341604] [gbkey=CDS]

MSNSYFIALTLGMAAVTFLIRFSFIGLAGKIQMSERVTKTLRFVPVTVLPAIITIQILSVNSSMEFDLKN

PKVIAAIICTLASFRLGLVWVVVSGVGSLVLLNYFM

>lcl|NZ\_FO834906.1\_prot\_WP\_004178266.1\_5075 [locus\_tag=BN49\_RS27490] [protein=Rid family detoxifying hydrolase] [protein\_id=WP\_004178266.1] [location=5341625..5342005] [gbkey=CDS]

MIITTADAPAAIGPYVQGVNLGAMTITSGQLPINPLDGTMPEDIAEQARQSLENVKAIVEAAGLTVGQIV

KTTVFVKDLADFAAINAAYEAFFIEHQAAFPARSCVEVARLPKDAGVEIEAIAFAR

>lcl|NZ\_FO834906.1\_prot\_WP\_042941031.1\_5076 [locus\_tag=BN49\_RS27495] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_042941031.1] [location=5342113..5342622] [gbkey=CDS]

MLTIRQACPEDAPQLSAMGYASYHHHFAHLWRDADELALFLKQEYAEDALRRSLADATQHWLIAEAPSPV

GFAKYSYQQRMADDGKIGTLLHKLYLMPGKTGHRYGEHIFHAVETRAKTAGESWLWLEVLAANPAARRFY

ERQGMQHIGDTTFHSASQQSTLHILAKPI

>lcl|NZ\_FO834906.1\_prot\_WP\_004177857.1\_5077 [locus\_tag=BN49\_RS27500] [protein=N-acetyltransferase] [protein\_id=WP\_004177857.1] [location=5342631..5343086] [gbkey=CDS]

MPELRDTGVRNVVCGENVVIYQPANLYDCQLGDNVFVGPFVEIQGNTRIGANSKIQSHTFICEYVTIGQR

CFIGHGVMFANDLFREGKPNADRASWGRIEIGDDVSIGSGATILAVSICDGVVIGAGSVVTKSITEKGVW

AGNPARLLRRL

>lcl|NZ\_FO834906.1\_prot\_WP\_002884631.1\_5078 [gene=pgi] [locus\_tag=BN49\_RS27505] [protein=glucose-6-phosphate isomerase] [protein\_id=WP\_002884631.1] [location=complement(5343136..5344785)] [gbkey=CDS]

MKNINPTQTSAWQALQKHFDEMKDVTISELFAKDSDRFSKFSATFDDLMLVDFSKNRITEETLAKLQDLA

KETDLAGAIKSMFSGEKINRTEDRAVLHVALRNRSNTPIVVDGKDVMPEVNAVLEKMKTFSEAIISGSWK

GYTGKPITDVVNIGIGGSDLGPFMVTEALRPYKNHLNMHFVSNVDGTHIAEVLKNVNPETTLFLVASKTF

TTQETMTNAHSARDWFLATAGDDKHVAKHFAALSTNAKAVGEFGIDTANMFEFWDWVGGRYSLWSAIGLS

IILSVGFDNFVELLSGAHAMDKHFSTTPAEKNLPVLLALIGIWYNNFFGAETEAILPYDQYMHRFAAYFQ

QGNMESNGKYVDRNGHAVDYQTGPIIWGEPGTNGQHAFYQLIHQGTKMVPCDFIAPAITHNPLSDHHQKL

LSNFFAQTEALAFGKSREVVEQEYRDQGKDPATLEHVVPFKVFEGNRPTNSILLREITPFSLGALIALYE

HKIFTQGAILNIFTFDQWGVELGKQLANRILPELKDGSEVSSHDSSTNGLINRYKAWRA

>lcl|NZ\_FO834906.1\_prot\_WP\_004146591.1\_5079 [gene=lysC] [locus\_tag=BN49\_RS27510] [protein=lysine-sensitive aspartokinase 3] [protein\_id=WP\_004146591.1] [location=5345550..5346899] [gbkey=CDS]

MTDLVVAKFGGTSVADFDAMNRSIDVALLDANTRIVVLSASAGVTNILVALAGGLEPTERFSQLDALRQI

QFNILERLRYPNVIREEIERLLENITTLAEAAALASSTALTDELVSHGELMSTLLFVEILRERGIQAQWF

DARKVLRTNDRFGRAEPDIAAVAELTQQQLAPRLAEGLVVTQGFIGSEAKGRTTTLGRGGSDYTAALLGE

ALNATRVDIWTDVPGIYTTDPRVAPAAKRIDVIAFEEAAEMATFGAKVLHPATLLPAVRSDIPVFVGSSK

EPKAGGTLVCKTTENPPLFRALALRRRQTLLTLHSLNMLHSRGFLAEVFGILARHNISVDLITTSEVSVA

LTMDTTGSTSAGDTLLTQALLTELSSLCRVEVEENLALVALIGNELSKACGVGKEVFGVLEPFNIRMICY

GASSHNLCFLVPGDDAEKVVQKLHHNLFE

>lcl|NZ\_FO834906.1\_prot\_WP\_002884627.1\_5080 [gene=panS] [locus\_tag=BN49\_RS27515] [protein=ketopantoate/pantoate/pantothenate transporter PanS] [protein\_id=WP\_002884627.1] [location=5347038..5347967] [gbkey=CDS]

MLATLTRLFPLWALLLSVLAYYTPTTFTPIGPWVTTLLMLIMFGMGVHLKLEDFKRVLSRPAPVAAGIFL

HYLVMPLAAWLLALLFHMPPELSAGMVLVGSVASGTASNVMIFLAKGDVALSVTISSVSTLVGVVATPLL

TRLYVDAHIQVDVMGMLLSILQIVVIPIALGLIVHHLLPKVVKAVEPFLPAFSMVCILAIISAVVAGSAA

HIASVGLVVIIAVILHNTIGLLGGYWGGRLFGFDESTCRTLAIEVGMQNSGLAAALGKIYFGPLAALPGA

LFSVWHNLSGSLLAGYWSGKPIAKKADKR

>lcl|NZ\_FO834906.1\_prot\_WP\_002884625.1\_5081 [locus\_tag=BN49\_RS27520] [protein=DUF3811 domain-containing protein] [protein\_id=WP\_002884625.1] [location=5348084..5348356] [gbkey=CDS]

MALPRITQKEMTEREQRELKTLLDRARIAHGRPLSNAETNSVKKEYIDKLMAQREAEAKKARQVRKQQAY

KTDKEATFSWSANTPTRGRR

>lcl|NZ\_FO834906.1\_prot\_WP\_009309459.1\_5082 [gene=rluF] [locus\_tag=BN49\_RS27525] [protein=23S rRNA pseudouridine(2604) synthase RluF] [protein\_id=WP\_009309459.1] [location=complement(5348353..5349228)] [gbkey=CDS]

MLPDSSTRLNKYISESGICSRREADRFIEQGNVFINGKRATIGDQVKPGDLVKVNGRLIEPREADDLVLI

ALNKPVGIVSTTEDGERDNIVDFVNHSKRIFPIGRLDKDSQGLIFLTNHGDLVNKILRAGNDHEKEYLVT

VDKPVTDEFIRGMGAGVPILGTVTKKCKVKKEAPFVFRITLVQGLNRQIRRMCEHFGYEVTKLERTRIMN

VSLTGIPLGEWRDLTDDELIDLFKLIENSSSEAKPKARPKPKAATPGIKRPVVKMENSNDKGRPAGNGKR

FTQPGRKKKGR

>lcl|NZ\_FO834906.1\_prot\_WP\_002884616.1\_5083 [locus\_tag=BN49\_RS27530] [protein=sugar-binding transcriptional regulator] [protein\_id=WP\_002884616.1] [location=5349578..5350525] [gbkey=CDS]

MENSDDIRLIVKIAQLYYEQDMTQAQIARELGIYRTTISRLLKRGREQGIVTIAINYDYNENLWLEQQLK

QKFGLKEAVVASSDGLLEEEQLSAMGQHGALLVDRLLEPGDIIGFSWGRAVRSLVENLPQASQSRQVICV

PIIGGPSGKLESRYHVNTLTYGAAARLKAESHLADFPALLDNPLIRNGIMQSQHFKTISSYWDSLDVALV

GIGSPAIRDGANWHAFYGSEESDDLNARHVAGDICSRFYDINGGLVDTNMSEKTLSIEMAKLRQARYSIG

IAMGEEKYSGILGALHGRYINCLVTNRETAELLLK

>lcl|NZ\_FO834906.1\_prot\_WP\_002884614.1\_5084 [locus\_tag=BN49\_RS27535] [protein=SDR family oxidoreductase] [protein\_id=WP\_002884614.1] [location=5350596..5351399] [gbkey=CDS]

MNTWLNLKDNVIIVTGGASGIGLAIVDELLSQGAHVQMIDIHGGDRHHNGDNYHFWPTDISSATEVQQTI

DAIIQRWSRIDGLVNNAGVNFPRLLVDEKAPAGRYELNEAAFEKMVNINQKGVFFMSQAVARQMVKQRAG

VIVNVSSESGLEGSEGQSCYAATKAALNSFTRSWSKELGKYGIRVVGVAPGILEKTGLRTPEYEEALAWT

RNITVEQLREGYTKNAIPIGRAGKLSEVADFVCYLLSARASYITGVTTNIAGGKTRG

>lcl|NZ\_FO834906.1\_prot\_WP\_016530854.1\_5085 [locus\_tag=BN49\_RS27540] [protein=mannose/fructose/sorbose PTS transporter subunit IIA] [protein\_id=WP\_016530854.1] [location=5351409..5351816] [gbkey=CDS]

MVHAIFCAHGQLAGAMLDSVRMVYGEVNVSAVAFVPGENAADIAINLEKLVSAHTDEEWVIAVDLQCGSP

WNAAAGLAMRHPQIRVISGLSLPLALELVDNQHTLSADDLCQHLQAIASQCCVVWQQPETVEEEF

>lcl|NZ\_FO834906.1\_prot\_WP\_004151751.1\_5086 [locus\_tag=BN49\_RS27545] [protein=mannose/fructose/sorbose PTS transporter subunit IIB] [protein\_id=WP\_004151751.1] [location=5351816..5352310] [gbkey=CDS]

MQITLARIDDRLIHGQVTTVWSKVANAQRIIICNDDVFNDEVRRTLLRQAAPPGMKVNVVSLEKAVAVYH

NPQYQDETVFYLFTNPHDVLTMVRQGVQIATLNIGGMAWRPGKKQLTKAVSLDPQDIQAFRELDKLGVKL

DLRVVASDPSVNILDKINETAFCE

>lcl|NZ\_FO834906.1\_prot\_WP\_046043977.1\_5087 [locus\_tag=BN49\_RS27550] [protein=PTS mannose/fructose/sorbose transporter subunit IIC] [protein\_id=WP\_046043977.1] [location=5352376..5353176] [gbkey=CDS]

MEISTLQIIAIFIFSCIAGMGSVLDEFQTHRPLIACTVIGLILGDLKTGVMLGGTLELIALGWMNVGAAQ

SPDSALASIISAILVIVGHQSIATGIAIALPVAAAGQVLTVFARTITVVFQHAADKAAEEARFRTIDLLH

VSALGVQALRVAIPALVVSLFVSADMVSSMLSAIPEFVTRGLQIAGGFIVVVGYAMVLRMMGVKYLMPFF

FLGFLAGGYLDFSLLAFGGVGVIIALIYIQLNPQWRKAEPAASTAPSAPALNQLDD

>lcl|NZ\_FO834906.1\_prot\_WP\_002884590.1\_5088 [locus\_tag=BN49\_RS27555] [protein=PTS system mannose/fructose/sorbose family transporter subunit IID] [protein\_id=WP\_002884590.1] [location=5353188..5354012] [gbkey=CDS]

MEQKKITQGDLVSMFLRSNLQQASFNFERIHGLGFCYDMIPAIKRLYPLKADQVAALKRHLVFFNTTPAV

CGPVIGVTAAMEEARANGAAIDDGAINGIKVGLMGPLAGVGDPLVWGTLRPITAALGASLALSGNILGPL

LFFFIFNAVRLAMKWYGLQLGFRKGVNIVSDMGGNLLQKLTEGASILGLFVMGVLVTKWTTINVPLVVSQ

TPGADGATVTMTVQNILDQLCPGLLALGLTLLMVRLLNKKVNPVWLIFALFGLGIIGNALGFLS

>lcl|NZ\_FO834906.1\_prot\_WP\_002884587.1\_5089 [gene=sorE] [locus\_tag=BN49\_RS27560] [protein=L-sorbose 1-phosphate reductase] [protein\_id=WP\_002884587.1] [location=5354085..5355317] [gbkey=CDS]

MQTTTALRLYGKRDLRLETFTLPAMQDDEILARVVTDSLCLSSWKEANQGADHKKVPDDVATRPIIIGHE

FCGEILAVGKKWQHKFQPGQRYVIQANLQLPDRPDCPGYSFPWIGGEATHVVIPNEVMAQDCLLTWEGDT

WFEGSLVEPLSCVIGAFNANYHLQEGSYNHVMGIRPQGHTLILGGTGPMGLLAIDYALHGPINPSLLVVT

DTNKPKLSYARRHYPSEPQTLIHYLDGHEASRDTLLALSGGHGFDDIFVFVPNEQLITLASSLLAPDGCL

NFFAGPQDKQFSAPINFYDVHYAFTHYVGTSGGNTDDMRAAVALMQAKKVQTAKVVTHILGLNAAGETTL

DLPAVGGGKKLVYTGKAFPLTPLGEIADPELAAIVARHHGIWSQEAEAYLLAHAEDITHD

>lcl|NZ\_FO834906.1\_prot\_WP\_002884583.1\_5090 [locus\_tag=BN49\_RS27565] [protein=shikimate 5-dehydrogenase] [protein\_id=WP\_002884583.1] [location=5355310..5356119] [gbkey=CDS]

MINRDTLLCISLAGRPGNFGTRFHNYLYDKLGLNYLYKAFTTKDIEAAVKGVRALGIRGCAVSMPFKESC

IPFLDAIDPSAKVIDSVNTIVNDDGKLTGLNTDYIAVKSLIASHRLDTNARVMIQGSGGMGKAVIAAFRD

AGFRDVIIAARNRQRGLALAKQYGFQWQPLPEGIAAEILVNVTPLGMAGGAESNTLAFSEAMVAQASVVF

DVVALPAETPLIRLAQQRGKQTISGAEVIALQAVEQFALYTGVRPDSALVAEASAFARS

>lcl|NZ\_FO834906.1\_prot\_WP\_004177864.1\_5091 [locus\_tag=BN49\_RS27570] [protein=Na/Pi cotransporter family protein] [protein\_id=WP\_004177864.1] [location=complement(5356207..5357838)] [gbkey=CDS]

MLTLLHLLSAVALLVWGTHIVRTGVMRVYGARLRTVLSSSVEKKPLAFCAGLGVTALVQSSNATTMLVTS

FVAQDLVGLMPALVMVLGADVGTALMARVLTFDLSWLSPLLIFIGVIFFLGRKQTRAGQLGRVGIGLGLI

LLALELIVQAVHPITQANGVQVIFASLTGDIMLDALIGAVFAIISYSSLAAVLLTATLTAAGAISFPVAL

CLVIGANLGSGLLAMLNNSAANAAARRVALGSLLFKLVGSLIILPFVHPLAAAMHKLPLAESELVIYFHV

FYNLLRCIAMVPFAGPMAKLCQRLIRDEPELDNHLKPKHLDPSALDTPALALANAARETLRIGDAMEQML

ESLHKVMHGEPRQEKELRRMADDINVLYTAIKLYLARMPKDELAEEESRRWAEIIEMSLNLEQASDIVER

MGSEIADKSLAARRAFSVEGLKELDALYDLLLSNLQLAMSVFFSSDVPSARRLRRSKHRFRILNRRYSHA

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MSSKVEQLHQQLKERILVLDGGMGTMIQGYRLSEQDFRGERFADWPCDLKGNNDLLVLSKPEVIREIHDA

YFEAGADIIETNTFNSTTIAMADYQMESLSAEINFAAAKLARASADAWTARTPEKPRYVAGVLGPTNRTA

SISPDVNDPAFRNITFDQLVAAYRESTRALVEGGVDLILIETVFDTLNAKAAIYAVKEELEALGVDLPLM

ISGTITDASGRTLSGQTTEAFYNSLRHAEALSFGLNCALGPDELRQYVQELSRIAECYVTAHPNAGLPNA

FGEYDLDADTMATQIREWAEAGFLNIVGGCCGTTPEHIAAMSRAVAGLPPRQLPEIAVACRLAGLEPLNI

GDDSLFVNVGERTNVTGSAKFKRLIKEEKYSEALDVARQQVESGAQIIDINMDEGMLDAEAAMVRFLNLI

AGEPDIARVPIMIDSSKWEVIEKGLKCIQGKGIVNSISMKEGVESFIHHAKLVRRYGAAVVVMAFDEVGQ

ADTRERKIEICRRAYKILTEEVGFPPEDIIFDPNIFAVATGIEEHNNYAQDFIGACEDIKRELPHALISG

GVSNVSFSFRGNDPVREAIHAVFLYYAIRNGMDMGIVNAGQLAIYDDLPGELRDAVEDVILNRRDDSTER

LLELAEKYRGSKADDGANAQQAEWRTWEVKKRLEYSLVKGITEFIEQDTEEARQQAARPIEVIEGPLMDG

MNVVGDLFGEGKMFLPQVVKSARVMKQAVAYLEPFIEASKEQGSSNGKMVIATVKGDVHDIGKNIVGVVL

QCNNYEIIDLGVMVPADKILKTAKEVNADLIGLSGLITPSLDEMVNVAKEMERQGFTIPLLIGGATTSKA

HTAVKIEQNYSGPTVYVQNASRTVGVVSALLSDTQRDEFVARTRKEYETVRIQHGRKKPRTPPVTLAAAR

ENDLAFDWESYTPPVAHRLGVQTVEASIETLRNYIDWTPFFMTWSLAGKYPRILEDEVVGEEAQRLFKDA

NELLDKLSAEKTLNPRGVVGLFPANRVGDDIEIYRDETRTHVLTVSHHLRQQTEKVGFANYCLADFVAPK

LSGKADYIGAFAVTGGLEEDALADAYEAQHDDYNKIMIKAIADRLAEAFAEYLHEKVRKVYWGYAANENL

SNEELIRENYQGIRPAPGYPACPEHTEKGTIWQLLDVEAHTGMKLTESFAMWPGASVSGWYFSHPDSKYF

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>lcl|NZ\_FO834906.1\_prot\_WP\_002884578.1\_5093 [gene=iclR] [locus\_tag=BN49\_RS27580] [protein=glyoxylate bypass operon transcriptional repressor IclR] [protein\_id=WP\_002884578.1] [location=5361846..5362676] [gbkey=CDS]

MATTPIPAKRGRKPAAATAQQAGGQVQSLTRGLKLLEWIAESHSSVALTELAQQAGLPNSTTHRLLTTMQ

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QCTQLMRMSAPIGGKLPMHASGAGKAFLAQLSEEQVTSLLHRKGLHAYTHATLVSPLHLKEDLAQTRKRG

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>lcl|NZ\_FO834906.1\_prot\_WP\_002884575.1\_5094 [gene=aceK] [locus\_tag=BN49\_RS27585] [protein=bifunctional isocitrate dehydrogenase kinase/phosphatase] [protein\_id=WP\_002884575.1] [location=complement(5362727..5364511)] [gbkey=CDS]

MTRGLELLIAQTILQGFDAQYGRFLEVTSGAQQRFEQADWHAVQQAMKQRIHLYDHHVGLVVEQLRCITE

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KDFFPERGWSHLLGKVLSDLPLRLPWQNKARDIGYIIASLQEALGEELLATCHLQVANELFYRNKAAWLV

GKLVMPMATLPFLLPIHRSEEGELFVDTCLTTHAEASIVFGFARSYFMVYAPLPGALVEWLREILPGKTT

AELYMAIGCQKHAKTESYREYLHYITRCDEQFIEAPGIRGMVMLVFTLPGFDRVFKVIKDRFAPQKEMTA

AHVRACYQLVKEHDRVGRMADTQEFENFVLDKRQIAPALLALLQAEAGNKLTDLGDRIVISHLYIERRMV

PLNLWLEQVNGQALRDAVEEYGNAIRQLAAANIFPGDMLFKNFGVTRHGRVVFYDYDEICYMTEVNFREI

PPPRYPEDELASEPWYSVSPGDVFPEEFRHWLCADPRIGPLFEEMHADLLRADYWRALQMRIKNGHVEDV

YAYRRKQRFSVRYGADSRPDKAFTPPSGKVRRSA

>lcl|NZ\_FO834906.1\_prot\_WP\_016531040.1\_5095 [gene=aceA] [locus\_tag=BN49\_RS27590] [protein=isocitrate lyase] [protein\_id=WP\_016531040.1] [location=complement(5364614..5365918)] [gbkey=CDS]

MKTRTQQIEELNKEWTNPRWEGITRPYSAEEVVKLRGSVNPECTLAQLGAAKLWRLLHGEAKKGYVNSLG

ALTGGQALQQAKAGIEAIYLSGWQVAADANLASSMYPDQSLYPANSVPAVVDRINNTFRRADQIQWSAGI

EPNDPRFIDYFLPIVADAEAGFGGVLNAFELMKSMIETGAAAVHFEDQLASVKKCGHMGGKVLVPTQEAI

QKLVAARLAADVMGVPTLVIARTDADAADLITSDCDPYDREFITGDRTSEGFFRTHAGIEQAISRGLAYA

PYADLVWCETSKPDLEQARRFAEAIHARFPGKLLAYNCSPSFNWKKNLDDKTIASFQQQLSDMGYKYQFI

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SVTALTGSTEEDQF

>lcl|NZ\_FO834906.1\_prot\_WP\_002884559.1\_5096 [gene=aceB] [locus\_tag=BN49\_RS27595] [protein=malate synthase A] [protein\_id=WP\_002884559.1] [location=complement(5365998..5367599)] [gbkey=CDS]

MTQQATITDELAFSQPYGEQEKQILTPEAVEFLTELVSRFTPARNKLLAARLQQQQAIDDGQLPDFISET

ASIRNGDWTIRGIPADLQDRRVEITGPVERKMVINALNANVKVFMADFEDSLAPDWRKVIDGQINLRDAV

NGTISYTNEAGKIYQLQPNPAVLVCRVRGLHLPEKHVTWRNEAIPGSLFDFALYFFHNYQALLAKGSGPY

FYLPKTQAWQEAAWWNDVFSFTEDRFDLPRGTIKATLLIETLPAVFQMDEILHALRDHIVGLNCGRWDYI

FSYIKTLKNHPDRVLPDRQVVTMDKPFLSAYSRLLIKTCHKRGAFAMGGMAAFIPSKDTERNRQVLSKVT

ADKELEANNGHDGTWIAHPGLADTAMAVFDRVLGDKPNQLSVTRSEDAPITAEQLLAPCEGERTEAGMRA

NIRVAVQYIEAWISGNGCVPIYGLMEDAATAEISRTSIWQWIHHQKTLNDGTPVTKALFRQWLAEELMVI

QEELGEHRFSHGRFDDAARLMEQITTSDELIDFLTLPGYRLLA

>lcl|NZ\_FO834906.1\_prot\_WP\_004146576.1\_5097 [gene=metA] [locus\_tag=BN49\_RS27600] [protein=homoserine O-succinyltransferase] [protein\_id=WP\_004146576.1] [location=complement(5367860..5368789)] [gbkey=CDS]

MPIRVQDELPAVNFLRNENVFVMTTTRATTQEIRPLKVLILNLMPKKIETENQFLRLLSNSPLQVDIQLL

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VCWAVQAALNILYGIPKQTRAEKISGVYEHHILHPHALLTRGFDDSFLAPHSRYADFPAGLIRDYTDLEI

LAETEEGDAYLFASKDKRIAFVTGHPEYDANTLASEYFRDVEAGLNPEIPHNYFPQNDPQNKPRATWRSH

GNLLFANWLNYYVYQITPYDLRHMNPTLE

>lcl|NZ\_FO834906.1\_prot\_WP\_004178258.1\_5098 [locus\_tag=BN49\_RS27605] [protein=acetyltransferase] [protein\_id=WP\_004178258.1] [location=5368946..5369407] [gbkey=CDS]

MVINIRRSRPDEGDKLTAIWCRSVDATHDFLTKAYRKELEEMVRAFLPEAPLWVAVNTEDQPIAFMLLTG

DHMDALFVDPDVRGCGVGKLLIEHALSLTPKLTTNVNEQNEQAVGFYQKMGFRVTGRSETDDLGQPYPLL

NLMYEQQAEADYD

>lcl|NZ\_FO834906.1\_prot\_WP\_002882540.1\_5099 [locus\_tag=BN49\_RS27630] [protein=FadR family transcriptional regulator] [protein\_id=WP\_002882540.1] [location=5375175..5375876] [gbkey=CDS]

MSLSAQQLAAQKNISWVLAEKLAQKILTGEYQPESILPGEMELGEQFGVSRTAVREAVKTLTAKGMLLPR

PRIGTRVMPRSSWNFLDKELLSWWLTEDNFEEVVSHFLVMRSSLEPQACFLAAANGTAGQKAQLNTLMEE

MIALKRHFQRERWIEVDMAWHEHIYEMSGNPFLSSFASLFHSVYHTYFTSITQNEVVKLDLHQAIVDAIL

NSDAPGALLACQALLNAPHHVNQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002882539.1\_5100 [gene=mdtD] [locus\_tag=BN49\_RS27635] [protein=multidrug transporter subunit MdtD] [protein\_id=WP\_002882539.1] [location=5375889..5377286] [gbkey=CDS]

MSGKKGRSMAGLPWIAAMAFFMQALDATILNTALPAIAHSLNRSPLAMQSAIISYTLTVAMLIPVSGWLA

DRFGTRRVFIIAVSLFTLGSLACALSSSLTELVIFRVIQGIGGAMMMPVARLALLRAYPRSELLPVLNFV

TMPGLVGPILGPVLGGVFVTWASWHWIFLINIPIGVIGILYARKYMPNFTTPRRRFDIGGFLLFGLSLVL

FSSGIELFGEKIVATWQALAVIAVSLLLLVAYVRHARRHPTPLISLSLFKTHTFSVGIAGNLATRLGTGC

VPFLMPLMLQVGFGYPAIIAGCMIAPTAIGSIIAKSTVTQVLRWFGYRKTLVGITVFIGLMIAQFSLQSP

EMPLWMLLLPLFVLGMAMSTQFTAMNTITLADLTDDNASSGNSLLAVTQQLSISLGVAISAAVLRFYEGF

DNASTVQQFHYTFITMGVITIISALMFMLLRAKDGRNLISERHKR

>lcl|NZ\_FO834906.1\_prot\_WP\_004187944.1\_5101 [gene=rbsR] [locus\_tag=BN49\_RS27640] [protein=ribose operon transcriptional repressor RbsR] [protein\_id=WP\_004187944.1] [location=complement(5377283..5378275)] [gbkey=CDS]

MATMKDVARIAGVSTSTVSHVINKDRFVSEAITAKVDAAIKSLNYAPSALARSLKLNQTRTIGMLITAST

NPFYSELVRGVERSCFERGYSLVLCNTEGDEQRMNRNLETLMQKRVDGLLLLCTETHQPSPEIMQRYPSV

PTVMMDWAPFDGDSDLIQDNSLLGGDMATQYLIDQGHSRIACIAGPLDKTPARLRLEGYHAAMARCGLPV

AEGYVVTSDFEFGGGFSAMQQLLALPQRPQAVFVGNDAMAVGAYQALYQAGLQIPQDMALVGYDDIELAR

YMTPPLTTIHQPKDELGELAIDVLIHRMADPQQKQQRVQLTPELVVRGSA

>lcl|NZ\_FO834906.1\_prot\_WP\_004173836.1\_5102 [gene=rbsK] [locus\_tag=BN49\_RS27645] [protein=ribokinase] [protein\_id=WP\_004173836.1] [location=complement(5378279..5379211)] [gbkey=CDS]

MMKTAGKLVVLGSINADHILNLDAFPTPGETVTGHHYQVAFGGKGANQAVAAGRSGADIAFIACTGDDDI

GERIRRQLASDKIDVAPVRAVAGEATGVALIFVNAEGENVIGIHAGANAALSVSQVEAEKERIASAQALL

MQLESPLESVIAAAKIAHHHHTTVVLNPAPARELPDELLALVDIITPNETEAEKLTGIRVESDEDAAKAA

NVLHAKGIGTVMITLGSRGVWLSAEGESRRIPGFRVQAIDTIAAGDTFNGALVTALLEGTALPEAIRFAH

AAAAIAVTRKGAQPSVPWRTEIDEFLAQQG

>lcl|NZ\_FO834906.1\_prot\_WP\_002882536.1\_5103 [gene=rbsB] [locus\_tag=BN49\_RS27650] [protein=ribose ABC transporter substrate-binding protein RbsB] [protein\_id=WP\_002882536.1] [location=complement(5379312..5380202)] [gbkey=CDS]

MNMKKLATLVSAVALSATVSANAMAKDTIALVISTLNNPFFVSLKDGAQKEADKLGYNLVVLDSQNNPAK

ELANVQDLTVRGTKLLLINPTDSDAVGNAVKMANQAKIPVITLDRQATKGDVVSHIASDNVQGGKMAGDY

IAKKVGESAKVIELQGIAGTSAARERGEGFKQAVAAHKFNVLASQPADFDRTKGLNVMQNLLTAHPDVQA

VFAQNDEMALGALRALQTAGKSDVMVVGFDGTPDGEKAVNSGKLAATVAQLPEQIGAKGVETADKVLKGE

KVEANYPVELKLVVKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_002882531.1\_5104 [gene=rbsC] [locus\_tag=BN49\_RS27655] [protein=ribose ABC transporter permease] [protein\_id=WP\_002882531.1] [location=complement(5380230..5381195)] [gbkey=CDS]

MTTQAVSGRRYFTKAWLMEQKSLIALLVLIAVVSTMSPNFFTVNNLFNILQQTSVNAIMAVGMTLVILTS

GIDLSVGSLLALTGAVAASIVGIEVNALVAVAAALALGAAIGAVTGVIVARGRVQAFIATLVMMLLLRGV

TMVYTNGSPINTGFSDNADLFGWFGIGRPLGIPTPVWIMAIVFLAAWYMLHHTRLGRYIYALGGNEAATR

LSGISVNKVKIIVYALCGMLASLAGIIEVARLSSAQPTAGTGYELDAIAAVVLGGTSLAGGKGRIVGTLI

GALILGFLNNGLNLLGVSSYYQMIVKAVVILLAVLVDNKKQ

>lcl|NZ\_FO834906.1\_prot\_WP\_016530467.1\_5105 [gene=rbsA] [locus\_tag=BN49\_RS27660] [protein=ribose ABC transporter ATP-binding protein RbsA] [protein\_id=WP\_016530467.1] [location=complement(5381201..5382706)] [gbkey=CDS]

MEALLQLKGIDKAFPGVKALSGAALNVYAGRVMALVGENGAGKSTMMKVLTGIYTRDAGSLLWLGKETTF

NGPKSSQEAGIGIIHQELNLIPQLTIAENIFLGREFVNRFGKIDWKQMYAEADKLLAKLNLRFTSQKLVG

DLSIGDQQMVEIAKVLSFESKVIIMDEPTDALTDTETESLFRVIRELKSQGRGIVYISHRMKEIFEICDD

VTVFRDGQFIAEREVSSLDEDRLIEMMVGRKLEDQYPHLDKAPGAVRLKVDNLCGPGGDNVTFTLRQGEI

LGVAGLMGAGRTELMKVLYGALPRSSGSVTLDGREVVTRSPQDGLANGIVYISEDRKRDGLVLGMSVKEN

MSLTALRYFSRAGGSLKHKDEQQAVSDFIRLFNVKTPSMEQAIGLLSGGNQQKVAIARGLMTRPKVLILD

EPTRGVDVGAKKEIYQLINQFKADGLSIILVSSEMPEVLGMSDRIIVMHEGHLGGEFTREQATQEVLMAA

AVGKLNRVNQE

>lcl|NZ\_FO834906.1\_prot\_WP\_009308849.1\_5106 [gene=rbsD] [locus\_tag=BN49\_RS27665] [protein=D-ribose pyranase] [protein\_id=WP\_009308849.1] [location=complement(5382717..5383136)] [gbkey=CDS]

MKKGTVLNADISAVISRLGHTDTLVVCDAGLPVPRSSTRIDMALTQGVPSFMQVLEVVTTEMQVEAAVIA

EEIKTHNPQLHATLLTHLEQLQQHQGTTIEIRYTSHEQFKKQTADSQAVIRSGECSPFANIILCAGVTF

>lcl|NZ\_FO834906.1\_prot\_WP\_016530298.1\_5107 [gene=kup] [locus\_tag=BN49\_RS27670] [protein=low affinity potassium transporter Kup] [protein\_id=WP\_016530298.1] [location=complement(5383322..5385190)] [gbkey=CDS]

MSTDNKQSLPALTLAAIGVVYGDIGTSPLYTLRECLSGQFGFGVERDAVFGFLSLIFWLLIFTVSIKYIT

FVMRADNAGEGGILTLMSLAGRNTSARMTSVLVILGLIGGSFFYGEVVITPAISVMSAIEGLEIIAPQLD

TWIVPISIIVLTLLFVIQKHGTGMVGKLFAPIMLIWFLLLAVLGARSIYANPEVLQALNPYWAVHFFLQY

KTVSFIALGAVVLSITGVEALYADMGHFGKLPIRVAWFSVVLPSLVLNYFGQGALLLKHPEAIKNPFFLL

APEWALIPMLIIATLATVIASQAVISGVFSLTRQAVRLGYLSPMRIIHTSEMESGQIYIPFINWLLYVSV

VIVIVSFEHSSNLAAAYGIAVTGTMVLTSILSATVARKNWQWNKLFVGLMLVAFLCIDIPLFSANLDKIV

SGGWLPLSLGMVMFTVMTTWKSERFRLLRRMHEHGNSLEAMISSLEKSPPVRVPGTAVYMSRALNVIPFA

LLHNLKHNKVLHERVILLTLRTEDAPYVHNVRRVQIEQLSPSFWRVVASYGWRETPNVEEVFHRCGLEGL

SCRMMETSFFMSHESLIIGKRPWYLRLRGKLYLLLQRNALRAPDQFEIPPNRVIELGTQVEI

>lcl|NZ\_FO834906.1\_prot\_WP\_004151555.1\_5108 [gene=ravA] [locus\_tag=BN49\_RS27675] [protein=ATPase RavA] [protein\_id=WP\_004151555.1] [location=5385407..5386906] [gbkey=CDS]

MAQTHLLAERISRLSAALEKGLFERSHAIRLCLLAALSGESVFLLGPPGIAKSLIARRLKFAFQQARAFE

YLMTRFSTPEEVFGPLSIQALKDEGRYERLTAGYLPEAEIVFLDEIWKAGPAILNTLLTAINERHFRNGA

HEEKIPMRLLVAASNELPEADSSLEALYDRMLIRLWLDKVQDKGNFRSMLVSQQDENSNPVPSALQVSDE

EFTQWQQQIGNIKLPDAVFELIFQLRQQLDALPNAPYVSDRRWKKAIRLLQASAFFSGRDSIAPIDLILL

KDCLWHNVESMNLMSQQLETLMTCHAWQQQAMLTRLGAIVQRRIQIQQQQSDKTALKVTRLGGMFSRKPH

YELPAEIQGTTLTLLLQQPLKLHDMEVIHITFEREALANWLEKGGEIRGKLNGIGFAQLLNMDVDTSQHL

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AQIKQAKQP

>lcl|NZ\_FO834906.1\_prot\_WP\_002882517.1\_5109 [gene=viaA] [locus\_tag=BN49\_RS27680] [protein=ATPase RavA stimulator ViaA] [protein\_id=WP\_002882517.1] [location=5386903..5388351] [gbkey=CDS]

MTLDMLNVMLAVSEEGMIEEMLLALLASPQLAVFFEKFPRLKNIIAADIPRWREAVRARLKEVNIPPDLD

AEVQTYQQAQLLSTSQFIVQLPQILGKLHQLQSPFAAQAQKLVDDNATFTPALHTLFLQRWRLSLVVQAT

SLNQQLLDEERDQLLSEVQERMTLSGQLDPVLAENDTAAGRLWDMSAGELKRGDYQLIVRYGDFLNQQPE

LLQLAEQLGRSREAKSVPKKDAPMETFRSLVREPATVPEQVDGLQQSDDILRLLPPELATLGITELEFEF

YRKLVEKQLLTYRLHGDAWREKITERPVTRQDFDEQPRGPFIVCVDTSGSMGGFNEQCAKAFCLALMRIA

LADNRRCFIMLFSSEVVHYELTSESGLEQAIRFLSQRFRGGTDLASCFRAIIERLQNPQWVDADAVVISD

FIAQRLPDEVIAQVGELQRKHQHRFHAVAMSVHGKPGIMRIFDHIWRFDTGLRSRLLRRWRR

>lcl|NZ\_FO834906.1\_prot\_WP\_002882514.1\_5110 [gene=asnA] [locus\_tag=BN49\_RS27685] [protein=aspartate--ammonia ligase] [protein\_id=WP\_002882514.1] [location=complement(5388355..5389347)] [gbkey=CDS]

MKTAYIAKQRQISFVKSHFSRQLEEKLGLIEVQAPILSRVGDGTQDNLSGCEKAVQVKVKTLPDAQFEVV

HSLAKWKRQTLGQHDFSAGEGLYTHMKALRPDEDRLTPIHSVYVDQWDWERVMGDEERHVGTLKATVEAI

YAGIKATELAVSQEFGLTPFLPEQIHFVHSQELLSRYPELDAKGRERAIAKELGAVFLIGIGGKLADGKR

HDVRAPDYDDWSTEVSEGFAGLNGDILVWNPVLEDAFEISSMGIRVDAEALKRQLALTGDEDRLKLEWHQ

ALLRGEMPQTIGGGIGQSRLTMLLLQLDHIGQVQCGVWPAQVRESVSALL

>lcl|NZ\_FO834906.1\_prot\_WP\_002882510.1\_5111 [gene=asnC] [locus\_tag=BN49\_RS27690] [protein=transcriptional regulator AsnC] [protein\_id=WP\_002882510.1] [location=5389499..5389957] [gbkey=CDS]

MENYQIDNLDRGILDALMANARTAYAELAKQFSVSPGTIHVRVEKMKQAGIITGARIDVSPKQLGYDVGC

FIGIILKSAKDYPSALARLESLEEVTEAYYTTGHYSIFIKVMCKSIDALQQVLINKIQTIDEIQSTETLI

VLQNPIMRTIKP

>lcl|NZ\_FO834906.1\_prot\_WP\_004144988.1\_5112 [gene=mioC] [locus\_tag=BN49\_RS27695] [protein=FMN-binding protein MioC] [protein\_id=WP\_004144988.1] [location=5390057..5390497] [gbkey=CDS]

MADITLISGSTLGSAEYVAEHLAEKLEEAGYSTEIQHGPLVDDLQAQGIWLIISSTHGAGDIPDNLVPFY

DALQEKQADLSAVRFGAIGIGSREYDTFCGAIDKLEAALKACGAKQIGETLKINVLEHEIPEDPAEIWLG

SWKNLL

>lcl|NZ\_FO834906.1\_prot\_WP\_016530810.1\_5113 [gene=mnmG] [locus\_tag=BN49\_RS27700] [protein=tRNA uridine-5-carboxymethylaminomethyl(34) synthesis enzyme MnmG] [protein\_id=WP\_016530810.1] [location=5390879..5392768] [gbkey=CDS]

MFYQDPFDVIIIGGGHAGTEAAMAAARMGQQTLLLTHNIDTLGQMSCNPAIGGIGKGHLVKEVDALGGLM

AKAIDQAGIQFRILNASKGPAVRATRAQADRVLYRQAVRTALENQPNLMIFQQAVEDLIVENDSVVGAVT

QMGLKFRAKAVVLTVGTFLDGKIHIGLDNYSGGRAGDPPSIPLSRRLRELPLRVSRLKTGTPPRINARTI

DFSVLAQQHGDNPMPVFSFMGSADQHPRQVPCYITHTNEKTHDVIRNNLDRSPMYAGVIEGIGPRYCPSI

EDKVMRFADRNQHQIFLEPEGLTSNEIYPNGISTSLPFDVQMQIVRSMQGMENARIVRPGYAIEYDFFDP

RDLKPTLESKFIQGLFFAGQINGTTGYEEAAAQGLLAGLNAARFSAEKEGWAPRRDQAYLGVLVDDLCTL

GTKEPYRMFTSRAEYRLMLREDNADLRLTEQGRELGLVDDERWARYNEKLESIERERQRLKSTWVNPQAE

SANEVNAHLTAPLSREASGEDLLRRPEMTYEQLVQLSPFTPGLEDRQAAEQVEIQVKYEGYIARQQDEIE

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151554.1\_5114 [gene=rsmG] [locus\_tag=BN49\_RS27705] [protein=16S rRNA (guanine(527)-N(7))-methyltransferase RsmG] [protein\_id=WP\_004151554.1] [location=5392884..5393507] [gbkey=CDS]

MLNKLSRLLDEAGISLTDHQKNQLVAYVGLLDKWNKAYNLTSVRDPNEMLVRHILDSIIVAPYLQGSRFI

DVGTGPGLPGIPLAIVCPESHFTLLDSLGKRVRFLRQVQHELKLDNVTPVQSRVEAFPAEPPFDGVISRA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004144991.1\_5115 [gene=atpI] [locus\_tag=BN49\_RS27710] [protein=F0F1 ATP synthase subunit I] [protein\_id=WP\_004144991.1] [location=5394124..5394504] [gbkey=CDS]

MSVSLLSRNVARKLLFIQLLAVMASGLLFSLKDPFWGISAVCGGLAVVLPNLMFIIFAWRHQAHTPAKGR

VAWTFAFGEAFKVLLTFALLAVALAVLKVVFLPLIVTWVLVLVVQVLAPAVINNKG

>lcl|NZ\_FO834906.1\_prot\_WP\_004173838.1\_5116 [gene=atpB] [locus\_tag=BN49\_RS27715] [protein=F0F1 ATP synthase subunit A] [protein\_id=WP\_004173838.1] [location=5394512..5395327] [gbkey=CDS]

MASENMTPQDYIGHHLNNLQLDLRTFSLVDPHNHTATFWTLNIDSMFFSVVLGLLFLAMFRSVAKKATSG

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VVPSADVNITLSMALGVFILIIFYSIKMKGVGGFVKELTMQPFNHWAFIPVNLILEGVSLLSKPVSLGLR

LFGNMYAGELIFILIAGLLPWWSQWVLNVPWAIFHILIITLQAFIFMVLTIVYLSMASEEH

>lcl|NZ\_FO834906.1\_prot\_WP\_000429386.1\_5117 [gene=atpE] [locus\_tag=BN49\_RS27720] [protein=F0F1 ATP synthase subunit C] [protein\_id=WP\_000429386.1] [location=5395377..5395616] [gbkey=CDS]

MENLNMDLLYMAAAVMMGLAAIGAAIGIGILGGKFLEGAARQPDLIPLLRTQFFIVMGLVDAIPMIAVGL

GLYVMFAVA

>lcl|NZ\_FO834906.1\_prot\_WP\_004107293.1\_5118 [gene=atpF] [locus\_tag=BN49\_RS27725] [protein=F0F1 ATP synthase subunit B] [protein\_id=WP\_004107293.1] [location=5395667..5396137] [gbkey=CDS]

MNMNATILGQAIAFVIFVWFCMKYVWPPLMAAIEKRQKEISDGLASAERAKKDLDLAQANATDQLKKAKA

EAQVIIEQANKRRSQILDEAKAEAEQERTKIVAQAQAEIDAERKRAREELRKQVAILAVAGAEKIIERSV

DEAANSDIVDKLVAEL

>lcl|NZ\_FO834906.1\_prot\_WP\_004144994.1\_5119 [gene=atpH] [locus\_tag=BN49\_RS27730] [protein=F0F1 ATP synthase subunit delta] [protein\_id=WP\_004144994.1] [location=5396152..5396685] [gbkey=CDS]

MSEFVTVARPYAKAAFDFAVEHNSVERWQDMLAFAAEVTKNDQMAELLSGALAPETLSEAFIAICGEQLD

ENGQNLIKVMAENNRLKVLPDVLEQFIHLRAASEAIAEVEVISANQLSDEQLARIVSAMEKRLSRKVKLN

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>lcl|NZ\_FO834906.1\_prot\_WP\_004144995.1\_5120 [gene=atpA] [locus\_tag=BN49\_RS27735] [protein=F0F1 ATP synthase subunit alpha] [protein\_id=WP\_004144995.1] [location=5396698..5398239] [gbkey=CDS]

MQLNSTEISELIKQRIAQFNVVSEAHNEGTIVSVSDGVIRIHGLAECMQGEMISLPGNRYAIALNLERDS

VGAVVMGPYADLAEGMKVKCTGRILEVPVGRGLLGRVVNTLGAPIDGKGPLENDGFSAVEAIAPGVIERQ

SVDQPVQTGYKSVDAMIPIGRGQRELIIGDRQTGKTALAIDAIINQRDSGIKCVYVAIGQKASTISNVVR

KLEEHGALANTIVVVATASESAALQYLAPYAGCAMGEYFRDRGEDALIVYDDLSKQAVAYRQISLLLRRP

PGREAFPGDVFYLHSRLLERAARVNAEYVEAFTKGEVKGKTGSLTALPIIETQAGDVSAFVPTNVISITD

GQIFLETNLFNAGIRPAVNPGISVSRVGGAAQTKIMKKLSGGIRTALAQYRELAAFSQFASDLDDATRKQ

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GYNDEIEGKLKGILDSFKATQSW

>lcl|NZ\_FO834906.1\_prot\_WP\_016529510.1\_5121 [gene=atpG] [locus\_tag=BN49\_RS27740] [protein=F0F1 ATP synthase subunit gamma] [protein\_id=WP\_016529510.1] [location=5398290..5399153] [gbkey=CDS]

MAGAKEIRSKIASVQNTQKITKAMEMVAASKMRKSQERMAASRPYADTMRKVIGHLANGNLEYKHPYLEE

RDVKRVGYLVVSTDRGLCGGLNINLFKKLLAEMKAWSDKGVQCDLAMIGSKGVSFFNSVGGNVVAQVTGM

GDNPSLSELIGPVKVLLQAYDEGRLDKLYVVSNKFINTMSQVPTITQLLPLPASEDADLKRKSWDYLYEP

DPKALLDTLLRRYVESQVYQGVVENLASEQAARMVAMKAATDNGGSLIKELQLVYNKARQASITQELTEI

VSGAAAV

>lcl|NZ\_FO834906.1\_prot\_WP\_004144997.1\_5122 [gene=atpD] [locus\_tag=BN49\_RS27745] [protein=F0F1 ATP synthase subunit beta] [protein\_id=WP\_004144997.1] [location=5399180..5400562] [gbkey=CDS]

MATGKIVQVIGAVVDVEFPQDAVPRVYEALEVQNGNEVLVLEVQQQLGGGIVRTIAMGSSDGLRRGLDVK

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NEPPGNRLRVALTGLTMAEKFRDEGRDVLLFVDNIYRYTLAGTEVSALLGRMPSAVGYQPTLAEEMGVLQ

ERITSTKTGSITSVQAVYVPADDLTDPSPATTFAHLDATVVLSRQIASLGIYPAVDPLDSTSRQLDPLVV

GQEHYDTARGVQSILQRYQELKDIIAILGMDELSEEDKLVVARARKIQRFLSQPFFVAEVFTGSPGKYVA

LKDTIRGFKGIMEGEYDHLPEQAFYMVGSIDEAVEKAKKL

>lcl|NZ\_FO834906.1\_prot\_WP\_001251971.1\_5123 [gene=atpC] [locus\_tag=BN49\_RS27750] [protein=F0F1 ATP synthase subunit epsilon] [protein\_id=WP\_001251971.1] [location=5400583..5401002] [gbkey=CDS]

MAMTYHLDVVSAEQQMFSGLVEKIQVTGSEGELGIYPGHAPLLTAIKPGMIRIVKQHGHEEFIYLSGGIL

EVQPGSVTVLADTAIRGQDLDEARALEAKRKAEEHIKSSHGDVDYAQASAELAKAIAKLRVIELTKKAM

>lcl|NZ\_FO834906.1\_prot\_WP\_004173839.1\_5124 [gene=glmU] [locus\_tag=BN49\_RS27770] [protein=bifunctional UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-phosphate N-acetyltransferase GlmU] [protein\_id=WP\_004173839.1] [location=5401699..5403069] [gbkey=CDS]

MSNSAMSVVILAAGKGTRMYSDLPKVLHTLAGKPMVQHVIDAANDLGACAVHLVYGHGGDLLRQTLHEDN

LNWVLQAEQLGTGHAMQQAAPFFNDDEDILMLYGDVPLISVETLQRLRAAKPQGGIGLLTVKLDDPTGYG

RITRENGQVTGIVEHKDASEAQRQIQEINTGILIAGGADLKRWLAKLTNNNAQGEYYITDIIAMAHQEGH

QIVAVHPQRLSEVEGVNNRLQLARLERVYQAEQAEKLLLAGVMLRDPARFDLRGTLQHGRDVEIDTNVIL

EGNVVLGDRVKIGAGCVIKNSTIGDDCEISPYSVVEDAQLQAACTIGPFARLRPGAELLEGAHVGNFVEM

KKARLGKGSKAGHLTYLGDAEIGDNVNIGAGTITCNYDGANKHKTIIGDDVFVGSDTQLVAPVTVGNGVT

IAAGTTVTRNIADNELVLSRVPQVHKQGWQRPVKKK

>lcl|NZ\_FO834906.1\_prot\_WP\_046043984.1\_5125 [gene=glmS] [locus\_tag=BN49\_RS27775] [protein=glutamine--fructose-6-phosphate transaminase (isomerizing)] [protein\_id=WP\_046043984.1] [location=5403253..5405082] [gbkey=CDS]

MCGIVGAVAQRDIAEILLEGLRRLEYRGYDSAGLAVVDSEGHMTRVRRLGKVQMLAQAVEEQPLHGGTGI

AHTRWATHGEPSESNAHPHVSEHIVVVHNGIIENHEPLRALLQSRGYVFVTETDTEVIAHLVHWELEQGA

TLREAVLRAIPQLRGAYGTVIMDTRDPGTLLAARSGSPLVIGLGMGENFIASDQLALLPVTRRFIFLEEG

DIAEVTRRSVVIFDKSAAQVKRQEIESNLQYDAGDKGIYRHYMQKEIFEQPNAIKNTLTGRISHGEVDLS

ELGPNANEMLAQVEHIQIVACGTSYNSGMVSRYWFEALAGVPCDVEIASEFRYRKSAVRRNSLMITLSQS

GETADTLAALRLSKELGYLGSLAICNVRGSSLVRESDLALMTKAGTEIGVASTKAFTTQLTVLLMLVAKL

ARLKGQDASIEHDIVHGLQALPNRIEQMLSQDKRIEQLAERFSDKHHALFLGRGDQYPIAMEGALKLKEI

SYIHAEAYAAGELKHGPLALIDAEMPVIVVAPNNELLEKLKSNIEEVRARGGELYVFADGEAGFNGSDNM

HIIEMPHVEETIAPIFYTVPLQLLAYHVALIKGTDVDQPRNLAKSVTVE

>lcl|NZ\_FO834906.1\_prot\_WP\_016531022.1\_5126 [gene=pstS] [locus\_tag=BN49\_RS27780] [protein=phosphate ABC transporter substrate-binding protein PstS] [protein\_id=WP\_016531022.1] [location=5405419..5406459] [gbkey=CDS]

MNVMRTTVATVVAATLSMSAFSAFAAASLTGAGATFPAPVYAKWADTYQKETGNKVNYQGIGSSGGVKQI

IANTVDFGASDAPLADDKLTQEGLFQFPTVIGGVVLAVNLPGVKSGELVLDGKTLGDIYLGKIKKWDDEA

IAKLNPGLKLPSQNIAVVRRADGSGTSFVFTSYLSKVNEEWKSKIGAGSTVNWPTGLGGKGNDGIAAFVQ

RLPGSIGYVEYAYAKQNNLAYTKLVSADGKPVSPTEDNFANAAKGVDWSKSFAQDLTNQKGENAWPITST

TFILVHKTTNKPEQTAEVLKFFDWAYKNGGKEANALDYATLPESVVEQVRAAWKTNVKDSSGKALY

>lcl|NZ\_FO834906.1\_prot\_WP\_004145004.1\_5127 [gene=pstC] [locus\_tag=BN49\_RS27785] [protein=phosphate ABC transporter permease PstC] [protein\_id=WP\_004145004.1] [location=5406588..5407547] [gbkey=CDS]

MAATKPAFTPPGKKGDMIFSALVKLAALIVLLMLGGIIVSLIISSWPSIQKFGFAFLWTKEWDAPNEIFG

ALVPIYGTLVTSFIALLIAVPVSFGIALFLTELSPAWLKRPLGIAIELLAAIPSIVYGMWGLFIFAPLFA

TYFQEPVGNVLSTIPFVGALFAGPAFGIGILAAGVILAIMIIPYIAAVMRDVFEQTPVMMKESAYGIGCT

TWEVIWRIVLPFTKNGVIGGVMLGLGRALGETMAVTFIIGNTYQLDSISLYMPGNSITSALANEFAEAET

GLHVAALMELGLILFVITFIVLAASKFMIMRLAKNEGAR

>lcl|NZ\_FO834906.1\_prot\_WP\_004151547.1\_5128 [gene=pstA] [locus\_tag=BN49\_RS27790] [protein=phosphate ABC transporter permease PstA] [protein\_id=WP\_004151547.1] [location=5407547..5408437] [gbkey=CDS]

MATIELQTTAELAESRRKMQAKRRMKNRIALALSMATMAFGLFWLIWILMATITRGFDGMSLALFTEMTP

PPNTAGGGLANALAGSGLLILWATVFGTPLGILAGIYLAEYGRKSVLAEIIRFINDILLSAPSIVVGLFV

YTIVVAQMQHFSGWAGVIALALLQVPIVIRTTENMLKLVPDSLREAAYALGTPKWKMISAITLKASVSGI

MTGILLAIARIAGETAPLLFTALSNQFWSTDMMQPIANLPVTIFKFAMSPFAEWQQLAWAGVLIITLCVL

LLNILARVIFAKKKHG

>lcl|NZ\_FO834906.1\_prot\_WP\_004145006.1\_5129 [gene=pstB] [locus\_tag=BN49\_RS27795] [protein=phosphate ABC transporter ATP-binding protein PstB] [protein\_id=WP\_004145006.1] [location=5408485..5409258] [gbkey=CDS]

MSMVNTAPGKISVRNLNFYYGKFHALKNINLDITKNQVTAFIGPSGCGKSTLLRTFNKMFELYPEQRAEG

EILLDGDNILTNTQDIALLRAKVGMVFQKPTPFPMSIYDNIAFGVRLFEKLSRADMDERVQWALTKAALW

NETKDKLHQSGYSLSGGQQQRLCIARGIAIRPEVLLLDEPCSALDPISTGRIEELITELKQDYTVVIVTH

NMQQAARCSDHTAFMYLGELIEFSNTDDLFTKPAKKQTEDYITGRYG

>lcl|NZ\_FO834906.1\_prot\_WP\_004145007.1\_5130 [gene=phoU] [locus\_tag=BN49\_RS27800] [protein=phosphate signaling complex protein PhoU] [protein\_id=WP\_004145007.1] [location=5409309..5410034] [gbkey=CDS]

MDNLNLNKHISGQFNAELEYIRTQVMTMGGLVEQQLSDAITAMHNQDSDLAKRVIDGDKQVNMMEVAIDE

ACVRIIAKRQPTASDLRLVMAIIKTIAELERIGDVADKICRTALEKFSQQHQPLLVSLESLGRHTVQMLH

DVLDAFARMDLDEAVRIYREDKKVDQEYEGIVRQLMTYMMEDSRTIPSVLTALFCARSIERIGDRCQNIC

EYIFYFVKGQDFRHVGGDELDKLLAGKDPKE

>lcl|NZ\_FO834906.1\_prot\_WP\_004150305.1\_5131 [locus\_tag=BN49\_RS27810] [protein=carbohydrate porin] [protein\_id=WP\_004150305.1] [location=5410512..5412146] [gbkey=CDS]

MMRKNRIASAIVLLAPLCYSTNLLASQLTVEQRLELLEKALKDTQKELKKYQDQERKRDQIWASWSPPAE

GQKRKTGGATAGPKTAVKPDAVLVKNQQPVTDGAPAYSAMTLKDFSKFVKDEIGFSYNGYFRSGWGTASH

GSPKSWAIGSLGRLGNEYSGWFDLQLKQRVFQEGDKRVDAIVMLDGNVGQQYSTGWFGDNAGGENYIQFS

DMYVNTKGFLPFAPEADFWVGKHGAPKIEIQMLDWKTQRTDAAAGVGLENWQVGAGKFDIALIREDVDDY

DRSLSNKQQINTNTLDVRYKEIPLWDKASLMVSGRYVAANQSSSEKYKEGNEGYYPWKDTWMAGTSLTQK

FANGGFNEFSFLLANNSIASSFSRYAGSSPYTTFNGRYYGDHTNGTAVRLTSQGETYLRDDVIMANAIVY

SFGNDVYSYETGAHSDFESIRTVLRPAYIWDKYNQTGVELGYFKQQNKDVTGKKYNESGYKTTLFHTFKV

NTSMLTSRPEIRFYATYIKAKDIDLDKAANNTTSIFEDGKNDQFAVGAQAEIWW

>lcl|NZ\_FO834906.1\_prot\_WP\_046043986.1\_5132 [locus\_tag=BN49\_RS27815] [protein=alpha/beta hydrolase-fold protein] [protein\_id=WP\_046043986.1] [location=5412185..5413351] [gbkey=CDS]

MKRHAIYFALALAGAAFTLQAAPLPAMPDPSLPVSHFITQVNADKSITYRLFAPDARRVSIVTGATPDSF

VSHDMTKAADGVWTWKSEPMKPNLYEYYFDVDGFRSVDTGSRYQKPQRQVNTSLILVPGSILDDREVAHG

DLRTLTYHSKALNAERRLYVWTPPGYSGTGDPLPVLYFYHGFGDSGLSAIDQGRIPQIMDNLLAEGKIKP

MLVVVPDTETDIPEAVAENFPPQERRKTFYPLNAQAADKELMQDIIPLIDARFNVRKDADGRALAGLSQG

GYQALVSGMNHLESFSWLATFSGVTTTTVPNAGVEAQLKQPDAINKQLRNFTVVVGEKDSVTGKDIAGLK

SELEKQQIKFDYHQYPGLNHEMDVWRPAYAEFVQKLFK

>lcl|NZ\_FO834906.1\_prot\_WP\_016529778.1\_5133 [locus\_tag=BN49\_RS27820] [protein=glucosamine-6-phosphate deaminase] [protein\_id=WP\_016529778.1] [location=5413401..5414120] [gbkey=CDS]

MKMIVTEDYEEMSLVASHHVLGYITAPRRVNLAVTAGSTPKRMYEHLTAAVKGKAFYDRVHYYNFDEIPF

RGQSREGVTISNLRQLFFTPAQIKEENIHKLTLDNAAQHDRQLEEAGGLDLRVLGLGADGHFCGNLPNTT

RFHDQTVEVPIHGEMIALIANSEMGGDISAVPDSYVTMGPRSVMAAKNLLLIVSGAAKAHALKQVVEGPV

SVQVPASVLKLHPSLVIIADKAAAAELQQ

>lcl|NZ\_FO834906.1\_prot\_WP\_004145102.1\_5134 [gene=yieH] [locus\_tag=BN49\_RS27825] [protein=6-phosphogluconate phosphatase] [protein\_id=WP\_004145102.1] [location=complement(5414200..5414865)] [gbkey=CDS]

MTQPEAVFFDCDGTLVDSEVICSRAYVHMFQEFGITLDLAEIFKRFKGVKLYEIIDTINAEYGVNLQKAT

LEPIYRAEVARLFDSELEVIPGAQALLDAVSVPMCVVSNGPVSKMQHSLGRTGLLRHFTDRLYSGYDIQR

WKPDPALMFHAAEAMQVKAENCILVDDSSAGAQSGIAAGMEVFYFCADPHNQPIDHPKVTTFTDLAELPA

LWQARGWDITR

>lcl|NZ\_FO834906.1\_prot\_WP\_016529777.1\_5135 [locus\_tag=BN49\_RS27835] [protein=NCS2 family permease] [protein\_id=WP\_016529777.1] [location=5415035..5416372] [gbkey=CDS]

MSQQQTSQSSGEGLLERVFKLREHGTTVRTEAIAGFTTFLTMVYIVFVNPQILGVAGMDTSAVFVTTCLI

AAFGSILMGLFANLPVALAPAMGLNAFFAFVVVQAMGLPWQVGMGAIFWGAVGLLLLTIFRVRYWMIANI

PLSLRVGITSGIGLFIGMMGLKNAGVIVANPETLVSIGHLTSHSVLLGVLGFFIIAILASRNIHAAVLVS

IVVTTLLGWMLGDVHYTGIVSAPPSVASVIGQVDLAGSLNLGLAGVIFSFMLVNLFDSSGTLIGVTDKAG

LADANGKFPCMKQALFVDSVSSVAGSFIGTSSVTAYIESSSGVSVGGRTGLTAVVVGILFLLVIFLSPLA

GMVPGYAAAGALIYVGVLMTSSLARVKWSDLTEAVPAFITAVMMPFSFSITEGIALGFISYCVMKIGTGR

LRELSPCVIIVSLLFVLKIVFIDAH

>lcl|NZ\_FO834906.1\_prot\_WP\_016529776.1\_5136 [locus\_tag=BN49\_RS27840] [protein=NAD(P)H-dependent oxidoreductase] [protein\_id=WP\_016529776.1] [location=complement(5416418..5416984)] [gbkey=CDS]

MSDTLKVVTLLGSLRKGSFNGMVARTLPGIAPAGMDISALPSIGDIPLYDADMQEVEGFPQRVQEIAQQI

READGVVIVTPEYNYSVPGGLKNAIDWLSRLPEQPLSGKPVLIQTSSMGAIGGARCQYHLRQILVFLDAM

VMNKPEFMGGVIQNKVDPQAGEVVDQSTLDHLRGQLTAFGDYIRRVKA

>lcl|NZ\_FO834906.1\_prot\_WP\_171819498.1\_5137 [locus\_tag=BN49\_RS27845] [protein=phosphopantetheinyl transferase] [protein\_id=WP\_171819498.1] [location=complement(5417021..5417596)] [gbkey=CDS]

MLYGISELPQIINEANGRPVFSDRQLPRFSIAYTGNIVGVALTTEGDCGLDMELQRTVRSHDADRHNFSN

NENLWINIQHDPDEARSQLVALRRSVLKLTGEASTQLQLLPGSGRLRTAGSQPIEAVCDAESLLVWSIAA

TPNIGSLKVWEYDAKGGDWRSLADAQQRAREPSARLMRFTSLPMEKTLSLN

>lcl|NZ\_FO834906.1\_prot\_WP\_004151541.1\_5138 [gene=yidZ] [locus\_tag=BN49\_RS27850] [protein=HTH-type transcriptional regulator YidZ] [protein\_id=WP\_004151541.1] [location=complement(5417906..5418865)] [gbkey=CDS]

MKKPLSSLDLNLLLCLQLLTQELSVTRTAKRMNVSPSAVSKSLAKLRAWFDDPLFVKTPLGLAPTPLVSS

MEQDLADWMQMGNQILDKPHHTMPSGLKFELAAETPLLMILFNTLSQRIYQRYPQALIRLRNWDYDSLDA

IIRGEVDIGFCGRESHPQSRELLSLLPWYIDFEVLFTDLPQVWLRADHPALREEWDLAAFLRYPHITICW

EQRDTWALDDVLQELGYKRNVALTVPGFEQSLFMAAQPQHTMLATAPRYCQHYNQQHQLPLVSRPLPLEA

QHLEKLRVPFTLLWHKRNSYNPKLVWLRDTLKALYSGTL

>lcl|NZ\_FO834906.1\_prot\_WP\_004181598.1\_5139 [locus\_tag=BN49\_RS27855] [protein=MFS transporter] [protein\_id=WP\_004181598.1] [location=complement(5418840..5420018)] [gbkey=CDS]

MTRFLLCSFALVLLYPSGIDMYLVGLPRIAQDLGASEAQLHIAFSVYLAGMASAMLFAGRIADRSGRKPV

AIVGAAIFVIASLICAQAHTSSHFLIGRFIQGIGAGSCYVVAFAILRDTLDDRRRAKVLSLLNGITCIIP

VLAPVLGHLIMLKYPWQSLFYTMTGMGVMVAVLSVFILRETRPTAPPQAASPQHDAGESLLNRFFLSRLL

ITTLSVTVILTYVNVSPVLMMEEMGFDRGTYSMAMALMAMISMAVSFSTPFALSLFNPRTLMLTSQVLFL

AAGVTLSLATRQAVTLIGLGMICAGFSVGFGVAMSQALGPFTLRAGVASSVLGIAQVCGSSLWIWLAAII

GLSAMNMLIGILIACSIVSLVLLLVVTPPRVAQYDEEAAVES

>lcl|NZ\_FO834906.1\_prot\_WP\_046043990.1\_5140 [locus\_tag=BN49\_RS27860] [protein=GNAT family N-acetyltransferase] [protein\_id=WP\_046043990.1] [location=complement(5420118..5420537)] [gbkey=CDS]

MTVEYTVIEKVPSAEAFCHLRVAAGMSPRPLEGARAGLPHSCYGVHILWQETPIAMGRIVGDGAINFDIV

DVAVDPAHQGKGLGRLVMEKLVAWLDANAFDGAYVTLVADVPELYAKFGFESVRPESEGMARVWLTRSR

>lcl|NZ\_FO834906.1\_prot\_WP\_171819487.1\_5141 [locus\_tag=BN49\_RS29745] [protein=AAA family ATPase] [protein\_id=WP\_171819487.1] [location=5421141..5422433] [gbkey=CDS]

MENKYLKRDFDSNEKNNAKMSFNIVNDGVGNEIRLEGRKFIDGDSKYLLPSVLTCISTSPFDKFSSERRF

YNSKHDINTFYHYFGLKDLGRKNAIHAFIEKILYSRINSSLKNDRESFEKILGFLNYQPKIKIEFRTRVR

LKKLFELDDEELIRQIEKPIFTPTGIYKWSKNQSNYDVPRIRNSLFLINDYILASSDIRSNSGSEARYFD

VEINALNENMINISEHVMHEMLYLMELNLLSIRDIYLYKKSGDEVILYEASSGEQCLLINTFGIANSIAD

NALILIDEPEVSLHPEWQEVYIELLMDVFSHKKGCHFIIATHSPQIISNLKKDNCFITTLENGKTYHAKD

FINKSADFQLATLMETPGHENEYLKRLAVNILSKISANEELSDQDINDVLWLKDISKNLEPNDTVMFLIG

LIVKSKVSLK

>lcl|NZ\_FO834906.1\_prot\_WP\_047084753.1\_5142 [locus\_tag=BN49\_RS29750] [protein=HNH endonuclease] [protein\_id=WP\_047084753.1] [location=5422430..5423068] [gbkey=CDS]

MISNAYLYNNDFQERINAKISSEGFCSDSWSDNDISDIKESIKQFYIPEQNHICPYCQQRFLTNNGRQWD

IEHIIPRQTQVGFMFTPQNLCVCCPDCNSHKGYKKTTTSVAKKTLPTKSHLYLIVHPHFDKYDDHIEVIE

PGYLYRAKSKKGENTMYVCSLNRFYQFSGYNSAVATDHRLMMLANGLSSAQSEEEKRQIRREMISISLRA

NI

>lcl|NZ\_FO834906.1\_prot\_WP\_071609141.1\_5143 [locus\_tag=BN49\_RS29755] [protein=ash family protein] [protein\_id=WP\_071609141.1] [location=5423211..5423447] [gbkey=CDS]

MFAVLLARPALAPSMVAQAGASKEAPGRDNRYANPVWVTTSEPGVSGGGVNLLITKRSAAYVSCPCIFRC

TSLRRRYL

>lcl|NZ\_FO834906.1\_prot\_WP\_015959185.1\_5144 [locus\_tag=BN49\_RS27870] [protein=hypothetical protein] [protein\_id=WP\_015959185.1] [location=5423444..5423647] [gbkey=CDS]

MKITVEQPSARELVDRSRVLVHVMLEHPDDIGPNYALLLILADQLQLLRDAFEEDEIRRLRDEKLPQ

>lcl|NZ\_FO834906.1\_prot\_WP\_042941246.1\_5145 [locus\_tag=BN49\_RS27875] [protein=helicase RepA family protein] [protein\_id=WP\_042941246.1] [location=complement(5423866..5424918)] [gbkey=CDS]

MTASDRTLTTSLPLRRGSEGFNTSQDYLVKGLIPAGALCSIYGPGGSFKSFLAVSLACHIASGTSWGGRR

VNQGAVLFIAGEGGTGVSRRIRAWELSVNDEMALDNLFRVDCPIFPAAPGSIEQVILAAKDIQNMTGMPV

RLIILDTLARCFGNSDENTARDMGAFIQGCDAIRYHTRAAMMIVHHSGKDQERGARGSSAFQAALDAEFN

VRREGRRNAITLSCTKMKDAEMPEVTAYDLEEVVIYTDSDGEPVTSLVLNDEPRQPDDDLLSSGIPPGVP

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>lcl|NZ\_FO834906.1\_prot\_WP\_042941247.1\_5146 [locus\_tag=BN49\_RS27880] [protein=toprim domain-containing protein] [protein\_id=WP\_042941247.1] [location=complement(5424921..5425904)] [gbkey=CDS]

MSYYVSAVSDRARNNWPKIFEQLGIFIPPNHRHGPCPCCGGKDRFRMDDLEGRGTWFCNQCGAGDGLDLV

SRFFGCALVAAAGMVQDMDPVPLVPPAREKSQALNMESRIKTLLRHCESGEAPYLTTRGWRRAQWLLTER

SSRTICGVHFGAGTLVLPIRNTGAQLTGAQFIHPGGKKYLLPGSHLKDCFCPVHQASRNGRPEPWAPDNK

PSEGIIITEGYATALAVSCLHHFPVVAALSAHNLKNVAIAFRAQWPECHLILAGDNDCSQEKNTGLLNAT

AAAGVVKGCVVLPADTTLSDWDEFYRHYGESISRIVFNQQLPANLRS

>lcl|NZ\_FO834906.1\_prot\_WP\_227504836.1\_5147 [locus\_tag=BN49\_RS27885] [protein=integrase domain-containing protein] [protein\_id=WP\_227504836.1] [location=complement(5425901..5426548)] [gbkey=CDS]

MSGDSGGQSTILAQSGRQKFAQSERISNKALGLGNASRAGTHLPLTSERWLSALSAFHEKDEGLALTLEL

ARAMGLRSQEAVQCCQSLKTWAAALERGENRLQVVFGTKGSRSRQTVVLEPERLRNILNQAIPLMAQRGG

RLLNKPDLRAAMNYWRASAVRAGLTGPYAPQAQEAMAHYQGLGLSIKEARAMVAMDLGHGDGRGRYIQQV

YGRQS

>lcl|NZ\_FO834906.1\_prot\_WP\_171819488.1\_5148 [locus\_tag=BN49\_RS29765] [protein=IS3 family transposase] [exception=ribosomal slippage] [protein\_id=WP\_171819488.1] [location=join(5426612..5426927,5426927..5427840)] [gbkey=CDS]

MIDVLGPEKRRRRTTQEKIAIVHPSFEPGMTVSLVARQHGVAASQLFLWRKQYQEGSLTAVAAGEQVVPA

SELAAAMKQIKELQRLLGKKTMENELLKEAVEYGRGKKVDSARALIARGWGVSFVSRCLRVSRAQLHVIL

RRTDDWKDGRRSRHTDDTDVLRRIHHVIGELPTYGYRRVWALLRRQTEPDGMPAINAKRVYRIMRQNALL

LERKPAVPPSKRAHTGRVAVKESNQRWCSDGFEFRCDNGEKLRVTFALDCCDREALHWAVTTGGFDSETV

QDVMPGAVERRFGSELPASPVEWLTDNGSCYRANETRQFARMLGLEPKNTAVRSPESNGIAESFVKTIKR

DYISIMPCVLRLMAAKNLAEAFEHYNEWHPHSALGYRSPREYLRQRASNGLSDNRCLEI

>lcl|NZ\_FO834906.1\_prot\_WP\_071829967.1\_5149 [locus\_tag=BN49\_RS27895] [protein=site-specific integrase] [protein\_id=WP\_071829967.1] [location=complement(5427765..5428094)] [gbkey=CDS]

MSKLTKRMEKLALLAGGSFKTVHDRLRIAGRLSQHLHKLNIQIQDLQHLKSSHIESYVMARREAGITPRT

LQNEMAALRTIWICPYISRHLLSLNPLLARCRRYSRGER

>lcl|NZ\_FO834906.1\_prot\_WP\_046043997.1\_5150 [locus\_tag=BN49\_RS28140] [protein=helicase-related protein] [protein\_id=WP\_046043997.1] [location=complement(5428854..5431022)] [gbkey=CDS]

MDNLYEIAKNNLSADNEHFDAFEYIKTINTLLDNPVQKTQGRDLTIRALNEKSKFSHHIKQLRAMIRKSG

LYPYLYSEFDDLDSDEKLATEIYRSPNSDDFIFHSMQMTVFHLLMNGANLALSAPTSMGKSIIIDSLVSC

GKYNTIVIVVPTIALIDETRRRLHKKFSNIYEIIYHSAQERNHEKTIYILTQERVNEREDLNEVDIFVID

EFYKLSFKNKTSEKYYDERVISLNVALSKLLTVSKQFYMIGPNIDFLRGLNNINEDFIFLSSDFNTVALN

IFEYNILPNNESLKQSTTLSIIEKNNGQFIIYCKSPKVAESIASFLIKSGVSSDTNEEEYSLWLEKYYSQ

FWVYTKAIRHGIGLHYGTLPRAIQQYTIDLFNNKKVNILICTSTIIEGVNTNAQHVIIYDNRDGNNSIDK

FTHNNIKGRAGRMKQHFIGNVHCLEESPEGKIEDSIVEIPIGLQDNTTPLNLIAGMQDEHVSSLSEDRLE

EYLSANRLPKEIIKKHASYEINKVLELFNEIDWLKDSEISDLCFQRYPDKKAMNQISKNLLITSRQTFTR

NSVSTEIEHISGMLFSYINAETHQTYFDSQLSRIINSQISEPEISELINRELKIIRNVFSYSIPKSLALQ

QDIINFICQKRKLNLTADYSFIINIFEKFHLPGNISALEEMGVPLQILQKINFPDDAIVDINKCIGYIKN

VYFLNKTLSRLERKFIERALII

>lcl|NZ\_FO834906.1\_prot\_WP\_071829968.1\_5151 [locus\_tag=BN49\_RS29770] [protein=dsDNA nuclease domain-containing protein] [protein\_id=WP\_071829968.1] [location=complement(5431015..5432667)] [gbkey=CDS]

MTMGLDNMDHSNSGGVGAKKGFLFQDYVAALYVTEMLRDKRIKGVCCEVKDDVDIIYENHVRFIQIKTTD

GDKKWSTKELCQRTKKKDSNRYNQDSIVHKSLNCDSSDKFKAIFGIISTRDVDSTLLYLKIEHDKRFDKT

SQRDKLINSITRQIKEFRSNNNNDIAYWVDNCEWNTFHNSDHIKLLCLSNIMKCASENGFYLDPNHDDEI

ILNSILAKVNKLSTLSKKEFLSKDKTYFRVDLITWFQAEIERISEEKPHKVYKTKSNNLPTILNELNKLK

DSTIDTISGTSYYQSYNRLSYRFDFISTNLVQWLPELLLRPEELSTITPTNMISRVRDVYKTISENNHDI

KNIISRVLLHSLVRHHCSSQPIPAHLYTEKKGDMIDFDNIHIVIRENDPDEMWFGLSLWCDGNIEKTVSL

FASKVLSFVDVTCDTQRKIILDIKSDEYLVKHDVNCVLDPATSITDHLSRIYFVVFIGYISETQTLEVKK

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MALSDTKLRTLTPRNRPWQLADHDGLVIEVLPTGRKIWRFRYRFDNKSQKITLGEYPAFSLAEARLWREK

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TTAHIQVVLDRIKQRGSDHVALLTRNVLKRMLAYAISRGIIFNNPAAAIEARYIAQATSRDVALTAEEIG

ILLRGIYISNMNRRHKLALHLLIICMVRKSEMIEATWSEVNFNALEWRIPGERMKMDNPHIVPLSKQALA

MFEELKFLAGDSPYVFPSRNDHRRPISKTTLNCAVRTLDLNVRDFVIHDFRRTASTLLHEQGYNSDWVEK

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>lcl|NZ\_FO834906.1\_prot\_WP\_004151538.1\_5153 [gene=mnmE] [locus\_tag=BN49\_RS27915] [protein=tRNA uridine-5-carboxymethylaminomethyl(34) synthesis GTPase MnmE] [protein\_id=WP\_004151538.1] [location=complement(5434392..5435756)] [gbkey=CDS]

MSHNDTIVAQATPPGRGGVGILRISGLKARDVAQAVLGKLPKPRYADYLPFNDVDGTPLDQGIALWFPGP

NSFTGEDVLELQGHGGPVILDLLLKRILTLPGLRIARPGEFSERAFLNDKLDLAQAEAIADLIDASSEQA

ARSALNSLQGAFSARVNHLVEALTHLRIYVEAAIDFPDEEIDFLSDGKIEAQLNEVMADLDAVRAEARQG

SLLREGMKVVIAGRPNAGKSSLLNALAGREAAIVTDIAGTTRDVLREHIHIDGMPLHIIDTAGLRDANDE

VERIGIERAWQEIAQADRVLFMVDGTTTGAVDPAEIWPDFIERLPAKLPITVVRNKADVTGEALGISEVN

GHSLIRLSARTGEGVEVLRNHLKQSMGFDTNMEGGFLARRRHLQALEEAANHLQQGKAQLLGAWAGELLA

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>lcl|NZ\_FO834906.1\_prot\_WP\_004150295.1\_5154 [gene=yidC] [locus\_tag=BN49\_RS27920] [protein=membrane protein insertase YidC] [protein\_id=WP\_004150295.1] [location=complement(5435879..5437525)] [gbkey=CDS]

MDSQRNLLIIALLFVSFMIWQAWEQDKNPQPQQQTTQTTTTAAGSAADQGVPASGQGKLITVKTDVLELT

INTNGGDIEQALLLAYPKTLKSTEPFQLLETTPQFVYQAQSGLTGRDGPDNPANGPRPLYNVDKEAFVLA

DGQDELVIPLTYTDKAGNVFTKTFTLKRGGYAVNVGYSVQNASEKPLEVSTFGQLKQTAALPTSRDTQTG

GLSTMHTFRGAAFSTADSKYEKYKFDTILDNENLNVSTKNGWVAMLQQYFTTAWVPRNNGTNNFYTANLG

NGVVAIGYKSQPVLVQPGQTDKLQSTLWVGPAIQDKMAAVAPHLDLTVDYGWLWFISQPLFKLLKFIHSF

LGNWGFSIIVITFIVRGIMYPLTKAQYTSMAKMRMLQPKIQAMRERLGDDKQRQSQEMMALYKAEKVNPL

GGCFPLIIQMPIFLALYYMLSASVELRHAPFILWIHDLSAQDPYYILPIIMGATMFFIQKMSPTTVTDPM

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GDDPVPPGPFDTREH

>lcl|NZ\_FO834906.1\_prot\_WP\_004151535.1\_5156 [gene=rnpA] [locus\_tag=BN49\_RS29775] [protein=ribonuclease P protein component] [protein\_id=WP\_004151535.1] [location=complement(5437749..5438108)] [gbkey=CDS]

MVKLAFPRELRLLTPSHFTFVFQQPQRAGTPQITILGRLNSLGHPRIGLTVAKKNVKRAHERNRIKRLTR

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>lcl|NZ\_FO834906.1\_prot\_WP\_000831330.1\_5157 [gene=rpmH] [locus\_tag=BN49\_RS27935] [protein=50S ribosomal protein L34] [protein\_id=WP\_000831330.1] [location=complement(5438124..5438264)] [gbkey=CDS]

MKRTFQPSVLKRNRSHGFRARMATKNGRQVLARRRAKGRARLTVSK