```
LOCUS       DMACINML_1            261035 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..261035
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                     PNYKPFNYKQDSKLTGFDTDLVEEIAQKNGIEIVWVETNFDGLIPALKAGKIDMIASA
                     MSATDERRQSVDFTKPYYMSKNLYIKLKNNEALQTKTDLEGKKIGVQLGTLQENTAKT
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                     /note="predicted cleavage at residue 20"
     gene            1394..2377
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                     /product="magnesium and cobalt transport protein"
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                     ISNEFNLEFPTKEEREEIELSAKYWEDNATITINAHFLIREFKNDNEEQNSIKLRTEI
                     VTFATAKNILFTIRYNEFSTFEEIQARILASPKNFEDGFDIIDKMFEVRVEKDADLLE
                     WIDKEARRLRTTVLEKKDEYSYDEMLKDISSLQELNMRVRDSLFDKRRAMTSLLKSDK
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                     VSLLARQLSRLIKANKF"
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                     TFWWFAAFVFAFCVIVIINVIYPTLIAPIFNKMEKLEDENLLSKINDLMKRCGFNANG
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                     KALINGAITMFLLFFIFAHLPDFAYLESHLEGVNGGVFALLFIFANIFSFIISPLINA
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     CDS             4434..5234
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                     YDFKQIKESYDFIFSNPPYIQNSYPIDLWVQNEPKEALFGGEKGYEILEEIITFSFER
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                     QKSMLRTEATRIQESINDSFNNATYNGKNVFQTMNFVVGSGTETTNLNPLATSGLSID
                     NQDSITSFMDQLGALRSEIGSGINAITSNINASVQNSINAKAAENNLLNNDMAKNVND
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                     LKSEFADGAEKQGYDRVKAEELWELIVKFAGYGFNKSHSAAYALITFQTAYLKTYYPS
                     EFMAALLTSEENNVDKIAVYIDEMKKMNIKLLPPSVNKAIREFSAVEQEDGKDAIVYG
                     LGAIKSVGIPAVENLLEARERGEFKNIDDFLSRIEPTKINKRTLESLIKAGAFDEFGY
                     TRKCLFDNMDNLTEGSKKMADARKNAASSLFGEDELTVGLQVNIVAKDEEFEVMEKLE
                     FEKEILGIYVSGHPLDRFYEKFKDIDYIKSIDFSTLKGNGEILSIGKIESFKSMMSKN
                     NKRYGRLEILDFYSTFEVTVFESNIEEIENILKNEASRNEAYGFLLSYKAEEGKLDSL
                     ALRSIKTLEELQEGEVKAVKKFSAKKNALENKDFVAEPKEFENNIIELDLSRLNRELV
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     gene            complement(11033..11362)
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     gene            complement(11359..12702)
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     CDS             complement(11359..12702)
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                     /transl_table=11
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                     /protein_id="Prokka:DMACINML_00012"
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                     RELQNALARVCRKEAFLLQGGDCAESFANFGAVNIRDMFKILLQMAIVLTFAGGCPVV
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                     TTLNLLRGFAKGGLANLHEVHRWNLGFLKKSELHQQYTDISEKISQALDFMEACGINT
                     YNTPSLKEVDVYTSHEALLLPYEEALTRVDSLSGEIYDCSAHMLWIGERTRGLDEAHV
                     HFLSGVRNPLGVKIGPNASADDVIALANALNPNNEEGRLNIIIRMGAEKIATQLPKIF
                     SKLKKEGLNLVYSIDPMHGNTVKAGDFKTREFDKIMQEVRYFFEIAMSEGVYAGGVHL
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                     TKFFRPDLFLEHERKK"
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                     /locus_tag="DMACINML_00016"
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                     HSYEIRILNYQFKAELDPSFAKLGFEIKNLDF"
     gene            complement(17572..18729)
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     CDS             complement(17572..18729)
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                     TIMSHRGLALMGVGSASGENAIEEALSNAIESPLLDGMDIKGAKGVILHFKTSSNCSL
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                     IEILEKAIKNYK"
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     gene            complement(70975..71850)
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     CDS             complement(70975..71850)
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     gene            complement(71840..72220)
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     gene            complement(72217..72987)
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                PKLHGMIKSKDEEEALVVDCLQKVGLFEEVKDKLKQNALALSGGQQQRLCIARALAIK
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gene            complement(94682..95770)
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                /locus_tag="DMACINML_00098"
CDS             complement(94682..95770)
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gene            complement(95767..96681)
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     CDS             98023..98523
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gene            100920..102089
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CDS             100920..102089
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CDS             complement(102159..103523)
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gene            complement(103525..105450)
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CDS             complement(103525..105450)
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gene            complement(105450..106625)
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CDS             complement(105450..106625)
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     gene            complement(106708..107898)
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     CDS             complement(106708..107898)
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                     KFVSDVQCIISRRLRPVDAGVITIGKFHAGTTFNVIPQNAILQGTVRFLSDENQKLLQ
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     CDS             complement(107903..108784)
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     gene            complement(131605..132807)
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     CDS             complement(131605..132807)
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                     QIDSKQDQIKKINEDLKDYNTQLAKLQNLRQKQVSEINKQKTDRAIYAKKLENLQDQQ
                     DELRKTLNQLKIIESKQEDKKQTQKTASDSKITNNTQKIRQIGSSYQGSSTKRYTGKK
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                     LARVVIVEHDNGIHTIYAHLDKIAPNIKVGKNVKKGAVVGRIKNDLTFEVTQKNFHIN
                     PLELISLN"
     sig_peptide     complement(132742..132807)
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     CDS             complement(132804..133610)
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                     /protein_id="Prokka:DMACINML_00130"
                     /translation="MKFFKTHLSLILPLLFMMFAFEFILLTNATLRYYEELVNKDYNI
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                     FVLFLKQMKIWLFEHTERVEIMCLFGAPFWFRSFMLYKIVVLDCFIAFVILFIFFTQI
                     YNLSIVQDSLKAVDIILPPINFIVHLGVIFLVTLFICLLCVNSVMFRVKK"
     gene            complement(133597..134262)
                     /locus_tag="DMACINML_00131"
     CDS             complement(133597..134262)
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                     /protein_id="Prokka:DMACINML_00131"
                     /translation="MSNLIQAHKLSLGYDELVIKEASFTFKDDDFVFITGKSGSGKST
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                     EIF"
     gene            complement(134311..135507)
                     /gene="trmB"
                     /locus_tag="DMACINML_00132"
     CDS             complement(134311..135507)
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                     /locus_tag="DMACINML_00132"
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                     /inference="ab initio prediction:Prodigal:2.6"
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                FLQVKKGENEFVVKVDKHTKPSKIAYLHKALYVFKQYFCEDIISEAFGIKNNALAEKT
                PLIANDFEEVLARLEGRIYIEIGFGSGRHLLYQAKNNPHVLILGIEIYNPAITQVAKL
                AKAQGIDNILLVQSDARLLLSVLQSHSVEKIFLHFPVPWDKKPHRRVVSKAFCKECAR
                VLTAQGVFELRTDSYEYFDFTFKEFLDFSSPQFSIRKNENLEISSKYEDRWKRQEKDI
                YDLWVWNLDKEENNPLSEEFDFSDIHLDKNDLMLLEKNFENFTLKKEDFFLHFENIYK
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gene            complement(135507..136739)
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CDS             complement(135507..136739)
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                /protein_id="Prokka:DMACINML_00133"
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                PRVASYIIERAKADGQEFKKIAEVKNRLNAEFIDEDLKPEESFNYRIIAVGFDGVQSE
                PSSVLNSTSKALPPQVEHLNASLDGANKIVLTWDAPKYKDFSYYKVYSTSSSLLPYTL
                LAKTEQNSYEDIVEGAAKSRYYKVTMVDIDGLESSMPKNGVEGKTLGSPSSPSVILAQ
                STSDGIELEWVDNDSRAVEYEVRRYGGGQNAIFKGIKEKRLKDIKALPGVEYSYEVIA
                IDSVGLRSEPSKRVKAGQ"
sig_peptide     complement(136674..136739)
                /locus_tag="DMACINML_00133"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 22"
gene            complement(136687..137652)
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CDS             complement(136687..137652)
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                /EC_number="4.2.1.70"
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                /inference="similar to AA sequence:RefSeq:CAL35395.1"
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                /transl_table=11
                /product="putative ribosomal pseudouridine synthase"
                /protein_id="Prokka:DMACINML_00134"
                /translation="MQTFLVDESSRLDTFLAKNLQQSRNQIALMIEKNCVWVNDKIQN
                KNSFKLKVGDRLVLNLPLVEEVKPKFDIDFDIEILYEDEDLLVLNKPSNLVVHGAKSV
                KSATLVDWLIEKQYTLSTLGGEVRAGLVHRLDKETSGAILIAKNNFTHQKLSEQLSDK
                TMGRIYLALIDLPLKEDKIIIDKALIRSSANAIKKIVTNSFVKGSKEAKSAFANLAKS
                EDVSLIAAKLFTGRTHQIRAHLASINRHILGDELYGYRGKYECRIMLHAYFLYFIHPR
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gene            137730..138836
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                /locus_tag="DMACINML_00135"
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                AMVLLIVGFGVLFIMGVHYKIWLSIIIAIGISSPIIYTHFLKPYQKQRIHDFISEKPS
                YQVAQSMIAIGNGGLIGKSQDEATQTHFNFLPISTSDFIFAYLIERFGFLGGFVLILL
                YTLLIFHLLSLNQKLKEDYFARVAINCVALFIFIYAAVNISMTIGFAPVVGIPLPFFS
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gene            138883..138959
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tRNA            138883..138959
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                /inference="COORDINATES: profile:Aragorn:1.2"
                /note="tRNA-Met(cat)"
gene            139328..139591
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CDS             139328..139591
                /locus_tag="DMACINML_00137"
                /inference="ab initio prediction:Prodigal:2.6"
                /codon_start=1
                /transl_table=11
                /product="hypothetical protein"
                /protein_id="Prokka:DMACINML_00137"
                /translation="MKHFIFSGLIGLGALAFLAGCGDEAKTSDYYKAHLDEAKARVAE
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gene            complement(140544..141023)
                /locus_tag="DMACINML_00138"
CDS             complement(140544..141023)
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                /transl_table=11
                /product="TPR repeat protein, Sel1 subfamily"
                /protein_id="Prokka:DMACINML_00138"
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                GKEQHKQGNYSKAKQYYEKACELNIKEACNGLGLLYFDGDGVKQDRTQAVSYFKKACE
                LEYGEACGILGLLYLDGDGVKQDRTQAVNYFKKACELGYGETCDILGLLYLDGDGVK"
repeat_region   141296..141925
                /note="CRISPR with 10 repeat units"
                /rpt_family="CRISPR"
                /rpt_type=direct
gene            complement(142072..142470)
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     CDS             complement(142072..142470)
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                     /protein_id="Prokka:DMACINML_00139"
                     /translation="MFDIPTKSKKEQKSANKFRVSLVKLGFFMMQFSVYVKICKGMTS
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                     TQDFKYSNDKIYKENKTKSNKIRQASLFEF"
     gene            complement(142490..142732)
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     CDS             complement(142490..142732)
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                     /transl_table=11
                     /product="putative CRISPR-associated protein"
                     /protein_id="Prokka:DMACINML_00140"
                     /translation="MIEVFRPLVDLCVFDLKDIKESEFLDKEAKQRLIGILQEEIIIE
                     NKAYPLNRAINFYIQNFKNALLENDELMMVNLYDRR"
     gene            complement(142852..143244)
                     /locus_tag="DMACINML_00141"
     CDS             complement(142852..143244)
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                     /product="CRISPR-associated protein Cas1"
                     /protein_id="Prokka:DMACINML_00141"
                     /translation="MAYDEAFKSILISNQAKLSLEFNHLVIKQDDKEAKFFLKDINFI
                     ILESLQASITSSLLSALAKYKIILLTCDESHHINGIFSPFLGHFISAKVAKKQIKVTL
                     QRKAILWQKIIKNKISNQAHILKITHHI"
     gene            complement(143234..146236)
                     /locus_tag="DMACINML_00142"
     CDS             complement(143234..146236)
                     /locus_tag="DMACINML_00142"
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                     /codon_start=1
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                     /protein_id="Prokka:DMACINML_00142"
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                     KSLEKESGELVSSQIINEILNHILDKGSITYKKFREYIKLHESMKFKSLKYDKDNAES
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                KSLENKSVIGLDTGFEDLNTMTKGFKGGELIIIAARPGMGKTTLCLNFIEKVLRQDKG
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                SGYATITDVRAILRRLKAQEESIGLCVIDYIGLMMSNSNFNDRHLQVSEISRGLKLLA
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gene            147836..148765
                /locus_tag="DMACINML_00144"
CDS             147836..148765
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                VFAKNKLDKESIEFDSLKREGNYHELELSYNYSLLNLGLIYDYNDADGKAQSYSRYGF
                KIGTHLVFARNYILTPSLSLNQYKADGTDPIFNQKQDGSITKFNLKLVKNQFLGYDSL
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sig_peptide     147836..147892
                /locus_tag="DMACINML_00144"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 19"
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gene            complement(148788..150119)
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CDS             complement(148788..150119)
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                /protein_id="Prokka:DMACINML_00145"
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gene            complement(150345..151280)
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CDS             complement(150345..151280)
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gene            151351..152583
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                /transl_table=11
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                /protein_id="Prokka:DMACINML_00147"
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                KISIPIGLISVIYEARPSLSAEIIALMIKSSNACVLKGGSEAKFTNSAIFDLVYKVLE
                EFNLQDCFAMFYERNEIMQILAFDDLIDVIIPRGSSNMIQEIASHTKIPLIKQDKGLC
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                     /transl_table=11
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                     AAFLYSVSVIYIFKNSPPKPVLQNGNLGFDIIFVDSIIIAFFVGFAVFLGAFLELDRS
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     CDS             complement(153776..154345)
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                     AKKWMLDGMMVDVLFHNGKAIGVEVPQVVELKIVETAPNFKGDTQGSNKKPATLETGA
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                FDAIILAMAGIKRLDLDKQVNFVYAFSKDELIPAASQGALGIESIDDEKILEFLKCLN
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gene            complement(160635..161021)
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                /inference="similar to AA sequence:RefSeq:CAL34690.1"
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                     CERLGVLSECDSLNNLKKYLDEYELFFSATNASSAIITNSLIDEVSHKRYFFDIAVPR
                     DIDVSENEKVSVFAVDDLEVVVRNNLALREQEARMAYGIIGRETAEFFRYLNDLALTP
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gene            complement(168701..169570)
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gene            complement(173966..176536)
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                     IAGLKIFKFGEKSGIDLPYEQKGEIPNSKRLRDIEKSVLSYGYGLKTTFIQLLAAYNV
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                     ELLRSIQELRAVDDEKMYLIIKNLQKGKEILKEIDGLTLNNVEHLILVRKITTAEGIS
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     gene            complement(182355..182789)
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                     LSGDAKKDSQLIGQFGVGFYSAFMVASKIEVLSKKALDDKAYLWISDANGYEIEDATK
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                     KISQINKANALWRMQKSSLKAEDYERFYEQNFHDSNKPLLYLHTKSEGKLEYNSLFFI
                     PQNAPFDLYRVDYQSGLKLYVKRVFISDDDKELLPTYLRFVRGIIDVEDLPLNVSREI
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                     LKLMLYKSTKGESLRSLEEYKNDIQGEQKEIFYIIGSNESLLRNSPLLEEYKQKNIEV
                     LLMDDEIDSLVTPMLGEYEGLKFVAINQVEDKNELSDEEKNEFASLVAKFKELLKDQV
                     EDVRLTSRLKDSPSCIVYDKNKPDFAMQQLLKQMGQEQNFKPILEINPKHAIFTGLKN
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                     /locus_tag="DMACINML_00180"
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     CDS             complement(185367..186068)
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                     PLFKIAIKKPKLLCIDRKNPRDLVRVLKEAKQRLGEDRVLAIFPEGTRSRNEKLLKFQ
                     SGAKVLSDKLDLKVQPILIVDSAKILDTKSFSASSGVLKIICMDLVDTSDDKWLENTR
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                     DFNITLQKSKDLVFLNPDLKWEYIKGDYRAVLWFEAKTSNANLEQISVSLLRNGKVFQ
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                     /note="predicted cleavage at residue 17"
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                     /gene="purQ"
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                     LFDDEKAMIRFDMSEFMEKHSVSRLLGAPPGYIGHEEGGELTEAVRRKPYSVLLFDEV
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                     KNELKNFFKPEFLNRLDDIITFNPLGKDEAYEIVKLLFKDLQKSLENKGIKASLSENA
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gene            complement(195292..195843)
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gene            complement(195847..198375)
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                     AAGGAAAAAEEKTEFDIVLVDGGAKKIEVIKIVRALTGLGLKEAKDAVEQTPSTLKEG
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     CDS             complement(221601..222080)
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                     /locus_tag="DMACINML_00212"
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                     EIQKGNMNFDVLIATPNLMGLVGKVGRILGPKGLMPNPKTGTVTMDVAQAVNNAKSGQ
                     VNFRVDKQGNIHAGLGKVSFSKEQLWDNISTFVKAINKHKPAAAKGRYIKSAALSLTM
                     SPSVKLETQELLDMK"
     gene            complement(222987..223412)
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                     /locus_tag="DMACINML_00213"
     CDS             complement(222987..223412)
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     gene            complement(223985..224164)
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                     ALVDWIMSSIVSAIV"
     gene            complement(224183..224258)
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     tRNA            complement(224183..224258)
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                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Trp(cca)"
     gene            complement(224270..224428)
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                     /locus_tag="DMACINML_00217"
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                     GDNVGVLLRGTKKEEVIRGMVLAKPKSITPHTDFEAEVYILNKDEGGRHTPFFNNYRP
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     gene            complement(225741..225815)
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                /inference="COORDINATES: profile:Aragorn:1.2"
                /note="tRNA-Thr(ggt)"
gene            complement(225910..225986)
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tRNA            complement(225910..225986)
                /locus_tag="DMACINML_00220"
                /product="tRNA-Gly"
                /inference="COORDINATES: profile:Aragorn:1.2"
                /note="tRNA-Gly(tcc)"
gene            complement(225993..226078)
                /locus_tag="DMACINML_00221"
tRNA            complement(225993..226078)
                /locus_tag="DMACINML_00221"
                /product="tRNA-Tyr"
                /inference="COORDINATES: profile:Aragorn:1.2"
                /note="tRNA-Tyr(gta)"
gene            complement(226140..226215)
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tRNA            complement(226140..226215)
                /locus_tag="DMACINML_00222"
                /product="tRNA-Thr"
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                /note="tRNA-Thr(tgt)"
gene            complement(226349..227086)
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CDS             complement(226349..227086)
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                GPLKVQKRAKEEVLQEAKIWLEKVGLAHKIDAYPRELSGGQKQRIAIVRSLCMNPELM
                LFDEVTAALDPEIVREVLEVILNLAKDGMTMLIVTHEMGFARAVADRIIFMDNGEIIE
                ENTPDDFFKNPKSERAKKFLNLFDYHK"
gene            complement(227088..227744)
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CDS             complement(227088..227744)
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                /transl_table=11
                /product="amino-acid ABC transporter integral membrane
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                /protein_id="Prokka:DMACINML_00224"
                /translation="MFDLLNPDTLSRLWKGLYITLEISIVSIIITSFGGLFLGILMSL
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gene            complement(227737..228438)
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CDS             complement(227737..228438)
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gene            complement(228449..229045)
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CDS             complement(228449..229045)
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gene            229127..229510
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CDS             229127..229510
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                /translation="MKYETINKESIAKLMELFYDKIRKDKDLGPIFNNAIGTSDEAWK
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gene            complement(229513..231327)
                /gene="recG"
                /locus_tag="DMACINML_00228"
CDS             complement(229513..231327)
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                     LMAPTSILAHQLYEEAKKLLPEFMDILFIKGGKKEKDLEEKIKKTNLIIGTHALIHLQ
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                     ISLSDLESFYKKNINLSNLVVILGGNLAQEKAKGLLDKLLAKLQKGSQNSQKTYEINS
                     KNKDIIQIRKESEQAYIYFAAPFFTKFNDKDFYLAKIALFILGQGGFGSRIMEEIRVK
                     RGLAYSAYAMLDMNASFTRVFGYLQTKNESAKEAKKIVKEVFKDFVKEGVSQNELVQA
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     gene            complement(232537..233583)
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     CDS             complement(232537..233583)
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                /protein_id="Prokka:DMACINML_00231"
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gene            236084..236326
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CDS             236084..236326
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                /transl_table=11
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                /protein_id="Prokka:DMACINML_00233"
                /translation="MDLKLARNLINEEPKNISLAKIEEAVNQEGQKFFYFDKENSHKD
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gene            236323..237624
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CDS             236323..237624
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CDS             237587..238231
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gene            238240..239229
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CDS             238240..239229
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CDS             239226..239750
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DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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                     EKDENGIDFYISLPKEAMKFMARKGSIGIDGVSLTINEIVENGVRLTIIPITFKETLF
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                     IADAMEKVGKDGVITVEEAKSINDELNVVEGMQFDRGYLSPYFITNAEKMTVELSNPY
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                     IAENAGFDAGVVVNSVENAKDENTGFDAAKGEYVNMLESGIIDPVKVERVALLNAVSV
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     gene            complement(20946..22151)
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     CDS             complement(20946..22151)
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                     KGRGIYDGKVFFLDRMNTDNYFLKHANEDNIHTESGLKILIQGEDVKKDLVWIRVKVF
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                     /protein_id="Prokka:DMACINML_00282"
                     /translation="MLPKWDSSFSVHNAKIDDQHKKLFELAAKVEIVSDRSVSKNEVK
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                     KLYIIAKKWLLEHILYEDMKVEKWRSSSLATDEGKDVSFEAADDSDDDKPQFYLYKCN
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     gene            23557..23922
                     /locus_tag="DMACINML_00283"
     CDS             23557..23922
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                     /transl_table=11
                     /product="Ribbon-helix-helix protein, copG family"
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tRNA            complement(24006..24080)
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gene            complement(24160..25410)
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CDS             complement(24160..25410)
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gene            complement(25407..26081)
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CDS             complement(25407..26081)
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gene            complement(26164..27582)
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CDS             complement(26164..27582)
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                     SDLKNYIGTLEIGQKIILDYERDGENKRVDFTLKGEKENPKAVQNDLIEGMTLRNLDP
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                     /inference="ab initio prediction:SignalP:4.1"
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     CDS             27791..28690
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                     /locus_tag="DMACINML_00289"
     CDS             28706..29080
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                     /protein_id="Prokka:DMACINML_00289"
                     /translation="MEHHYDEPVYLISVVAKVLSIHPQTLRQYEREGLIEPSRTDGKI
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                     NASSKAVVKHKNSFDLIFYEKK"
     gene            29081..30703
                     /gene="kefB"
                     /locus_tag="DMACINML_00290"
     CDS             29081..30703
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                     system protein"
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                     ALAIFSLLQAKSMLDVETAQILIVVSIITMIITPFVLNNIRKIANVVEDMTLNTNVVQ
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     gene            30713..31045
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     CDS             30713..31045
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                     TYLKDYYD"
     gene            31038..31658
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     CDS             31038..31658
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                     /protein_id="Prokka:DMACINML_00292"
                     /translation="MINVFFDMDGTLIDSANAISCAVNEIRNELNLSPLSREKIMQTI
                     NTPNVDWAKELYSIDNFHHSSFKDGFEKYFIKHYEQSVVLFEGIKDILEFLKEQNCFL
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     gene            31712..33706
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                     /locus_tag="DMACINML_00293"
     CDS             31712..33706
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                     /locus_tag="DMACINML_00293"
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                     /protein_id="Prokka:DMACINML_00293"
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                     LDTLIGLFSIGKIPSGTKDPYALRRAANGIIKIALNLNKEFDIQALLEKLASHYKNFD
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                     TFKRLANIANKTSHKVDENLFIEEAENKLYKAFKEKIQAHSLQEKLENLFSLKPFIDE
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                     NEKVASYHSGTDFRAAVGTPIYAANSGIVKIAKDRYFAGKSVVIDHGFGIYSQYYHLS
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     CDS             34521..35471
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                     PMKAKLKEKCEILNLKKGELSLELEEFFKDLDKASKKFIFASFDYGVFNPEQFSIRIY
                     QKHEVFNPFEITLKDFFGKSDLTYNVNFTQIQQLIKEHDFKLLALKKQNQALIDFGFE
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     gene            complement(35543..36508)
                     /locus_tag="DMACINML_00296"
     CDS             complement(35543..36508)
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     gene            36564..37337
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gene            45269..46804
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CDS             complement(47740..48297)
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                     /gene="purD"
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                     PYVLEFNVRFGDPECEVLMPLIENPLELILATTQKRLRHTKIKIKKDYAVGVVCASEN
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gene            51821..53869
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CDS             51821..53869
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gene            53886..56102
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gene            complement(59754..60623)
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                FLPSGTGTSAAFLAKNSKFKVFTCACVGDEYYLKTQILNLIKNYDFSNLEILKSDKKY
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CDS             complement(60633..61583)
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                     EQLSKELNSSIDSKDKQILILLGQLEKKDEEIRNLQESFDKAKEKVQNLSLIRENLSK
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                     WTKEELDQRYLSESLQHFEKIGAIFKQVSNQDFFAELDHTIDRKFGIFQDMLNVEEKA
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                     DISNEKIQHFDKTLLAFDEKVDRFGKNFELYEKAILESQEKVFEGFKTSLFEGMHKFK
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                     /note="predicted cleavage at residue 22"
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                     LILYGKNPKFIKNGIAIPSSYIKIIKTPRFKECYEVPNNDIQSEEINDYKISCNKF"
     sig_peptide     65724..65774
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gene            67094..67312
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CDS             67094..67312
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     CDS             complement(69575..70579)
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                     LDALGVKESILDVGIGFGKSAEHNMILIKHLEHFLQFKKPLLVGASRKSVINAYYESE
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     CDS             complement(73643..74254)
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     gene            complement(74254..74787)
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     gene            complement(74788..75990)
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                     GALKADLCEIYTDVDGVYTTDPRIEPKAKKLDKISYEEMLELASLGAKVLQNRSVELA
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gene            complement(80812..81276)
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CDS             complement(80812..81276)
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                     ICEIVKDDGDMARRSDLEEFCAKHNLNMIAVSDIIEYRLKNESLIKLQEKSDAILAGF
                     KAQKFIFTDHNNAQHIAFAFKEIQKCENVKFHISGSDFELLTSDKFSKLLDQICFLSE
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                     ICNFN"
     gene            84637..84711
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                     /inference="COORDINATES: profile:Aragorn:1.2"
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                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Phe(gaa)"
     gene            85250..86593
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                     FHSISAFNNSGFTIFENGLLAYKHDVAINLIFTSLIIIGGLGYFVLVELYFFQRKRLQ
                     NLSLHTKVVIMATLFLIVSSTLIIFLLEYANPKSIGSFSLFDKILSSYFIAINYRTAG
                     FNTLDMSGLHDASLFFGSLFMVIGGAPGGTAGGMKITTVVVLLFYAYWSIRNGRVRIF
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     gene            86606..87256
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     gene            complement(87257..87964)
                     /locus_tag="DMACINML_00353"
     CDS             complement(87257..87964)
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                     SCVQKKALYKQILKKFPKTKIKIPYYILQNYATTRNLDIKDMRYYLDEIIYYKISTKE
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     gene            complement(87930..88559)
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     CDS             complement(87930..88559)
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                     /protein_id="Prokka:DMACINML_00354"
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                     AAPQGLENFAKIHSDVELYVASIDESLNEKGYIVPGLGDAGDRVFNTLD"
     gene            complement(88556..89791)
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                     /protein_id="Prokka:DMACINML_00355"
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                     IASNNELAYTYTNKANLVAIVSDGSAVLGLGNIGAQASKPVMEGKACLFKKFADVNAY
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                     AIISTAGLMNAMEISGKKFEDIKVVVSGAGAAGIASARMYRNLGVKNIILVDSKGVVN
                     KKRTDLNQYKLEFVSDTQADTLKEAMKDADVFLGLSAPKILDDEMILSMAKDPVIFAL
                     ANPIPEVMPEDVARLRKDAIVGTGRSDYPNQINNVLGFPFIFRGALDVRATKITENMK
                     VAAARALADLAKLPVSDAVKNAYNISHLEFGKDYVIPKPFDERVKAVVSTAVAAAAVK
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                     IECRITAEDPKTFLPSPGKIIKYVPPAGRNVRMESHCYQDYSVPPYYDSMIGKLVVWA
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gene            94037..94597
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gene            94651..95655
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CDS             94651..95655
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gene            95656..96786
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     gene            98092..98877
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     CDS             98092..98877
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                     YTFTHFIEEQARVPYRYFKPFKGDIIYENSNKKTYKINYYVRDLHKKSEVSILKQIAL
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     gene            98879..100387
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                ELLVFDESMNLISSKQVGVKGELYVRGTSLSLGYYNDKEKTQKAFIQNPLHDNYLDLL
                YKTGDIVAYNERGELLCYGRADNQIKYMGHRIELGEIESVINSHPKVKNSACIFKDKI
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gene            100374..101117
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CDS             100374..101117
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                     IFEKEFTNQKVYSFEAVSKNYDLMLKTLELNNSKRIIPVKNALGSKEEKLQISISGYS
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gene            142510..142600
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                     PALDELIATFEKKVKEFEGIIKIGRTHLQDATPLTLAQEFSGYLSMLLHSKEQIITSL
                     PTLRELAIGGTAVGTGLNAHPELSEKVSEELSKLIGTKFVSSPNKFHALTSHDAINFT
                     HGAMKGLAANLMKIANDIRWLASGPRCGLGELNIPENEPGSSIMPGKVNPTQCEAITM
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                     VENLKTLELLHTLTWLKAKALNRNPFFYKVIDRILENAKQGFDDENLLDETARRVKKE
                     LTLKRTKLFLDQNAILQDKITHIKSNLFIIKNTFEDIVEIARFAKENDFKFWFSNSTN
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                     AFTLFLLPLFKAIPANAIYPVLVMVGILMFMEVKNIDFKDSAIAVASFFTIIMMPFTY
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gene            167933..169228
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                /protein_id="Prokka:DMACINML_00431"
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                GAGAIGAVATAMISDFITEENRGKAMAIMGSFIGLSFAASMVISPLMSAKWGLSSLFD
                LSAALSLLCIILLYTVVPKENKITHENTKTPFLHLIKQKNLALMNFTNFMQKMLMSIA
                FLSIPIILVKHLGFDEHKLWIVYTASMIAGFIAMGFSGSLGEKRGLAKQILLLGIAFF
                ILSYIFFVFSNSITFFIVAVVIFFIGFNLHEPIMQSCASKFCKVHEKGAALGLFNAFG
                YGGSFIGGVIGGIFLHLNKLELLAIILVALSIVWFIALLYLKNPSEFKNIYLPLETTL
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gene            complement(169230..169757)
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CDS             complement(169230..169757)
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                /inference="similar to AA sequence:RefSeq:EAQ72915.1"
                /codon_start=1
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                /product="lipoprotein, putative"
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                /translation="MRKIHLISALFLALFLSACAKSAFVQSSIQTSNEGIFLKAKQGQ
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sig_peptide     complement(169695..169757)
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                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 21"
gene            complement(169757..170467)
                /locus_tag="DMACINML_00433"
CDS             complement(169757..170467)
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                     RANFTKNVKPVVQEETMLIALGDKSKPAIYVFSDPECPYCRDHLAQIKDELKNYQVNY
                     ILTPVHGKSAFEKSALIYKESKKAKSDDEKIAILNKYYDANIKSYPKVSDSELKEVFS
                     LYEKYRSLGLSATPTIIK"
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                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 17"
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     CDS             complement(170516..172315)
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                     NPVSEPLKKEQKNKFLMLLKNKELKKAFEFLKNTHKYGFGLLSSYQRFKLSHEEALNL
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                     EFGLQNLSNLLEFEKGVYFKKGIDYEKLRERNNDELYNILKKQGIKPQAPYNLYEFLE
                     LDRKSGDEILKKLTKQNRVIRLSHNLFVEKNALDKLMQECLEILKSQSLDIQSMKERF
                     NLSRKYAIAYLEYLDKDERVQKKDEKRFLKTNI"
     gene            complement(172312..173634)
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     CDS             complement(172312..173634)
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                     /product="L-seryl-tRNA(SeC) selenium transferase"
                     /protein_id="Prokka:DMACINML_00435"
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                KITSLKLLNDEITYIKEKALRVQNEIQVKSELKMSKSLVGGGSMPDKTLETCILAFDG
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gene            173704..175365
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                FTRQSGCYNISNFKDQESLLEFLQDKSPKYTYKTYITYDSSVCQYHERRSEHCAKCAE
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                LKFNASLCTTCGYCEVSCAEKDTLKLTRSGMEFNPSYFEYQTMAKDELFACIECGKEF
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CDS             complement(175528..176019)
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                HFA"
gene            complement(176019..176714)
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CDS             complement(176019..176714)
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                     KIWPHSIVPLMDIGEMILNQNPQNYFNEVEQAAFSPSNIVPGIGFSPDKMLQARIFSY
                     PDAQRYRIGTNYHLLPVNRARSEVNTYNVAGAMNFDSYKNGAAYYEPNSYEESPKEDK
                     SYLEPDLVLEGNAQRYAPLDNDFYTQPRALFNIMNQNQKEQLFENIAASMEGVEEKII
                     ARALGHFEKISPDYAQGIKKALGK"
     gene            178704..179171
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                     /transl_table=11
                     /product="ankyrin-repeat containing protein"
                     /protein_id="Prokka:DMACINML_00441"
                     /translation="MITLSLEEEKRFAELCKMAFNFARNNEYENLKIMIEAGLNVNLK
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     gene            complement(179175..179843)
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                     ILCINHDTSMMRDLVCKIIDIEKLDDMGEFLNQNKENNTSVDSLGNIETLSHSIEEIL
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                     TFVAIAFEMIRYKSVVETLNSIMIFFKGMGHLFVITVSLIVCGQVFASGLLSVGFVDT
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     CDS             183094..184461
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     CDS             184470..185810
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     gene            complement(185980..186144)
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     CDS             complement(186110..186382)
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     CDS             complement(186559..187149)
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                     IQMQKLENESQKIMSDEQKYLKILNNMKLNQVRFVYNDKLWQFNDFDFNEFKIIAVEL
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     CDS             187802..187894
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     CDS             188003..188209
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     CDS             complement(188587..188859)
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     CDS             complement(189007..189129)
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                     EQSVANPSRFVDIIPAIKDLVEFLISNENKLLLDKAYVLGFAVAHLIGRYQISIACNA
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                     IYKIMLLDLPFFQIQTLEFIKRTQLRTLSHGIVMLCYLLKHRERLKDFAYYGFSLEEQ
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                     RKKSIMKLTLAFSVVKVSVQHQKEVRRYKKDIKRDVLNKRLPLEFYRDYQKAIKLKNF
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                VDVMTSGKLGLCLVLENEKLVGIITDGDLRRALKANDKPRFDFKAKEIMSINPKVVDA
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CDS             complement(219963..221594)
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                /inference="similar to AA sequence:RefSeq:CAL35553.1"
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                /protein_id="Prokka:DMACINML_00483"
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                AIKAEQAKLILEFIQRARELEPKGQIVIDKPKSYGEVILEEGDTINVPSKNNLIIVQG
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CDS             complement(221596..222711)
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                AKAGLVTQLESDIAQREAKLLTMQSYMNDHAPEIVTLKAEIAALKKQLVKERSKISAD
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CDS             complement(222711..223373)
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                LHEKVKFVEDFAELGKFFDEPMNTYSSGMSARIAFGLSMAFDFDYYLIDEAGAVGDPK
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                KK"
gene            complement(223370..224152)
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CDS             complement(223370..224152)
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                     permease protein"
                     /protein_id="Prokka:DMACINML_00486"
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                     FIARTLLEFCIYFVIFVAVLFIVGWFFRLEVIPRHFLSVMICIFLLMCSGFALGMVFA
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     gene            225307..225996
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     CDS             225307..225996
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                     /locus_tag="DMACINML_00489"
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gene            225998..226708
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CDS             225998..226708
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                SYLKENDIFYFQDESNENEKYFRNYIRKNFSNAFVSKFHQGLKRSFFYLDEDRKKLYD
                LESIKEIQGLMICPKNESLIAKVVKMKGLLLSAAQRKEFLKGDCVLGGKIGIVYKDEK
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                     MEQVPFKVINKRLKIIEKIVDEVIEKSFEKEVGKKRLVVCTGESSEGEFFIAAKDLRW
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gene            232722..233795
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CDS             232722..233795
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                     FFFIFNEIKNNDGQIIMTSDNPPNMLKGITERLKSRFAHGIIADITPPQLDTKIAIIR
                     KKCEFNDINLSNDIINYIATSLGDNIREIEGIIISLNAYANILGQEITLELAKSVMKD
                     HIKEKKENISIEDILSLICKEFNIKPSDVKSSKKTQNVVTARRIAIYLARELTSLTFS
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                     ADIEKITQIAKKHKIATICDNTVATPFLLQPFKYGVDIIVHSLSKYVSGQGSALGGAL
                     IERKDLNDLLKNNDRYKAFNTPDPSYHGLNLNTLDLPIFSIRIIITWLRDLGASLAPQ
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                     IVTGAPVEQMDFEKVAYWEELLEIFDFLQQNVTSSMYICWGAMAALKHFYGVDKIALD
                     KKIFGIYKHDKVSPDLLLTNLDEKVLMPHSRHSSMDEEQISALQKQGKLKVLLRNKKI
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                     GVTTMVACAMGSANEAACAILSDIKGVVSVYHDTPTTRN"
     sig_peptide     complement(45089..45271)
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                     /note="predicted cleavage at residue 61"
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     CDS             45430..45813
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                     /protein_id="Prokka:DMACINML_00555"
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     gene            45810..46607
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                     ISDLKKFKDKFLFTCQNMLKYLEKSRYFALVIADLYRNSEIVPLGFELMNLIKQNFKV
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     gene            48977..49984
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gene            50063..50707
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                AIFELGTSNELEVGFKAEQIEYNTRNYYQETIGSNFYDPRQTNYGLYLGYTYKF"
sig_peptide     50063..50128
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gene            complement(50731..51360)
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CDS             complement(50731..51360)
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gene            51697..53232
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gene            complement(56288..56818)
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gene            complement(57045..57120)
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tRNA            complement(57045..57120)
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gene            complement(57122..57197)
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                /inference="COORDINATES: profile:Aragorn:1.2"
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gene            complement(57331..58296)
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                     /translation="MEYIVEKIGMSRTIANPSIAVTLLRVVNAKVCEVDNGKAIVAYS
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gene            72038..72394
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                KALDTVFMLHADHEQNASTSTVRAVGSTHAHPYACISAGIGALWGHAHGGANEGVIRM
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gene            81639..82418
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CDS             82443..83204
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sig_peptide     82443..82502
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                /inference="ab initio prediction:SignalP:4.1"
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gene            complement(83211..83384)
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CDS             complement(83211..83384)
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     CDS             complement(83498..84274)
                     /gene="murB"
                     /locus_tag="DMACINML_00608"
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                     FDKIKDENLKNARNNQPSGASFGSIFKNPKGDFAGRLIEAVGLKGFSKGGAMLSDKHA
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     CDS             complement(84271..84540)
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                     /protein_id="Prokka:DMACINML_00609"
                     /translation="MDESTLVALGVQTFKITLLLSLPMLLAGLIAGLIISIFQATTQI
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     gene            complement(84552..85415)
                     /locus_tag="DMACINML_00610"
     CDS             complement(84552..85415)
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                     EIWDIWLELAQENLPLPLGGMALRRSLPLSDAIKIERDLTNAVKIADSNRRILAPMLM
                     ERNLIRVDEKKLDTYLNLYANKNSICMNEMQFKAVDVLFKLGYDYKFYDKIIHAKDYL
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     gene            85525..86556
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gene            86556..87800
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gene            87866..88069
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CDS             87866..88069
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gene            88059..88721
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                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Pro(tgg)"
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                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-His(gtg)"
     gene            89790..89866
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     tRNA            89790..89866
                     /locus_tag="DMACINML_00618"
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                     /inference="COORDINATES: profile:Aragorn:1.2"
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     gene            89881..89957
                     /locus_tag="DMACINML_00619"
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                     /note="tRNA-Arg(tct)"
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     tRNA            89963..90047
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                     /note="tRNA-Leu(tag)"
     gene            90248..91003
                     /gene="proB"
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     CDS             90248..91003
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                     /codon_start=1
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                     /inference="ab initio prediction:SignalP:4.1"
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     CDS             93988..94773
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                     NNEKKMILKNQIQEVLDEYDFIIIDSPPALGSITINAFVASDSVIIPIQCEFYALEGV
                     AMVLNTIKIIKKTINPKLKVRGFLPTMYSSQNNLSKDVVEDLKQNFKKQLFTINGNED
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                     FVSDSDESKLRELALIENIQRENLNPIELANSYKDLIEVYNITQENLAELIHKSRTQI
                     TNTLRLLNLDSKTQELIASGKISQGHAKVLVGLDKEDEKVLVDSILGQKLSVRDTERL
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                     RGQRELIIGDRQTGKTTVAVDTIISQKGQGVVCIYVAIGQKQSTVAQVVKRLEEHGAM
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                     ISITDGQIFLETDLFNSGIRPAINVGLSVSRVGGAAQIKATKQVSGTLRLDLAQYREL
                     QAFAQFASDLDEASRKQLERGQRMVELLKQPPYSPLSVEKQVVLIFAGTKGYLDDVAV
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                     /product="putative MotA/TolQ/ExbB proton channel family
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                     /translation="MPFDDEKPELNITPLVDIMLVLLAILMVTAPSITYEEKINLPQG
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                     NQKTGIYDEFLGKVVRTITQRWRQYHPNSENISVKVKIFIDENGNFGYTSVEKSGNSL
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                     DYTLTYQKVIIDGGLNLFPKWGNKEQSIFYYTAYDHDRPTLYRYDLRTNKASKILSSG
                     GMVVASDVSLDGSKLLVTMAPKDQPDIYLYDLKSKNLTQLTNYSGIDVNGNFIGVDDS
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                     /locus_tag="DMACINML_00639"
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                     YENSKIKLNYLIQKQYKPARANFWLGEIEYKQKKYNNAIVYYKKSSALSTKGDYFPKL
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     CDS             109332..109946
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                     /protein_id="Prokka:DMACINML_00647"
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     CDS             110482..111684
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gene            114829..115425
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CDS             114829..115425
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sig_peptide     114829..114894
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gene            115442..116137
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gene            complement(117420..118346)
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CDS             complement(117420..118346)
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gene            complement(118343..119329)
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CDS             complement(118343..119329)
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                /translation="MRIRLFFIASFIYIALIFALAWYLELGNYTLNFNTYSFELPIMI
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                KNHIKNDINYAYSKIKNLSQTQDEFQDLAFESLIKKGTYEQIKNIKITKKPCHILTLI
                KRFKEGNLELNTAEYEVLLSHNILGEKDYLDIAKLSTKLLNPDALIGIFNKIKNEKGE
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gene            complement(119326..119679)
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CDS             complement(119326..119679)
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     gene            complement(119691..120140)
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     CDS             complement(119691..120140)
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                     /gene="accD"
                     /locus_tag="DMACINML_00660"
     CDS             complement(120142..120984)
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                     GRKSAVISGECLIDGLKTQLVVFDFSFMGGSLGSVEGEKIVRAIQRAITDKTPVVIVS
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                     FCGK"
     gene            complement(120999..121715)
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     CDS             complement(120999..121715)
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gene            complement(121715..123931)
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CDS             complement(121715..123931)
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gene            124007..124834
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                /protein_id="Prokka:DMACINML_00663"
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                AKLTKQTLFAHPMAGTENSGPKAAFKELYKDAVCVLCDSEVADDLHQKRAVEIFSHLG
                MRIVFMDSTAHDHHAAIISHLPHVISFSLANFVMKEEDKRNIVHLAGGSFKGMSRIAK
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gene            124931..126304
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CDS             124931..126304
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CDS                131365..131724
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gene               132601..133314
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gene               133304..133747
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CDS                133304..133747
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                NEKEKIEAKIISVEDENITLENLENQEKTTLKFSDIKKARTFVEW"
gene            complement(133757..134743)
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CDS             complement(133757..134743)
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                QRNNIIRLSKIDPLSLEYDKITIYNPYSTRVNGALLALTFFNHIDNNQFFHDNIDKEY
                FASICQLSQELKKHGLEPNQIFMLIFNESINQSIISNSGSNYESRILEKLESIGINQE
                AIIKKHDENDSSTEFDFFFNLNGKSYGIGAKRTLRERYKQFIKTVQMSTIDVMIEITL
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gene            complement(134730..135695)
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CDS             complement(134730..135695)
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                NRERIYIVAFLKNKFKNISFSFNELKNIKIKSKLGDILEKNIDEKYTISDKLWAGHQR
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gene            135914..136225
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CDS             135914..136225
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                /protein_id="Prokka:DMACINML_00676"
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                F"
gene            complement(136214..137020)
                /locus_tag="DMACINML_00677"
CDS             complement(136214..137020)
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                protein"
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                HGAFGGIGIAFYFSLPILISTGIFTLFLAFLVAFLSKRYEHRSDSIVAVIWAFGMAFG
                IILIDLSPGYSTDLMAYLFGNILAVGMQDLWLMAIVDGVVIVLMLLFYRQFEALSFDV
                EFAKVRGINTSFFHYLLIALMAFCIVISIRLVGIILIMALLSIPSFIAENFTKKLGLI
                MILASVLSMIFCVLGLIISYYFNLSSGACIIAVACFGFLIHLLAKFLLKR"
gene            complement(137013..137867)
                /locus_tag="DMACINML_00678"
CDS             complement(137013..137867)
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                VDSKSAIQIFELLSSLHEKGIGILLICHDINLVLAYSDKIAYLNKELFLHTNTKEKDK
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                KFSKESHV"
gene            complement(137881..138735)
                /locus_tag="DMACINML_00679"
CDS             complement(137881..138735)
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                RNLDKFLTELDVLNLQISSKLQKVKNKEFITYHPAWSYFAKRYNLVQNHVEFLGKKLK
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gene            complement(138906..139844)
                /gene="trxB_1"
                /locus_tag="DMACINML_00680"
CDS             complement(138906..139844)
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                /locus_tag="DMACINML_00680"
                /EC_number="1.8.1.9"
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                LAKAVIVCTGSAPKRAGFKGEDEFFGKGVSTCATCDGFFYKNKEVAVLGGGDTALEEA
                LYLANICSKVYLIHRRDEFRAAPSTVEKVKKNEKIELITSASIDEVYGDKMGVTGVKV
                KLKDGSIRDLNVPGIFTFVGLNVRNEILKQDDGKFLCDMEEGGQVSVNLKMQTSVPGL
                FAAGDLRKDAPKQVICAAGDGAVAALSAMAYIESLH"
gene            complement(139979..140293)
                /gene="trxA"
                /locus_tag="DMACINML_00681"
CDS             complement(139979..140293)
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                /locus_tag="DMACINML_00681"
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                LL"
gene            complement(140348..140686)
                /locus_tag="DMACINML_00682"
CDS             complement(140348..140686)
                /locus_tag="DMACINML_00682"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:CAL34319.1"
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                KDGILHFIEVKFTQNNYEVSERLNIKKYERILKTIEFYELKHGILNDFQIDLICISDD
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gene            complement(140686..141936)
                /gene="hom"
                /locus_tag="DMACINML_00683"
CDS             complement(140686..141936)
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                KENPLIPIVTNVDEILQRDDIDVFVELMGGVETPFKIISEILKKNKPVVTANKAMLAY
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gene            complement(141938..143143)
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CDS             complement(141938..143143)
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                FFEDLDKTLHESIPRPKYVVVNFPHNPTTVTCEKSFYERLVATAKKERFYIISDIAYA
                DLTYDDYKTPSILEVEGAKDVAVETYTLSKSYNMAGWRVGFTVGNKRLVAALKKIKSW
                FDYGMYTPIQVAATVALDGDQSCVDEIRATYDKRMHILLEAFENAGWKLHKPRASMFV
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                NIKKYLKEE"
gene            complement(143156..143962)
                /locus_tag="DMACINML_00685"
CDS             complement(143156..143962)
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                /transl_table=11
                /product="putative periplasmic protein"
                /protein_id="Prokka:DMACINML_00685"
                /translation="MVKKIFIFLFLANSVFAVSSLELAKNLVANPSKDSQLRLLFPDS
                SYIDNKGNPDIAKISRILKTNSLINLTLSDPQTLRLNFKAKADSVVFFKILTDALTNL
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                DLNFENAQLNTNIDLKLNSTQTLERPLKDYVFTLQGASNLIIDAHDADFWFPKVLFLD
                KNLNLIKAIKSQAQNNHFSELIPSGAVYAIVSDMYNLDNIRRGLKITLKK"
sig_peptide     complement(143888..143962)
                /locus_tag="DMACINML_00685"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 25"
gene            complement(143956..144900)
                /locus_tag="DMACINML_00686"
CDS             complement(143956..144900)
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                /product="putative membrane protein"
                /protein_id="Prokka:DMACINML_00686"
                /translation="MLNWKKIEDLNLKEVAARTKIELDFLEALVKKDFVTLNRFNVRG
                FVKILSREYELDFTDFNEEFETYLNENNLNDTAKPKIITPKLDAYTQKSTGFVSFIVI
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                VIILALVGFGIYYFDYIKSFFQNDQNNSSAAVVDIIGQAQSNLKALENNVVVIDNQAE
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                APNKEAHFKASGKIWIGLIDLSNYRKTGLVKENDFNLSLEVNRLVLTGAAALSVFDEN
                GKEQKFPAGNSKRFLIKDGKITSISAAEFMKLNKGKEW"
gene            complement(144893..145576)
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CDS             complement(144893..145576)
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gene            complement(145589..146413)
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CDS             complement(145589..146413)
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                IIYESPKRILSLIEQIAILDSQREIFAIKEISKKFETKFKAKAIDLFDILKQTNLKGE
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gene            complement(146416..146616)
                /gene="rpmE"
                /locus_tag="DMACINML_00689"
CDS             complement(146416..146616)
                /gene="rpmE"
                /locus_tag="DMACINML_00689"
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                /inference="similar to AA sequence:RefSeq:CAL34326.1"
                /codon_start=1
                /transl_table=11
                /product="50S ribosomal protein L31"
                /protein_id="Prokka:DMACINML_00689"
                /translation="MKKEIHPEYVECKVSCACGNTFVTKSNKSELRVDICSSCHPFFT
                GSEKIVDAAGRVEKFKKKYAMQ"
gene            complement(146695..147348)
                /locus_tag="DMACINML_00690"
CDS             complement(146695..147348)
                /locus_tag="DMACINML_00690"
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     gene            complement(147349..147756)
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     CDS             complement(147349..147756)
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                     /protein_id="Prokka:DMACINML_00691"
                     /translation="MDKSYEFFLALHLYSLYASGFLMLFYLVLTQGNFKTEFIFIRRI
                     RLFLPIYYVFLALMLFTGFLLLAIKQFQMHLNLWLMIFSWIFIFALAIFHFTQFKKAR
                     RLRRYITFRRISFMILFCELVLLILPFLTGKYL"
     gene            complement(147760..148179)
                     /locus_tag="DMACINML_00692"
     CDS             complement(147760..148179)
                     /locus_tag="DMACINML_00692"
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                     /protein_id="Prokka:DMACINML_00692"
                     /translation="MGKNLSILISLFVILFLNACSNDKEFNHKNQDTTEEIVQIEQND
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                     NLSSEKFIQRLQNLKDEAHNFLTQEQRENLAKYIGKE"
     sig_peptide     complement(148120..148179)
                     /locus_tag="DMACINML_00692"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 20"
     gene            complement(148179..148760)
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     CDS             complement(148179..148760)
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                     /transl_table=11
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                     /protein_id="Prokka:DMACINML_00693"
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                     /protein_id="Prokka:DMACINML_00694"
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     gene            complement(149503..150465)
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                     /locus_tag="DMACINML_00695"
     CDS             complement(149503..150465)
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                     LKGLNDDELISLLEFAKSKNIQIRFIEFMENIHAYGKLQGLKRDEIIQILSQKYQIKL
                     IKKAEKAPVSIYSADDYEFGIIDPHSHEFCDSCNRIRLSAEGLLIPCLYFDEALSIKE
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     gene            complement(150481..150999)
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     CDS             complement(150481..150999)
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     gene            complement(150992..151492)
                     /locus_tag="DMACINML_00697"
     CDS             complement(150992..151492)
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                KKDKNE"
gene            complement(151483..152367)
                /gene="ubiA"
                /locus_tag="DMACINML_00698"
CDS             complement(151483..152367)
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                GFKALILGIICAVSARNFAMATNRLMDEDIDKDNPRCANRPNVSGKIGRKSVWIFIIL
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                VMGEIHIYSVILCLGVTFWTAGFDLLYSLQDMEYDKKVGLHSIPAKFGSKATLFISAF
                CHVLAVLFWLLFVWQVWGVALGNIALLGVIISGIILAFEHKIVHKNFAHIDKAFFTLN
                GYLSIIFFIFIWVDLLWG"
gene            152438..153307
                /gene="miaA"
                /locus_tag="DMACINML_00699"
CDS             152438..153307
                /gene="miaA"
                /locus_tag="DMACINML_00699"
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                transferase"
                /protein_id="Prokka:DMACINML_00699"
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                ANAKPSKDELMNLNYFGVNLLSVDEHFNVELFIREYQKAKEFALMNDLPLIIVGGTGF
                YLKTMIDGLSQKIQDTTSILSNDEIYTLLLKIDPAYKIEKNDTYRLRKWLSIYENTKE
                IPSDFLKRTQKDGVLKDIEIYELVWDREILRKRIEARTKEMIDSGLIEEARMLFSNFD
                NNLKALNSIGLKECKEYLENKISLKELENLITIHTSQLAKRQRTFNKKFQSTPLEFSK
                ALTLLRNKFLAKK"
gene            complement(153293..153856)
                /locus_tag="DMACINML_00700"
CDS             complement(153293..153856)
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                KNKAEFLGGAVLIILGIKILIEHLFFS"
gene            154029..154103
                /locus_tag="DMACINML_00701"
tRNA            154029..154103
                /locus_tag="DMACINML_00701"
                /product="tRNA-Glu"
                /inference="COORDINATES: profile:Aragorn:1.2"
                /note="tRNA-Glu(ttc)"
gene            154265..154672
                /locus_tag="DMACINML_00702"
CDS             154265..154672
                /locus_tag="DMACINML_00702"
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                /transl_table=11
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                /translation="MSYDTNFFLLYFKDKVPKDSLIFLKESLEKASEEQKEKLLFTKL
                KNPLYGLLFAFLFPGLDRIYNGNIILGILKIISVILVSMGLVIAEDKNDESTMLIFIN
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gene            154669..155097
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CDS             154669..155097
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                PLVGLVLSITVGLFGVDRFYKGDILLACIKLAFFIIPLFATFAAFIALLNKSHSIFID
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gene            155205..155843
                /gene="sodB"
                /locus_tag="DMACINML_00704"
CDS             155205..155843
                /gene="sodB"
                /locus_tag="DMACINML_00704"
                /EC_number="1.15.1.1"
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                /transl_table=11
                /product="superoxide dismutase (Fe)"
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                     /protein_id="Prokka:DMACINML_00704"
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                     ENFKAEFIKGATGVFGSGWFWLVYNTKNQKLEFVGTSNAATPITEDKVPLLVVDVWEH
                     AYYVDHRNARPAYLEKFYAHINWEFVAKAYEWALKEGMGSVSFYANELHPVK"
     gene            complement(155871..157076)
                     /locus_tag="DMACINML_00705"
     CDS             complement(155871..157076)
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                     /EC_number="1.5.1.7"
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                     /inference="similar to AA sequence:RefSeq:CAL34341.1"
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                     /protein_id="Prokka:DMACINML_00705"
                     /translation="MKNLLIIGAGGVSRVATVKCAMNSDTFSKITLASRTKSKCDEIA
                     SFIKERLGVEIQTAQIDADDSDAVVELIKKTGAQILLNVALPYQDLSLMDACIKAGID
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                     EISYIDILDCNAGDHGYAFATNFNPEINLREVSAKGRYWEKGEWIETEPMEIKMEWDY
                     PEVGVKDSYLLYHEELESLVKNIKGLKRIRFFMTFGQSYLTHMKCLENVGMLGIKPVM
                     HQGKEIIPIEFLKTLLPDPASLGPRTKGYTNIGCVIRGVKDGKDRQVYIYNVCNHEEC
                     YKETGAQAVSYTTGVPAMIGTKLIAKGIWQGKGVFNMEEFDAKPFMDELNSQGLPWKI
                     IEMTPSLGE"
     gene            complement(157112..158017)
                     /gene="cfbpC"
                     /locus_tag="DMACINML_00706"
     CDS             complement(157112..158017)
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                     /inference="similar to AA sequence:RefSeq:CAL34342.1"
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                     /transl_table=11
                     /product="putative iron-uptake ABC transport system
                     ATP-binding protein"
                     /protein_id="Prokka:DMACINML_00706"
                     /translation="MLEIKNLSKNFGKIQALKNINLHVKEGEFLSILGGSGSGKSTLL
                     RIIAQLEQASSYEFLKCKGEVAMMFQNYALFPHLNVEKNILFALYDKKDKKQILEDLL
                     KTFEIENLRYKKIDEISGGQAQRVAFARAVARGCKLLLLDEPFSNLDQNLKQDLRREL
                     KKLIQKQKITAIMVTHDIEDAYCMSDKIAFLDKGEILAHADPKELYFKPNHKSARILP
                     DLNIIEEELDLEDEFFQWIASKNYTFGYAELKIGNRFEATILQKEFLGAFYRLKVRYK
                     NIEFFMLLSSNYPLKEKINFDIINF"
     gene            complement(158004..159620)
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                     /locus_tag="DMACINML_00707"
     CDS             complement(158004..159620)
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                     /locus_tag="DMACINML_00707"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL34343.1"
                     /codon_start=1
                     /transl_table=11
                     /product="putative iron-uptake ABC transport system
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                EISSIKENLSHFFDYLFLKFIKDTLIVSIGVLLLSLILGVSSAYLMANYNFYFCRILE
                KLLILPLAIPAYILAFVYVGIMDFQGFFHEIFGFRIDFFNHYGVIFVLGISLYPYIYL
                FAKTAFKSEAIEAYEVAKIMGYSEFRIFSRVMLLSARPAIFSGALLVLMETLSDYGAS
                AYLGVDTFSAGIFKLWYDLNDSYSSSILSGILMIFVFLIMYIDYYYKNKHHYSFNQNL
                TLFIKKRKLSHIKQILACFYCFIIALLGFILPFIWLVYWGLKDFKLFETEFYIISFQT
                IILAFITALITTLLAYFLMFSSRIIKNNFFSLCILKLSSLGYSIPAAALGISMIVLFV
                FLDKIFHLNLLGTSLIILVFAYIIRFLASAIYSLEGGYNKIHLNTDEASLNLRPSYLI
                LFFKIHTPLMKHFLFLAFIIVFIDTIKELPLSRILAPFGFETLSVKAFWFASDERIYD
                AALPSLLIVLLSLIVVIWMDKITRKDDVRN"
gene            complement(159620..160624)
                /gene="futA1"
                /locus_tag="DMACINML_00708"
CDS             complement(159620..160624)
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                /locus_tag="DMACINML_00708"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:SQE23619.1"
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                /transl_table=11
                /product="iron ABC transporter periplasmic iron-binding
                protein"
                /protein_id="Prokka:DMACINML_00708"
                /translation="MKKIFSLCLLGFSLLGAAELNIYSARHYDADFQIIKKFEEKTGI
                KVNHTQAKASELIKRLSLEGSNSPADIFITADISNLTEAKNSGLLSPVKSKYLEDTIP
                AHLRDKDGEWFAITKRARIIAYNKNANTDISKMKNYEDLAKPEFKGQIVMRSATAPYS
                KTLLASIIANDGDENAKAWAKGVLDNLATKPKGGDRDQARQVFAGEAKFAVMNTYYIG
                LLKNSKNPKDVEVGNSLGIIFPNQDNRGTHINISGIAMTKSSKNQEAAKKFMEFMLTP
                EIQKILTDSNYEFPIRNDVELSQTVKDFGTFKEDQIPVSQIAEKVKEAVKIYDQVGFR
                "
sig_peptide     complement(160571..160624)
                /gene="futA1"
                /locus_tag="DMACINML_00708"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 18"
gene            complement(160625..160747)
                /locus_tag="DMACINML_00709"
CDS             complement(160625..160747)
                /locus_tag="DMACINML_00709"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:CAL34345.1"
                /codon_start=1
                /transl_table=11
                /product="putative lipoprotein"
                /protein_id="Prokka:DMACINML_00709"
                /translation="MKKLVLFLFCLGFAFACSEHSNADFKDHDKTKYNSQYKDK"
sig_peptide     complement(160676..160747)
                /locus_tag="DMACINML_00709"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 24"
gene            160989..161840
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CDS             160989..161840
                /locus_tag="DMACINML_00710"
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                /inference="similar to AA sequence:RefSeq:CAL34346.1"
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                /product="putative iron transport protein"
                /protein_id="Prokka:DMACINML_00710"
                /translation="MKFYTMLSTLFISFMLSACAVLQKPSPLQENKDFYILNTHTQEK
                ISFEDMILELLKADVILLGEKHDEAKHKISQVMIFNALEGNLSSQNISFDVALEMLAS
                TEQNHLDKAFKNKKNIKVNELANALNWDKGWKWKDYDQFVNAVFYSRAKILGANLSRS
                EITSIYNGVQPLKGYVSTTNEVKKQIFDIISLSHKLNPQENKELLDKLVEIQQFKDRR
                MADVLVHHTNKVLLLAGNYHTSKKIGVPLHIQDFKSDKKIVVVNLNYGKVDLKDSDYI
                FIYKGGE"
sig_peptide     160989..161051
                /locus_tag="DMACINML_00710"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 21"
gene            161837..164113
                /locus_tag="DMACINML_00711"
CDS             161837..164113
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                /codon_start=1
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                /product="Putative outer membrane siderophore receptor"
                /protein_id="Prokka:DMACINML_00711"
                /translation="MKKLSLICVMGLCFANFAFSEELEFDSLEISGSRIKNDEKPFVT
                PGATSTRDNLNSSTQSIDSIVRSVPGAYTQVDQAQGGVSVNIRGMTGLGRVNTQIDGV
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                IGVDDIVQEGRVFGLLGKYSYGSNAIGPDFMGAIAGKTMLENNTSLGVLFAYSGQNVS
                QNYKIGGGGYIGDQKPPIDTDDDGIPDDNLAAPINPNNLYNQPRSQLFKVEYKSDISE
                AILNYRAYKNNLAGRKITNDTYQIDYRLNPDSNLLDLKFLFAYNDGKQKYNQGSTWGY
                HDMSGVKTKNRAVTFDLSNTMNKEFSQDSNLYFTYGVNILNNHYSNDFPQDRVLLPYI
                LTSFYPKGKQDIKTLYLDTSFTQGIFTLNSNVNWTNAQLSGYKGICSMANPYCQPKNA
                TNLEKDYNNFNYSLMLSADIHPLFNPFISYSKSHRIPNVQEYFFTHDASFEHNMNTFL
                KAESADTYQIGFNSFTHEILNDSDTLGFKMLYYDTKVKNYIYNRRYWQKADDAVFLMQ
                LNDDEKAKFHGVELEFKYDTGFFYSILSYTYQKSKHKFSDTESLEFGGAQSGQSQFAQ
                LPEHYANLDMGVRLFEEKLTLGALAKYTGKAKRIVPVGSLDDDPSNPDAMAPLKTTDE
                LPKIPTIVDLYANYKILKNFTIKAEVQNLFDKNYMDALYSYNTGENQNAGGLFDPIYI
                YNNSARGRTFIVSFEYKY"
sig_peptide     161837..161899
                /locus_tag="DMACINML_00711"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 21"
gene            164126..164887
                /gene="exbB1"
                /locus_tag="DMACINML_00712"
CDS             164126..164887
                /gene="exbB1"
                /locus_tag="DMACINML_00712"
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                /inference="similar to AA sequence:RefSeq:CAL34348.1"
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                /codon_start=1
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                /product="biopolymer transport protein"
                /protein_id="Prokka:DMACINML_00712"
                /translation="MLKKIFLFCFLLLNLNAEVNVTDTNLSFDSPKIEAEVPKIELSL
                SSLYQNADEVVKGVIYILVLFSVLAWAVFISKLMQFYFMKKNLDFSIHKIKELKNLNE
                LDQTKGFAGVLSLEIQDELEKSEYKNDHIKERIELRLQNTISKQITASKNGLSLLASI
                GASAPFIGLFGTVWGIMNAFIGIANLGNASLAVVAPGIAEALFATAFGLVAAIPAVLF
                YNYLTRKNLKLMHHLDELANFVYILFHRSYFNDKN"
sig_peptide     164126..164185
                /gene="exbB1"
                /locus_tag="DMACINML_00712"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 20"
gene            164874..165284
                /gene="exbD1"
                /locus_tag="DMACINML_00713"
CDS             164874..165284
                /gene="exbD1"
                /locus_tag="DMACINML_00713"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:CAL34349.1"
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                /transl_table=11
                /product="biopolymer transport protein"
                /protein_id="Prokka:DMACINML_00713"
                /translation="MIKTEIAHKEEELSEINITPFIDIMLVLLIVFMAVTPLITSSIK
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gene            165286..166077
                /gene="tonB1"
                /locus_tag="DMACINML_00714"
CDS             165286..166077
                /gene="tonB1"
                /locus_tag="DMACINML_00714"
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                /inference="similar to AA sequence:RefSeq:CAL34350.1"
                /codon_start=1
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                /product="TonB transport protein"
                /protein_id="Prokka:DMACINML_00714"
                /translation="MKSSVIFGFVSSLVLHALVLMFFLFSFYTQEKSSGVDFKQGVEF
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                KNAVLKAQKKIEKQDENQAQKEIANASENSKFKNETLSAPLQSNEDKTQTIVSGNAKE
                QIKSYQALLMAHLAKFKKYPQEAIMQKQEGVVRIRVSIDESGNVLSKELKKSCPYAVL
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gene            166133..167353
                /locus_tag="DMACINML_00715"
CDS             166133..167353
                /locus_tag="DMACINML_00715"
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                     /translation="MFSSFFASKKWALWAYLGLFLLLFFLYMQTSLNVAINSWYSDFY
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                     LEYFFNSRAMIEKESYSASDFYALILVFLAIAIPYVLIATINIYFASVYAFKWREAMT
                     FSYLKFWKNKDDNIEGSSQRIQEDTYNFSKIVESLGLSFIRALMTLVAFIPILWTLSD
                     VVSKALFANLSENSSFYFLKNIDGLLVYVALLISLGGLIVSWFVGIKLPGLEYNNQKA
                     EAAFRKELVYAEDNRKEYAKNETMIELFTGLKFNYKRLFLHYGYFNIWLILFEQMIVI
                     VPFLIMAPGLFAGAIGLGIVMQINNAFDQVRSSFSVFITNWTTITQLRSIYKRLKEFE
                     KNIEYAKNKNKNHL"
     gene            complement(167344..168477)
                     /gene="ynfM"
                     /locus_tag="DMACINML_00716"
     CDS             complement(167344..168477)
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                     /locus_tag="DMACINML_00716"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:UniProtKB:P43531"
                     /codon_start=1
                     /transl_table=11
                     /product="Inner membrane transport protein YnfM"
                     /protein_id="Prokka:DMACINML_00716"
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                     LCIPAILTALLTLLSRLESDNIQKNIAIYVGATTFGGFVGRVFGSFLSDLFSWHFALN
                     FFSILMMVCAFLFLFFKEHPISLNTQTSLRDFLPFIKELRFMVILFCVFTIFFSFQSI
                     VSFLPFHLKESIKDITQTQIGLVYLGFLTGVISSLLIGKTIEILGSKIRTAIFGFLVF
                     ITGCFCMIVGNFYFAFFAMFVFCSGMFISHCIFSGILNSIADKKGLANGIYLTFYYSG
                     GALGSVLPSFYYESFGWEFLCIFTAFLLFIALIIFGKFRHFYK"
     gene            168589..169950
                     /locus_tag="DMACINML_00717"
     CDS             168589..169950
                     /locus_tag="DMACINML_00717"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL34352.1"
                     /codon_start=1
                     /transl_table=11
                     /product="putative integral membrane protein with
                     hemolysin domain protein"
                     /protein_id="Prokka:DMACINML_00717"
                     /translation="MDPSQVLDLNQTLPTASFDAGYSILMVVIALALVLLNGFFVLSE
                     FSIVKVRRSKLEEMVKEKKVGAKKALEVTSRLDTYLSACQLGITLSSLALGWIGEPAI
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                     RPLHWFWILFLPCIKIFDFLAAMTLKLFGIKPAKESELTHSEEEIKIIASESQKGGVL
                     DEFETEIIRNAVDFSDTVAKEVMTPRKDMICLNKQKTYAENMQIICDHKHTRFPYIDG
                     SKDTILGMIHIRDIVQNELSDKSENLDTFVKPLILVPENISISKVLVMMNKERSHTAL
                     VIDEYGGTAGILTMEDIMEEIIGEIKSENEEDSYKKLAENIYEFQGRCDIETVEEMLL
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                     DEE"
     gene            complement(169963..171147)
                     /locus_tag="DMACINML_00718"
     CDS             complement(169963..171147)
                     /locus_tag="DMACINML_00718"
                     /inference="ab initio prediction:Prodigal:2.6"
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                     /protein_id="Prokka:DMACINML_00718"
                     /translation="MRILLILRGNYYAGQEEFIKENRLKDYTLDLNSLRLLSGSVSKI
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                     IDFKSSLEECLEKNEQKAKERGYIVSQSLLKKTHHLLERIPKKYTILNPNDWKKCLYQ
                     MPNLSKYRKIHHIGDIQGCFSVLKEYLQELKDDECYIFLGDYIDRGIENGKVLKFLLK
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                     ECLYYKFHEKQVFCSHGGVNFLPSKAYQISFMSSYDFIYGVGNYEESQKVASQFCEFT
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                     KK"
     gene            complement(171156..171365)
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     CDS             complement(171156..171365)
                     /locus_tag="DMACINML_00719"
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                     /transl_table=11
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                     /protein_id="Prokka:DMACINML_00719"
                     /translation="MPKDANGTELNAGDSVSVIKDLKVKGASTTLKRGTTIKNIKLTS
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     gene            complement(171415..172155)
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     CDS             complement(171415..172155)
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ACCESSION
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SOURCE      Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
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                protein"
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CDS             complement(18666..19610)
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                    TGTSDIGFEDDFFNRLEHLILPVLVLVLSHLALFLRIARNCINETFSQIFVQNLYARA
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                    EDVCFNIEDLADGIKSIQELFYKYGFSDNGIIFGHALAGNIHFIITPDLNNKLEFDNF
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                    KRLESLNDDESKAKLKDIKKYYNHLVDSSCAACGVCSFSCPLGINFADFSLKYRKNNI
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                     KKKNNTLGNLFNNLSSNFTNVALLALVGVEFYLALEFKWASVAEATTIALSILFLRTP
                     LVSMIGSFPTLLLAKIALDKIAKLELDDYKEHFEKTNFIKDWRQISFKNTSFSYDDNF
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                     NINDKGEKFDEIVKNELKATEVIRIRAIETKLDDDEENILKPMGIKDLLNKSYNLLPE
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                     DNPIVQQINAFGVFAAGFFMRPIGSWLFGSLADKVGRKKSMVVSVVLMALGSFMIAAL
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                     GQLLAVASISIMLFFFSIDEMKDYAWRILFVVGGILALGSLLVRKVMNESATQIHKHD
                     DRGTLKALFTSSWKQFLMVLGITAGGSLAFYTITTYTKTFMENSGMDKTLVNNLFLGA
                     LFILMIIQPLFGYIGDKIGHKRSLIIFCILAFVGIYPIFNLISSNAQSNSSLVFILVV
                     LLFIILSFYTSVAGIFKAKLFPEHVRALGTGLGYAISNAIFGGSAPWVALQFKNAGME
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     gene            complement(58886..59905)
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                     /codon_start=1
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                     /product="A/G-specific adenine glycosylase"
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                     AYGVYISEIMLQQTQVKSVLERFYFPFLQKFPTLQSLAKANEDELLKAWQGLGYYTRA
                     RNLKKSALECVDKFEGKLPKKLDELKKLSGIGAYTAGAIACFAYDQKVSFVDGNIRRV
                     LSRLFALENPKMNELERKAKELLNLEDAFNHNQALLDIGALICVSKNAKCGICPLYDF
                     CQGKFNTELYPKAKKISYENASLNLFIFEWGKKFAIQKSQDKLYKGMYNFPFFKEEEG
                     EISKNMKFLGEFKHNYTKYKLNIKVYHQILKEENKNYQFKSLKELESTALSILSLKAL
                     RLIKL"
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                     /inference="similar to AA sequence:RefSeq:AII23819.1"
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                     /product="hemerythrin family protein"
                     /protein_id="Prokka:DMACINML_00798"
                     /translation="MDHHKLIPLWDERYNINHQKIDTQHQRLFELAAQVENAVFKFVK
                     RDELKEILTELFTYMKEHFHDEEEFMQEIRYPRLYEHKQMHKNIVHEMSQLIQNIKST
                     NDLKEKLYSIMSNWLSRHILSHDVMIIAWVNENLKKDENKTLELNDLPPKQILTQEEN
                     FEFIYSCPCKIDHRLSFKEHESIANEGKIMRCKKCQELLFFIRSQEKTYKG"
     gene            60869..61465
                     /locus_tag="DMACINML_00799"
     CDS             60869..61465
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                     /transl_table=11
                     /product="putative iron-binding protein"
                     /protein_id="Prokka:DMACINML_00799"
                     /translation="MLPKWDKIYSVHNGKIDNQHKKLFELAAKVEHIFDKPVHRDEIK
                     ALLTDFFNYMKYHFDDEEKYMQFIRYPDFERHRQIHKEIIQSMIKIIQNIKTTNDLKE
                     KLYIMVKKWLLEHILYEDMRVEQWRIGSLSSENGADITFEEIKDDEEEAVIYFYACEC
                     IGQIHDVPSGIHKKIQNEGAKFKCKKCKFPLEFFKKGY"
     gene            61518..62276
                     /locus_tag="DMACINML_00800"
     CDS             61518..62276
                     /locus_tag="DMACINML_00800"
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                     /inference="similar to AA sequence:RefSeq:CAL35718.1"
                     /codon_start=1
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                     /product="putative periplasmic protein"
                     /protein_id="Prokka:DMACINML_00800"
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                     /translation="MLAFFKGLGIGFLCLVLFIAGVIFNVEFLNKNKTTQTLNFSRSI
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                     PALEPKFSKQTLKDNKEKLYSELLKKAYSYENIYSLDLNKTCILKNLNIESIPNFYPR
                     ALNSMKSADNMELSLPIIKDEEQSISGTALFICK"
     gene            62335..62409
                     /locus_tag="DMACINML_00801"
     tRNA            62335..62409
                     /locus_tag="DMACINML_00801"
                     /product="tRNA-Gly"
                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Gly(gcc)"
     gene            62420..62508
                     /locus_tag="DMACINML_00802"
     tRNA            62420..62508
                     /locus_tag="DMACINML_00802"
                     /product="tRNA-Leu"
                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Leu(taa)"
     gene            62530..62603
                     /locus_tag="DMACINML_00803"
     tRNA            62530..62603
                     /locus_tag="DMACINML_00803"
                     /product="tRNA-Cys"
                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Cys(gca)"
     gene            62635..62722
                     /locus_tag="DMACINML_00804"
     tRNA            62635..62722
                     /locus_tag="DMACINML_00804"
                     /product="tRNA-Ser"
                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Ser(tga)"
     gene            62800..63129
                     /locus_tag="DMACINML_00805"
     CDS             62800..63129
                     /locus_tag="DMACINML_00805"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_00805"
                     /translation="MKKFILISSILSSFFVFTQASELPGDEIQPEVKAIKEHFKDKVE
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                     VHKCNKF"
     sig_peptide     62800..62862
                     /locus_tag="DMACINML_00805"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 21"
     gene            63223..64311
                     /gene="trxB_2"
                     /locus_tag="DMACINML_00806"
     CDS             63223..64311
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                     /inference="similar to AA sequence:RefSeq:CKG86610.1"
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                     /product="thioredoxin reductase"
                     /protein_id="Prokka:DMACINML_00806"
                     /translation="MFKIVLLISIIFGLNACKGEDMNNNEDTNKDIKTVYAPNAVGID
                     LNTKTNEFLFNQRKKPTGKYTKEYTKALLEAVNIVDNSPYKKFYEPKYLDPEFHTGQK
                     STLIEFKEWQSIYLKDPVKGSLAPWTKAEKAYYNSLDGEGRYNYLVKRSGLVCTPIDL
                     KDSALIRPKRPKEKRFINAYKEGMKDYKEAKRLDYKGYDLFQKAIKNLSYAYEEGKDY
                     KAGLALAELGYSKDYFRAIIGKLDQDENNEVLLDKLINEFLNANYRSIRIYEELIEKY
                     DLGDAYWGLYVYSRKIEDTVFDDRFYFAQLKDSSEELYKNAFEHGAYGAFGAKANTIY
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     gene            64289..64981
                     /gene="trxB_3"
                     /locus_tag="DMACINML_00807"
     CDS             64289..64981
                     /gene="trxB_3"
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                     /inference="similar to AA sequence:RefSeq:CKG86610.1"
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                     IDKGKYKDPRDVDSTPESRWEFDQEIDAYKEGSVRSYSYDLPNHWSEADVEIYLEELY
                     LHAKLAALTPPQGYPNAPRYYSPERLEFIYEKHKLDAKLDPRIPAIYRANFPEELRAK
                     IRAFAKEHGIEE"
     gene            64983..65963
                     /gene="ribD"
                     /locus_tag="DMACINML_00808"
     CDS             64983..65963
                     /gene="ribD"
                     /locus_tag="DMACINML_00808"
                     /EC_number="3.5.4.-"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL35719.1"
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                     /transl_table=11
                     /product="riboflavin-specific deaminase/reductase"
                     /protein_id="Prokka:DMACINML_00808"
                     /translation="MKNFYMNLALNEAWKYQFLTYPNPAVGCVILDKNEKILAIKAHE
                     KAGCAHAELNAIAHAFTSLNPEISLPQEANAMHEFICKNHRGIFKDSIAFVTLEPCSH
                     QGKTPPCAKLFSELGFKKVFISVKDENEIASKGADFLKKQGVEIEFGVLEDEGKKLLK
                     PFLKWQKGQFKLFKLALSMNGSPFGKIVSNELSRTYAHKIRSVIDLLVLGGETIRKDR
                     PILDARLCKGKAPNLCILSHHNLENFDKSIPLFNVPHRQIYTHIPNKAKFLMYEGGEN
                     FLKNFKDEMDMFLIFQSSSLNDEKNVTMSLNFKPLYRNFLGSDTYGIYEL"
     gene            65944..66465
                     /locus_tag="DMACINML_00809"
     CDS             65944..66465
                     /locus_tag="DMACINML_00809"
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                     /inference="similar to AA sequence:RefSeq:CAL35720.1"
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                     /transl_table=11
                     /product="putative membrane protein"
                     /protein_id="Prokka:DMACINML_00809"
                     /translation="MAFMSFSGFFYARNDLRLFKIEKKNEIKSFFYKDYTLASFKDEL
                     NLNNEIFFYQSLKENLFKENDEILISNLGKKIILFRNFTQNSDNFAEAKLKQVLLLTF
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                     EFLTQRMKKYTKK"
     gene            complement(66524..67888)
                     /gene="tdcG"
                     /locus_tag="DMACINML_00810"
     CDS             complement(66524..67888)
                     /gene="tdcG"
                     /locus_tag="DMACINML_00810"
                     /EC_number="4.3.1.17"
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                     /inference="similar to AA sequence:RefSeq:AJA55834.1"
                     /codon_start=1
                     /transl_table=11
                     /product="L-serine dehydratase TdcG"
                     /protein_id="Prokka:DMACINML_00810"
                     /translation="MSNLNIFKIGVGPSSSHTLGPMLAGNLFCKKIAKKLEKIEKIQI
                     ILYGSLSLTGKGHLSDKAVIWGLNALEAKNLSAAIQEEVNKNATDKGKINLCGEKELR
                     FDYEKDLIFSKDFLPLHENGMQIQAFNASGEIVDQETYYSIGGGFVLTAAELEKRNKG
                     ISQGRKKKLDIELNNAKQALELCEKRDWDLAELSYRYELQFHTKEEIRSYCLEIWEVM
                     QEVYYNGTHPNEDYLPGKLHLKRRAKGLKERVTMTADPMGIIDFISLYAIAIAEENAS
                     GAKVVTAPTNGACAVIPAVMLYLKNHTIGFNDEKAIEFLLVAMLIGSFYKKNASISGA
                     EAGCQAEIGSASSMAAGAMATVLGANAFKACNAAEMAMEHHLGLTCDPVGGLVQIPCI
                     ERNAFGAIKAISAARMAMTRKSIPIVSLDEVIETMYETGKDMNYKYKETSLGGLATNL
                     KTVC"
     gene            complement(67899..69221)
                     /locus_tag="DMACINML_00811"
     CDS             complement(67899..69221)
                     /locus_tag="DMACINML_00811"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:ABS43832.1"
                     /codon_start=1
                     /transl_table=11
                     /product="serine transporter"
                     /protein_id="Prokka:DMACINML_00811"
                     /translation="MNTPKWTRYDTRWVLSLFGTAVGAGILFLPIKAGVGGFWPVIAM
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                     AYCVGITNTFESFIYHQFLPLLNSEGVFADIIRAMYEVSADDKGKVVASLFPFYRLLL
                     AFILVSIFMLIMLFSEELITKVCEWLVYPLCAILFIFSLYLIPQWSFESFSAIPGVKE
                     FITIVWLTLPVLVFSFNHSPAISTFSLSVKRQYKEHAVEKADQILFRTSTMLLFFVMF
                     FVISCVLSLSPAELNEARAQNIPVLSYFANKLDNPFISYGGPLIAFLAISSSFFGHYF
                     GAREGAYGIVRKCCKLAGSENPDLKKIAICSTLVMYIIMLITAYINPSILVFIESLGG
                     PIIAAILFLMPIIAIYTVSKMKKFQNKALDAFVFVTGVLTIITVIYTF"
     gene            complement(69491..69907)
                     /locus_tag="DMACINML_00812"
     CDS             complement(69491..69907)
                     /locus_tag="DMACINML_00812"
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                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL35723.1"
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                     /transl_table=11
                     /product="putative periplasmic protein"
                     /protein_id="Prokka:DMACINML_00812"
                     /translation="MKLKLGLAALLGATVLFARDIIVPASELPRNAQDFISKNFKTAQ
                     IALVKKDIDSYDVTLNDGTEIDFIITGEWKDVDGKYKALPNSILPNIMPKISASSNAQ
                     IIEVSKEINGYKFELSNQLKIYTDAQGNILGQKFDY"
     sig_peptide     complement(69851..69907)
                     /locus_tag="DMACINML_00812"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 19"
     gene            complement(69976..70713)
                     /locus_tag="DMACINML_00813"
     CDS             complement(69976..70713)
                     /locus_tag="DMACINML_00813"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL35724.1"
                     /note="hypothetical protein Cj1627c"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_00813"
                     /translation="MQENHNFISFVLLDEAKFDFLKLKKILEDDFDIWIADENFTQDG
                     VIFSFKNMLITLNLIKNPIPNNEAEYYANFNFMWKDALEQTQKHKAHLLISVLSQSET
                     KLDQAKLFTQISSVCLQDKHALGFYTGGVVLEPKFYIENAKMLEDNRLPVYNWIYVSV
                     YPGDNGNNAYTYGLRNFDKLELEVCDANIEEKELFFTLYDIILHILTYDLTLKDNDTL
                     KFEDGRILSFKKSQGIGVENESLKIIF"
     gene            70880..71305
                     /gene="exbB-2"
                     /locus_tag="DMACINML_00814"
     CDS             70880..71305
                     /gene="exbB-2"
                     /locus_tag="DMACINML_00814"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:EAQ72747.2"
                     /codon_start=1
                     /transl_table=11
                     /product="TonB system transport protein ExbB"
                     /protein_id="Prokka:DMACINML_00814"
                     /translation="MEFLKDYIDLIIFIILGVMAFIAFWCVIERVLFFRKIDFKNYEN
                     QEQFDDAISENLTTIYIIYSNAPYIGLLGTVVGIMITFYEMGIAGNIDVKSIVVGLSL
                     ALKATALGLLVAIPALMAYNALLRKVSLLSNAYKVSKNA"
     gene            71298..71687
                     /gene="exbD"
                     /locus_tag="DMACINML_00815"
     CDS             71298..71687
                     /gene="exbD"
                     /locus_tag="DMACINML_00815"
                     /inference="ab initio prediction:Prodigal:2.6"
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                     /codon_start=1
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                     /product="biopolymer transport exbD protein"
                     /protein_id="Prokka:DMACINML_00815"
                     /translation="MLKLPKNEGLNIVPFIDIMLVLLAIILSISTFIAHGKIEINLPV
                     SENALSLNNDEKKLSISIDENNIFYLDDKTTDLKGLSDAISSLHKKTIVELKSDKNAK
                     FESFVQIIDLLKAKEHENFQIITEKNR"
     gene            71684..72367
                     /gene="tonB2"
                     /locus_tag="DMACINML_00816"
     CDS             71684..72367
                     /gene="tonB2"
                     /locus_tag="DMACINML_00816"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL35727.1"
                     /codon_start=1
                     /transl_table=11
                     /product="putative TonB transport protein"
                     /protein_id="Prokka:DMACINML_00816"
                     /translation="MKNALSNHKSQAFYISFLFFLPLAFLLFNSANFFKIEFKSEDSF
                     TLAMKQFTQNQPTQTPPIPTNSEPIQHHKPKPIKQPIKKTKKAAENQVKPIQAINPIQ
                     KSTPFIAQTHTTHNQALKNSDAKPTQLTYGKDNHPALEKIQKAIMEQARKNYPRQARK
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                     LPIVYNLKA"
     gene            complement(72413..73297)
                     /locus_tag="DMACINML_00817"
     CDS             complement(72413..73297)
                     /locus_tag="DMACINML_00817"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:SQE25111.1"
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                     /transl_table=11
                     /product="hypothetical protein"
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                     /translation="MDKLTINDFNVSLPSSQNITNRKEILELKKEEQEKVKVNDISDN
                     QISGFKVVFENKQGELMALKISDENYKNLQSHFGSFTNYIARDDGTIRLNGEANEFIA
                     NWFEKISSEFFNPNSLNNKEESNHINVKFHKNTLFESMQNLAFKGEDELSLSANLQTR
                     LNFAIEKDVNFDGNINEFDVKKESLTDILRDIKNASGGSADATKITDPQKSDENDEVK
                     IKKKKDEKDVKDLLEIAKEKGLSALSADEQAKLKASNPQIFEELQNKSLGNLEQNLKK
                     DLMVQIGNNEAIFVDKRV"
     gene            complement(73337..73537)
                     /locus_tag="DMACINML_00818"
     CDS             complement(73337..73537)
                     /locus_tag="DMACINML_00818"
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                     /inference="similar to AA sequence:RefSeq:CKH06754.1"
                     /codon_start=1
                     /transl_table=11
                     /product="periplasmic protein"
                     /protein_id="Prokka:DMACINML_00818"
                     /translation="MRKLLFIALVACFVNSFAYGKTENNNKNSQVRNSCVDYEIRLKQ
                     CNSLPTQHKRQACRLGLFAACK"
     sig_peptide     complement(73481..73537)
                     /locus_tag="DMACINML_00818"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 19"
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gene            73670..74653
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CDS             73670..74653
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                /inference="similar to AA sequence:RefSeq:ABS44159.1"
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                /protein_id="Prokka:DMACINML_00819"
                /translation="MKALALFSGGLDSMLAMKLITSQGIEVKALNINIGFGSTSDKSE
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                DREKLEGISGRSRKRQLELAAKFGLEDFESPGGGCLLTLDSFAKKIRDFIEFDKDMQV
                NDAQLLKYGRHLRLPNGAKMIIGRNELENELLRNLKTPKYEVIELGDLIGAYSLLSAN
                ADEKDLELALKIALTYTKHEANKSYELRFKNQNYKSIAFEDKKEINPFFIS"
gene            complement(74656..76308)
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                /locus_tag="DMACINML_00820"
CDS             complement(74656..76308)
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                /inference="similar to AA sequence:UniProtKB:P35077"
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                /transl_table=11
                /product="Filamentous hemagglutinin transporter protein
                FhaC"
                /protein_id="Prokka:DMACINML_00820"
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                NMIKELTNFIVSKGYSTSSVTIDGINQERDILFLDLKYGFVGEVYLNGDNNTTRLDFG
                MPLKKGDKFNIYDLDTGIENLNNGARDVKIAVKASENYGYSDIFINLQSKPPDLILDF
                DNSGYKAKGEYKASAYLSLSNIFNLNDSIRFGFIKGLLKDMSQERENVYYVANYTLPIQ
                SYQLSYSMQYSDNINMIEGYDNSFIKNTDTSLRHKIMLKKILHRTSKDKFSIYANLGI
                KDDVNEIDNFRLESSSGRYSSIASGVEYSTLAFGGFLFLNLEYEKGIPFLGSKKDSKD
                SLYKIEFNKVNFNLSYQKSFYANDGLAFLYQNSSGASYSNESLLYADKFLIGDEYTVR
                GFKESSAALDYGAYSNNTIYLQFLNAPKYLRALEPFVGLDMGYGRDYLLPNKDFLAGV
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sig_peptide     complement(76249..76308)
                /gene="fhaC"
                /locus_tag="DMACINML_00820"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 20"
gene            complement(76309..81933)
                /gene="fhaB"
                /locus_tag="DMACINML_00821"
CDS             complement(76309..81933)
                /gene="fhaB"
                /locus_tag="DMACINML_00821"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:UniProtKB:P12255"
                /codon_start=1
                /transl_table=11
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                /product="Filamentous hemagglutinin"
                /protein_id="Prokka:DMACINML_00821"
                /translation="MEFNKKKIVRLSLNLTLLGALFPCVLFSADLRQRNGNVIVSRTA
                DLTQSSNKTDVINIKNPNQNGVSHNQFDEFSVQDGVIFNNSLKDGNSQIGGWVGKNPN
                LKQNANTIINEISSKQASSINGAVEVFGKSANLIFANENGFSVNGAAFLNTKGVTLST
                GKFNGDFTEVTSNGRVAIGEKGVMVDGDYFNVISRGIDLAGSIAHYQSGKNLSDINFI
                AGLNKVDLSTPNAPKIVASKQKDEKIDYGIDGKYLGSMYANTVTLISTEEGVGVRHSG
                VIRGIEDVIVKVKDKAEFQAIGVNSNGSVKIDAKDIKTSLINADNIDLKASGKVTNEG
                LYKGKQIQINANNFENAKQVNFSQETKDIFDINEENSKIYADNLALNTLDKTSNFGFI
                NALNDIKVDTNSFDNQGEISANKDISLTLNDDAFVNNGKILSQKDIQIQANKDLTLNH
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gene            96300..96902
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                     VNLSNIDLNAIFSGVSIGIFLGLFIGKQLGVFLFSYFAIKFKLASLPQNANLKQLYGV
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CDS             complement(102207..102389)
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gene            102562..104634
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CDS             102562..104634
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                LFYVGFWLLSNAQNKKWVSFIKQGAIDAISNNSAKTLWFTVFLAVYREGAETVLFYQA
                LFFDAKTSTDLSAIFGGLGLGILVLIVLYFLLKAGAIRIPIKQFFYICSYIIFYMIFV
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sig_peptide     102562..102627
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gene            104631..105170
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CDS             104631..105170
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                /translation="MIKKFLSVVAAAAAISTNLFAGEVPIGDPKELNGMEIAAVYLQP
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                     ACAICGDMGYIKKEGELICISCNVRIFLPSVGKTGGCNPIPLKYDYDGEKITIDVKDV
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     gene            106645..107940
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                     /transl_table=11
                     /product="putative ABC transport system permease"
                     /protein_id="Prokka:DMACINML_00848"
                     /translation="MLVKMITHSIFRNKIQKFLAFLTCFLATLLLCTMLNITLSIGDE
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                     DDSNEIMLGEDFAKNNDLKINDTIKLIGENKISKEVKVVGILLHANPKMSNKIIAPLN
                     LAQELLEKKGLYASAEVRAFTIPESALSEKVRRMGEEKLDQIEYDKWYCSAYVGSIAS
                     QISDGLPGADAKALNAISDAQSLVVKKIQSLMAITCIICLIVASIAISSLMSSEIHRR
                     KKEIGLLKVLGANTFQIYLLFAGENLIIALVSAVFGFIFGIGLSELISLGIFGYFIDI
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     gene            107930..109048
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                     /product="putative integral membrane protein"
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                     ENGKTTKLTIKGILLSNDELDSIVLAPLSVVQNLSDTFGIQYANAVVYGNFDEINTKT
                     KNISNESINAKPISSVSLSEGLVLDKIKALMFLIILVVLIIVTTSVNTTLSSIIFSRK
                     KEIALRLALGAKKSEIFKLFACEYFIISLFASIIGAFCGIFLANIFGYLIFNASIDFR
                     FKAVFMALIISLFFAFLAAFFPIKKALKINVCENLKGE"
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                     /protein_id="Prokka:DMACINML_00850"
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                     VMLSQYYHSSVDEEDAKAVLEKVGLSHRLSHLPSQLSGGEQQRVCIARALINNPEILL
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     CDS             109692..110180
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                     LL"
     sig_peptide     109692..109748
                     /locus_tag="DMACINML_00851"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 19"
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     CDS             110141..110644
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                     /product="putative lipoprotein thioredoxin"
                     /protein_id="Prokka:DMACINML_00852"
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CDS             complement(110746..111792)
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                VGLVGFPNVGKSTLISVVSNAKPEIANYEFTTLTPKLGLVDVDEYNSFVMADIPGIIE
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gene            complement(112159..112467)
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                /locus_tag="DMACINML_00855"
CDS             complement(112159..112467)
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                /translation="MYAIIKHSGKQYKVSVGDELKLDHFEAESKANIEVSEVLAINDK
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gene            complement(112625..113611)
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CDS             complement(112625..113611)
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                /codon_start=1
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                     YILEFEILDITQAKQSKISYQNNTKASINIAYKLIFYPTRELVFSKTFNTTFTLSGDS
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     CDS             complement(113611..114234)
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                     /transl_table=11
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                     REDFEKTAEIMIDSMLNDPAFANIQPGQRKVIAIGKIINDTPQRIDTDKLISKITIAL
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                     DNVKLKNGDIQAEYFFYLSVTDLNSGLAYWEDERTIDKTGSSKSVTW"
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                     /locus_tag="DMACINML_00860"
     CDS             complement(117409..118815)
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                     RKLILEINLGGTAIGTGINSHPNYPKVVERKIREVTGFEYTVAEDLIEATQDTGAYVQ
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CDS             119874..120566
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gene            complement(120563..120763)
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gene            complement(121598..121702)
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CDS             complement(121598..121702)
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                GSKGCSKTIFTLGFGSVLTVFALFLSIGLGSSAFYPSLSDLQSSLTIHNASSSYYTLS
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gene            complement(122840..124402)
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                /locus_tag="DMACINML_00867"
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CDS             complement(124402..124632)
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                /protein_id="Prokka:DMACINML_00868"
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                AAECFWATLKEMAIPCLTIGLVVAFAFISKNSGMSTTLGLAFAHTGDAFAFFSPIIGW
                IGVFLTGSDTSANLLFGTLQQVSAQKLGVSEALFLAANSVGGVVGKMISPQSIAIACA
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gene            126939..127676
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CDS             126939..127676
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                ELVELQYEEECCGFGGTFSVKEPEISNAMVRNKIKDIQNTGVKYLISGDGGCLLNIDG
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gene            127673..129112
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CDS             127673..129112
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gene            130651..131262
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CDS             130651..131262
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gene            complement(131491..132522)
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CDS             complement(131491..132522)
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     gene            complement(132636..133532)
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gene            137239..138105
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gene            139154..140233
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CDS             139154..140233
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DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
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                     GFPLMIRASYTLGGAGSGVVYNMDEFKELANAALALSPIHEILIEESLLGWKEYEMEV
                     IRDKNDNCIIVCSIENLDPMGVHTGDSITVAPALTLTDKEYQVMRNASFAILREIGVD
                     TGGSNVQFAVNPTNGRMIVIEMNPRVSRSSALASKATGYPIAKVATLLAIGFSLDEIK
                     NDITGTPASFEPVIDYIVTKIPRFTFEKFPGANTTLGTAMKSVGEVMAIGRTFKESIQ
                     KALCSLERNLSGFDRVKFEDKNDLIFKIRNANEKRLLYVAQAFREGFDVKELYELCKI
                     DPWFLSQIKEIVDFEEQIDMDILHNKTLLRKAKTMGFSDKMIALLVNLKDNLELSQND
                     IYYARMKQKIIAEFSEVDTCAGEFEALTPYLYSSINVSELTQSKNEARDKKEKKVMII
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                     EHLRGVIEREKPDGVIVHFGGQTPLKFAKRLSAFGAKIIGTSARVIDMAEDRKKFAEF
                     ITKLGINQPKNSTATSVEEAVLKASEIGYPVLVRPSYVLGGRAMRVVNDESELRLYMQ
                     EAVDVSDKSPVLIDQYLDNATEIDVDAISDGKDVYVAGIMEHIEEAGIHSGDSACSLP
                     PCNIDEKMQEQIIQKTANIALNLGVVGLLNIQFAIYNNELYMIEVNPRASRTVPFVSK
                     ATGIPLAKVATRVMWQGNLKEALKFYDTFDVVNFDNTILRPKLSKHISVKEAVFPFAK
                     LSGSDLELGPEMRSTGEVMGISKDFANSYAKSQISSFNHLPENGVVFISLKEKDKKYA
                     KKLASEYSKLGFKLMATSGTCKEIVENGFECELVHKISEGRPNVEDKLKNGEIQLVIN
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     CDS             22917..23339
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                     /translation="MKKFSLWCDFIENSFLDDDFLNLLSRGINGATSNPAIFKNAILN
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                     FEALNAGLVEFRKNNIALQGKNTRLRTPQAVISIFVSRFDRLLNSKAKEQNRIGILNA
                     NLAYNNIISKNEPNIRALFASTGVKGDDLPKDYYIKELLFENSINTAPLDAINAFKTE
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     gene            complement(24324..24947)
                     /gene="serB"
                     /locus_tag="DMACINML_00927"
     CDS             complement(24324..24947)
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                     /locus_tag="DMACINML_00927"
                     /EC_number="3.1.3.3"
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                     DFFESLQERVSFLKGMPYDLVLKIGQDLPLMNGAYELIEFLNSKNIFVVIFSGGFHEG
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     gene            complement(24947..25468)
                     /locus_tag="DMACINML_00928"
     CDS             complement(24947..25468)
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                     /codon_start=1
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                     /product="chemotaxis protein"
                     /protein_id="Prokka:DMACINML_00928"
                     /translation="MSNEKLEQILQKQQTQIAGPVGDQKEDDIIQLVGFVVGDEEYAI
                     PILNIQEIIKPIEYTRVPSVPDYVLGVFNMRGNVMPLIDLAQRFNLGSSKMTPQTRYI
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                     TILKVEALLKREF"
     gene            complement(25473..27770)
                     /gene="cheA"
                     /locus_tag="DMACINML_00929"
     CDS             complement(25473..27770)
                     /gene="cheA"
                     /locus_tag="DMACINML_00929"
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                     VNQLSDSEVEAEIERLLKARKAEDQARRAQKKQNAASPTNSKPAASTPKAENTEKKVP
                     ASGGGGGGMDQTIRVEVKRLDHLMNLIGELVLGKNRLLKIYDDVEERYEGEKFLEELN
                     QVVSQLSIITTDVQLAVMKTRMQPIAKVFNKFPRVVRDLSRELGKHIELEITGEETEL
                     DKSIVEEIGDPIMHMIRNSCDHGIEDPATRAANGKPEKGIVQLKAYNEGNHIVVEITD
                     DGKGLDANGLKAKAIEKNLITEREADQMTDKEAFALIFKPGFSTATKVTNVSGRGVGM
                     DVVKTNIEKLNGVIEIDSELGKGSSFKLKIPLTLAIIQSLLVGTQEEYYAIPLASVLE
                     TVRVPIDDIYTIEGKNVLRLRDEVLSLVRLSDVFGVKQVLESGDQTYVVVIGVAESKL
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                     IKAQLESSAKKPKEKPSDYKVLIVDDSKMDRTLMQKALEPLGVSLIEATNGVEALNII
                     KSGDHDIDAILIDIEMPRMDGYTLAGEIRKYSKYRNLPLIAVTSRTSKTDRLRGVEVG
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                     /gene="cheV"
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                     /locus_tag="DMACINML_00930"
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                     IKIPSLTELPGVPDYIEGIFDLRGVVIPVVNLAKWMQITEPESTMLKPRVIITEFSNI
                     LIGFIVHEAKRIRRINWKDIEPATFSTGSGALDKGKITGVTRIENDEVLLILDLESVV
                     EDLGIYSPKTDIDFSKIEKFSGSALILDDSMTARKRVKEMMQQMGFQVIEVKDGVEGL
                     NKLEELSQIYGENLSSILKIIVSDVEMPQMDGFHFAARIKEDARFKDIPIVFNSSLSN
                     EFMNEKGVHEAGGESYLVKFNASDFFNEIAKVIKKHQSQEQG"
     gene            complement(28723..29358)
                     /locus_tag="DMACINML_00931"
     CDS             complement(28723..29358)
                     /locus_tag="DMACINML_00931"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:AAW34924.1"
                     /note="conserved hypothetical protein"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
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                     NLARFFQRVKIFSLQEQPLKLNLHTSKGKNTDFKNSFITLAHGDIFLSPCLQFTLKSL
                     RNHYLLVFLNFLNQISSNSISNKILKNQNKKNLFYKIENFKNLAKERYKKYGNLGFWV
                     CEGHYHQNLILDEKDIKYFNLASFAYERSFFVVECYQEIKFREQKLRGQNV"
     gene            complement(29491..29976)
                     /gene="greA"
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                F"
gene            complement(29993..31084)
                /locus_tag="DMACINML_00933"
CDS             complement(29993..31084)
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                /EC_number="2.4.1.182"
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                GHPLLDEIKDFKNENDIKILLNKNESEKTIAFLPGSRRSEIKRLMPVFRELSRKFEGE
                KILCVPPFNLERLEIYGDIKDFKIQSNTPQVLKKADFAFICSGTATLEAALVGTPFVL
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gene            31230..32105
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CDS             31230..32105
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                EGFATFISSLDNLSFGVAIAVAVAIHNIPEGMAVSLPIYHATKDKKKAFIYSALSGIA
                EPMGAIVGAFLILPIMNELTLAITFAVVAGIMVFISFDELLPAAKTYDKAHDSLYGLV
                LGMAVMAVSLILLNP"
gene            complement(32229..32801)
                /gene="cdtC"
                /locus_tag="DMACINML_00935"
CDS             complement(32229..32801)
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                     /protein_id="Prokka:DMACINML_00935"
                     /translation="MKKIFILFFALLSFLKAGPSLDELEDFTPMFAIRSLETGISLSP
                     FRKTSKRLEDQNWFLKEIVPSEELKAKDMHAKDLPFGYVQFVSPKGDDICLAVLSEKS
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     sig_peptide     complement(32733..32801)
                     /gene="cdtC"
                     /locus_tag="DMACINML_00935"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 23"
     gene            complement(32811..33614)
                     /gene="cdtB"
                     /locus_tag="DMACINML_00936"
     CDS             complement(32811..33614)
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                     /locus_tag="DMACINML_00936"
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                     /inference="similar to AA sequence:RefSeq:CAL34251.1"
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                     /translation="MKKIVFLILSFNVLFAALENYNTGTWNLQGSSAATESKWNVSIR
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                     YYSRVDVGANRVNLAIVSRVQADEVFVLPPPTVASRPIIGIRIGNDAFFNIHALASGG
                     NDAGAIVAAVDMFFRNRPEINWMILGDFNRESGALVTLLDPDLRARTRVVVPPSSTQT
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                     /gene="cdtB"
                     /locus_tag="DMACINML_00936"
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     gene            complement(33639..34415)
                     /gene="cdtA"
                     /locus_tag="DMACINML_00937"
     CDS             complement(33639..34415)
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                     /locus_tag="DMACINML_00937"
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                     NNTVMIKNAKTFTCLNAYRNGIVHYPCDQTNFAQFWRLYPMTNGAYQIQNFATQQCIQ
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     sig_peptide     complement(34350..34415)
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                     /locus_tag="DMACINML_00937"
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                     /gene="surE"
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     CDS             34938..35714
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                     /locus_tag="DMACINML_00938"
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                     EDITYSGTCAGAMEAVLQGIPAIALSQFYKKSEKELDFKNALKVTKKIVQNIFDKGFP
                     LGKKEFLNINFPAKSNIKGIKICKAGKRVYNFEAHSNINPRGMEYYWLAAANLDFEDE
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     CDS             35707..36363
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                     /product="putative acetyltransferase"
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     CDS             complement(36917..37297)
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                     /locus_tag="DMACINML_00941"
                     /EC_number="4.1.1.11"
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                     /transl_table=11
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                     /protein_id="Prokka:DMACINML_00941"
                     /translation="MNITLLKSKIHRASVTEARLDYVGSISIDEKLLQASGILEYEKV
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     gene            complement(37294..38142)
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                     /locus_tag="DMACINML_00942"
     CDS             complement(37294..38142)
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                     /protein_id="Prokka:DMACINML_00942"
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     CDS             complement(39332..39709)
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     gene            39799..40050
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     CDS             39799..40050
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                     LDFKMRSFLQDELVKILQHFKITTLLVSHDLAEIYKLSHRILELSDGKIIKDARTNEF
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                     PFMVNPLQSAFSSINQNLLDASYTLGKGKIYTLFRVILPNSKVGIFSACAMSFAHTIG
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                     QKHYDHYENIIILSEALFSMDGDFSDFNTLIAFKEKYPKIKLYIDEAHSVGCFDEEGL
                     GLVKALNLEEKVDFIVFTFGKALASMGACMICKNLYKSFFINKARAFIYSTALPPINI
                     AWTKFIFEKMSELKEKREKLQIIGNFFKNQLIEKNHQILGDAYIISLVLGENQKAIEL
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                     /gene="pth"
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                     STAQNIKIFNIKDLNLSSFIEAKSGVFEKKNWTLKEGNLTLLPKEYELGDKGLNISEF
                     KELDTLEGFKPKIIEGVASNSDYSILDILESLELFKTQNISIEALKINLYKLVFMPFF
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                     LKIFGEIYMDIHHSFVGINENLKEIKRIYSHPQGYNQCRKFLESHELSNIEFVPSKST
                     ANAAYLASQDKYSAAICSKIAAKLYNVPVLFDKIEDNAANRTRFLILSDIKNPKMPNC
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CDS             complement(62328..63821)
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                MLKYSIHSQNQSLFNTPPTFAIYMFNLEMKWLLDQGGLDAIDAKNSQKAAMLYECIDS
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gene            complement(67801..68778)
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CDS             complement(67801..68778)
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gene            complement(68771..69757)
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CDS             complement(68771..69757)
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                /product="putative fatty acid/phospholipid synthesis
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                /protein_id="Prokka:DMACINML_00977"
                /translation="MISIAIDAMGGDFGEKPIIEGVIEALKEKPFNAILVGDPHILEP
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                     VCDGFDGNVILKACEGVATAIIQILKNEIKQSLVSKIGALLMKPSFKRLKKHIDWQEY
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                     /protein_id="Prokka:DMACINML_00980"
                     /translation="MEKTLSIIKPDAVKKGVIGKILDRFESNGLRIAAMKKVQLSKEQ
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                     ADFAESIDANAVHGSDSLENAKIEIEFFFKSNEIC"
     gene            complement(70808..71092)
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                     FTNEHGEVCPAGWNKGDAGMKADPKGVAEYLDKNEDKL"
     gene            72067..73155
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                     VLLKFMQELPLVERYNIIGQLIWLRDRAIILAAIVIIAFLVIAVLDIFLVRFQYFKGL
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                     YDTTKEQAPRVVAKGVDFLALRIKQVAYDNNVVVYENPPLARELYKACDINDLIPREM
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     gene            complement(73170..73901)
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                     /locus_tag="DMACINML_00984"
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     gene            complement(74696..77335)
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     gene            complement(77399..77842)
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     gene            complement(77835..78425)
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     CDS             complement(78406..79110)
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                     QNLVAITGVSGSGKSSLILQTLLPFAQEELNRAKKVKKLGGVQIEGLEKLDKVIYLDQ
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     gene            complement(82586..83371)
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     CDS             complement(82586..83371)
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                     GDNFKSINVSTASAFILAALGVKVAKHGNRAISSSSGSTDVLDALDIKIPDNLECALN
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     gene            86568..87167
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                     INEALSLKPKIIDLNSKIEKENHLKDVEKIKYILKEMKK"
     gene            87164..88342
                     /gene="trpB"
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                ENFVKKAKALGISALIVPELSYEESKPLYKECQKYDIALITLVSITTPKERVEELVKN
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                DGVIVGTNIVKLFASNDVNQILKGVEEIFEK"
gene            89154..89576
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CDS             89154..89576
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CDS             89576..89884
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                     SINDKFGVRIRAVQQGKESINPEQNNLSTNEEPILNSKKTSLEGYDYTNYILVMLVLF
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     gene            complement(90672..92132)
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     CDS             complement(90672..92132)
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                     /protein_id="Prokka:DMACINML_01001"
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                     IGTVRLKELFYDKGKTDALDDFINPILEQIPSEFCNQNLIAIGGSLRAISNSIMQKNS
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                     KTKQIITSGVGIREGIYLQDLLRPKHTFPINFNPSLKSLQDRFLQGNINNKTPYFSMQ
                     IFKVLQTLHKIHEKYKQSLLNAAKLCHLGEYLNFYFANEHSAYFILNGLNYGFSHQEK
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                     NTLYIYSESKILDLPKDELKKITKPATIALAINQKP"
     gene            complement(92132..92377)
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     gene            complement(93241..93558)
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                     /protein_id="Prokka:DMACINML_01005"
                     /translation="MENLIIYAIAYLLGSIPFGLILAKQFAKINIQNQGSKSIGATNV
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                     IYLLFEGGKGVATGAGAMIVLLPLELLTAFIVWFIVGKIFKISSLASLLALLVFIGSS
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     gene            94333..95358
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     gene            97237..97689
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     gene            complement(97721..99031)
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     CDS             complement(97721..99031)
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                     /protein_id="Prokka:DMACINML_01012"
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                     GEYEIAQSRANLESTALQYNEAKLNKENYLKALKILTSNDLNDILYQDQAYQVFKLKD
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     CDS             complement(100908..104030)
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                     YKSQGRLNGNDAVPIMINLQSGANALNTAKLVEAKMQELSKSFPEGLEYKIPYDTTKF
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                     LNIVRNTQDGKWDLSNIYADLNLNGEVVKGKLYFIDSVIDADSGTVKAKAVFDNNDST
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                     TLEEDTQGFEEYYQGWKILFSSVAGSKEEEITTKLLAHIANEAGFQTDFSFVDEVEFS
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     gene            complement(115526..116305)
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     CDS             complement(115526..116305)
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                     IKEHTSSNFLTLTPGIRPFGETSDDQKRVANLTMARENLSDYIVVGRPIYKNEDPRAV
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                     FILAPFVMPSLTAWLIIAIMGALGTIYQIHVTKAYGIAKQAGVVAGISYLDVVFSMIV
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gene            122693..123928
                /gene="serS"
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CDS             122693..123928
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                VLKNEGALLSRALVNYMIDFNRSRGFEFVNVPFLVNSATMFGTGQLPKFKDDMYKIDD
                EDLYLISTSEIPVTNLYSGEILTSESLPIKMTCYSACFRKEAGSAGRDTRGIIRQHQF
                EKVELVSITKPEQSDSVFNEMVECASDLLSSLGLAHRHLMLCTGDLGFSAAKTIDLEV
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gene            123938..126400
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CDS             123938..126400
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                VCALKLNDREKFKYYIDLAQVYLPKEGKSKLYDYYLALINYYKGYYPEALQMLQRVNS
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                FKANMQKNMLFLANGDYVSMLPYLDENGQKTPLNLIFEAIIAKNNNLNNQVDVKIAKL
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                LMHIAGLLNLERQKFKTLINTSKVKDEGMVQTLAYLDIFAQQYEESYALYNILIDEYG
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gene            complement(126429..127043)
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CDS             complement(126429..127043)
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                GYNGKNPLAMNTDELNQLISEEGFFGIDNTANRIADFVIKGAGNDVEKLKKGLEGIKQ
                GFEQAEKIWGGELPQISQDTIEATIKKVSDRIDELGGKTLDLKA"
gene            complement(127136..128578)
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                /locus_tag="DMACINML_01039"
CDS             complement(127136..128578)
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                TPNHYKLSINQSEILNMLKLDEYIYLYDGSIKAKVTAKDNEKIETLIENDGFLNSNKG
                INFPNTKINIDVITQKDKKDLLWGIENGVDFLAISFVQNAHDIDEVREILAQNNAKIS
                IFAKIEKFDAVENIDEIIASSDGIMVARGDLGIEVPYYKVPNIQKAIIHKANNASKPV
                ITATQMLFSLAKSKTATRAEISDVANAVLDGTDAVMLSEESAVGIDPANAVDIMCQTI
                IETEKRYPYNKFNEFVNLDNTDKIMRSSAHLATDLNADAIFSLTSSGKSAIKIARYRP
                NMEIIAVAHSEKTLNSLSIVWGVNPAILVNKSEDLTDLLRDSVKSSVEKGFMDKDKCY
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gene            complement(128630..129976)
                /gene="mqo"
                /locus_tag="DMACINML_01040"
CDS             complement(128630..129976)
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                EAGEVFTTVDFGKMSASLIEQGQKQGKNTFVAFNQEIVHIEKKDDIFILKTNTYQEYR
                SKAVVVNAGAHSLYLAHKMNLGMDKSCWPVAGSFYLTKQKLLNGKVYMVQNPKLPFAA
                LHGDPDLLADMNTRFGPTALVIPKLERYHGLKSVPEFFEALKLDKTVLKVTFSMFKDP
                TIRNYILYNYLFELPFIDKGLFVKDAKKIVPSLKTSDIYYAKGFGGVRPQVIDKTKGE
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gene            complement(130102..130731)
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CDS             complement(130102..130731)
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                /translation="MLFCDIGNSNASFLDDNKFFTLSIEQFLEFKSEQKIFYINVNEH
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                IHLGGFILPGIANYRKIYAHISPRLKHEFNTQISLDAFPQKTSDALSYGVFKSIYLLI
                KDAAQNKKLYFTGGDGQFLANYFDYAIYDKLLIFRGMKKIIQENPNLLF"
gene            complement(130718..131005)
                /locus_tag="DMACINML_01042"
CDS             complement(130718..131005)
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                     /translation="MNILNEAMKVLKLDLKPFDLTNLTKKKTYLCALNDENLLLIYTG
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     gene            complement(131002..132000)
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     CDS             complement(131002..132000)
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                     EVYSYKFDAAVLGIALHGDDLALILANNSIVLANRSLGIKFNQNLTPAPAQDSRVANP
                     IFLDNIIIYPTLDGKIIIVSKNTFEVVKDVVISAESFFNNVIHLGISDDKMIAATAKK
                     VIVVSPARTLYLDADIKDIAFDNNAIFILEKNGNIIKTDYNLRKITEKKFDFAIFTKV
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     gene            complement(131997..132575)
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     CDS             complement(131997..132575)
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                     LIVWFAISFISGKIDQYNVEESNKIYTNLLKNPNDKVLLEQLKNKNTNLYAIFLMKEL
                     AKDINNTEIKSQLQTLSTHSDTNHLLKNIASLSLGEKSIFLKNYDKILQAYRLLGEGK
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     gene            132708..132995
                     /gene="gatC"
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     CDS             132708..132995
                     /gene="gatC"
                     /locus_tag="DMACINML_01045"
                     /EC_number="6.3.5.-"
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                     /transl_table=11
                     /product="Glu-tRNAGln amidotransferase subunit C"
                     /protein_id="Prokka:DMACINML_01045"
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CDS             133075..133635
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gene            133639..134109
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CDS             133639..134109
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                /protein_id="Prokka:DMACINML_01047"
                /translation="MLIENVEYDVLLERFKKILRQGGLKYTKQREILLKTLYHSDTHY
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CDS             134109..135617
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                /protein_id="Prokka:DMACINML_01048"
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                SLGVERFLRIAPELYLKRLVVGGFEAVFEINRCFRNEGMDLTHNPEFTTIEFYWAYHN
                YKDLMDLTEELFALLLEKLQLGKIIEFDGQKIDFSKPFERITYKDALKKYGALSDEII
                ENKDKILEKLKKDGFEANDKLDLGHLQAELFDNYVESKLIDPTFITDFPISISPLSRR
                SDKNSEIAERFELFVCGRELANGFNELNDPLDQYERFLKQIEAKNAGDEEACEMDEDF
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gene            135614..136858
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CDS             135614..136858
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                KPKLIVCGASAYARIIDFSKFREIADEVGAYLFADIAHIAGLVVAGEHPSPFPHAHVV
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gene            136855..137400
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CDS             136855..137400
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gene            137413..138258
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CDS             137413..138258
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                VKQTVTKKEPAKQAPKQETKQESKTNANDLFKNVDAKPVHPNGLASGIYVQIFSVSNL
                DQKSRELAAVKQKGYEYKLYKTTVGGKEITKVLIGPFEKANVATELAKIRKEVAKDAF
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gene            138255..139046
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CDS             138255..139046
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                DALGDFDFDLVINSTSAGLKDDDLPCDKILLDKILSRAKFAFDVIYGKETSFLKLSKE
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gene            complement(139122..140027)
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CDS             complement(139122..140027)
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                TSHTKLDSLVDLNYPIKTKDGINMFKTTISTVPTQLNKGLEKPAFEIDKSFLHFYKNT
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sig_peptide     complement(139968..140027)
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                /inference="ab initio prediction:SignalP:4.1"
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gene            140118..140933
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CDS             140118..140933
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                FVGIRGMSYHGAIIGFLIATFLFCKKYKENPWKFLDLVALSVPLAYVFGRIGNFLNQE
                LFGRITNVPWGIYVEGVLRHPSQLYEAFLEGVVVFIVIYLVKMKQKFQGELILVYACV
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gene            141001..141786
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CDS             141001..141786
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                /product="Fumarate reductase, cytochrome b subunit"
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gene            141770..143761
                /gene="frdA"
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CDS             141770..143761
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                /EC_number="1.3.99.1"
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                GILRDVDGYRFMPDYEPEKKELASRDVVSRRMMEHIRKGKGVKSPYGDHLWLDISILG
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                     /locus_tag="DMACINML_01071"
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LOCUS       DMACINML_6            142271 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
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ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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CDS             complement(4326..5096)
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                PKNLKFVELKDAQLTRSLDDVDYSLINSNFAILSGLNPIKDGLYTENKYSEYGNIIAV
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CDS             complement(5109..6101)
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                     KNGIYQKLSNYWDNNTSTNFYLGKIPTDYIQNDLNKIYKEK"
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                     VVVAVMAMFGATLTLPGMAGLVLTVGMAVDANVIINERIRELLREGANIKASIEQGYK
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                LPITLPEDIQITGEGNPLEKHPTWKNCTCPKCGQEAQKESDTLDTFFESSWYFARFAS
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gene            108395..108907
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CDS             108395..108907
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                     IAKYDDFDTVVRKLLNKLEERSLEVFAELLTSCLNPSLVEDLKIHGFAQNLLQRPFLL
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                EFHPGIDLRAAVGTPIYAPANGVVEFSGYSDNGYGYNVILLHNFGFKTVFAHMVRKDV
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gene            112387..112674
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gene            115610..116374
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                     DELREQPFKFILFCDDFSFEKNDDSYKFLKPLLEGSIEAPPRNIIIYASSNRRHLLSE
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     CDS             complement(119537..120205)
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ACCESSION
VERSION
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gene            complement(43666..44184)
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CDS             complement(44177..44605)
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                     dehydrogenase"
                     /protein_id="Prokka:DMACINML_01267"
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gene            complement(54632..55363)
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                     subunit"
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     gene            complement(60708..60899)
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CDS             complement(60708..60899)
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gene            63180..64721
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CDS             63180..64721
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gene            64945..65391
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CDS             64945..65391
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gene            65435..66625
                /gene="moeA2"
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CDS             65435..66625
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                GFFHISVFIKPIIGVLSSGSEIKDLGEALENPAQIRSSNHIAIASLAKNLNCDTRVFP
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                IKIAKANEKFIIALPGFPYSAMVMFNLYAREILNSWLLQPKDYICKAFLQGSYKKKTP
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gene            complement(66642..67904)
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CDS             complement(66642..67904)
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                /product="2-amino-4-hydroxy-6-
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                /protein_id="Prokka:DMACINML_01283"
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                GIGLVFLLASLIFWIFAWIKFEELDKQEFSHSQEMAVKTQKKVFDFDLKWIKITMALF
                LVLSFVIFGLKFTQRIIFQSIRRGFFYFEDYDKLIYNLVDIRYVLVHIATFLALLSVF
                LFCKKLKTYKMFIYFLIWQVLVIFGWNLRFILKLIMGEDVFIENFILDKIISIVCIII
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gene            68213..69667
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CDS             68213..69667
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                /protein_id="Prokka:DMACINML_01284"
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                IPFYFAWVDKRDKEKGILNDEVEIPPIIDPKCPTFYILFPWLPVVFLFIAYFFTIKLD
                VVTANFLSISLVFLVEFARHKNARKLGEDMMVILKAMAEIFISVVSIIIAAGVFAEGI
                KALGGINILANAVSDLGTGNFAWFGILLSITVLSFLVYFATVIMGSGIAAFNAFGKLA
                PDIATKLGVAPITFVLPIEIASCLGRAASPIAGGIIALAGFVKVDPMDIIKRTTPLLL
                IAMIINIAVAFYLAQSNPLPKENNIKTQTLLKTN"
gene            complement(69701..70681)
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CDS             complement(69701..70681)
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                ISSKKFTTPFPFFRAKKHMSEIVLKLVRAINAKHFDKNFAKINFSKVKNLLPYDTKLS
                DDFFNKIDIEYEKIIGINAFSNYSEYVGCNFFIKDWIGLARQLSLKYPKYLFVLLNYD
                KNSIQYNIDQSSNLKVFVNNASIASLVSISKKLDFLVTIDTGNLHLCDILQIPTLAFT
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gene            complement(70729..71949)
                /locus_tag="DMACINML_01286"
CDS             complement(70729..71949)
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                /transl_table=11
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                /protein_id="Prokka:DMACINML_01286"
                /translation="MQSLNEILVQKKIKEIRFKAIASIVCGFLSIIPYLGVLFNLVSW
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                GIGVVFLLASLVFWILAWIKFKEFDEQELSNLEERLAKTQKKVFDFDLKWIKITMASF
                IILNLLVLTFSFILEIIDFEDFRFYYTKKTLFYTAIILALLSVFLFCKKIKNYKLFIY
                FFIWQGLSVFGSYLLFIPALIINDILIAYGSLMMALNLCYIILAFLFFKTLVQITKEK
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gene            complement(71959..72666)
                /gene="tam"
                /locus_tag="DMACINML_01287"
CDS             complement(71959..72666)
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                /inference="protein motif:HAMAP:MF_00560"
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                /transl_table=11
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                /protein_id="Prokka:DMACINML_01287"
                /translation="MYEILHTKAPKNELDFYLSYANKKDKILELMCGSGRFLLPFIES
                GFDISGVDNSTSMLEKLKEKAPNAKITKCDVLAYHSDEDFDYIFISSGSLCLITDINE
                CKRLLRNLKSFLKKGGKLVFALDTIMTRCKDDSDYKISIKVKTEQNLDLILKNKNHYD
                EISKTQFSPSIYELYDKDKLLQSEKMDFKIHLYDLKEIENILEELEFERFFIYSSFDK
                KIAKDDKSEMFLCECIK"
gene            complement(72699..73688)
                /gene="purM"
                /locus_tag="DMACINML_01288"
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                     /protein_id="Prokka:DMACINML_01288"
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                     FRMPSGFKNPVILGATDGVGTKLRLAIDAKKYDTIGQDLVAMCVNDLICNFATPLFFL
                     DYYATAKLEVEVAKSVVAGIASGCKMANCALIGGETAEMPGMYAKDDFDLAGFAVGMA
                     EEDEIDRSKFVKNGDILLALPSSGLHSNGYSLARKVLFESLKLKFDDKIEGKNLIDVL
                     LEPTRIYVRDFLTLKPYINALAHITGGGLVENLPRVLPRGMGATIRKHHLKTPEIFYT
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     gene            73749..74354
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                     /product="dephospho-CoA kinase"
                     /protein_id="Prokka:DMACINML_01289"
                     /translation="MKNAFFVTASIACGKSTFIEIANSLGFKSISADSIAHEILDKYA
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                     SQMDIEEKLKKADFIIKNTGSYVDFRQECVKVIQNISKGQM"
     gene            74351..75100
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                     /locus_tag="DMACINML_01290"
     CDS             74351..75100
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                     /locus_tag="DMACINML_01290"
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                     /protein_id="Prokka:DMACINML_01290"
                     /translation="MKLYKYCASGNDFVIMNANEKKDRSALAKELCNRYEGIGADGFI
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                     YNANVNFVKVENDNTLKVRTFERGVEDETQACGTGMGACFYLAFLNKKIHNQARIIPK
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     gene            75075..75806
                     /locus_tag="DMACINML_01291"
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                     /product="putative FlgJ-related protein (Bax domain)"
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                     /translation="MKRIIIFLSFYLLPLFGDSELKNGFGEEYYKLNVEQKRQIFFTK
                     MNAMFDKSFEEIAKERAFVEAFFYDVYKNGLRHSNQSNLEKLIDLKNKYRVENLYDFT
                     EYKKRIQKIPKSMGMAQALVESATGTSRFAREANNLFGEWTWGEKGLTPDLRHPDKKH
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                     IHPISHDEKKLQKIYFRDFGLRNNLCIQKDFTHLFENLILNELFKFKQEFFYNKFFTF
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     gene            complement(77006..78163)
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     CDS             complement(77006..78163)
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                     MVMFGSKRGLCLLLSKENILGCFHEGLALARINKKYGFIDKNENWVIEAKYDEVEDFY
                     KGLAIAKLDKKSGLLDKNGRVIVDFLYEKILVVNKDIIILVKNNEILIQKI"
     gene            complement(78235..79716)
                     /locus_tag="DMACINML_01294"
     CDS             complement(78235..79716)
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                     /inference="ab initio prediction:Prodigal:2.6"
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                     WIKQRNLCEKDSIFNISRLNSNKKFEFYYKNIISFKDIKDLSVFNKNQQIQIQASLNK
                     EIYINKEKIKEFLNTLTYPIYHLDFETFMQAVPEFKGVKPYMQIPFQYSLHIDYKDKL
                     EHKEFLSECGVDPRYELAKNLINDIPKDACVLAYNASFERGVIKNLALVFPEFSEHLL
                     NIEKNIKDLMIPFQNKDYYHYKMQGSYSIKKVLPALIPDMEQAYKDLNLIHNGSEAMQ
                     SFEAMQNMSEDDKKAYRQALLEYCKLDTLAMVKILKHLEEIAS"
     gene            complement(79778..80419)
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     CDS             complement(79778..80419)
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                     /product="McrBC 5-methylcytosine restriction system,
                     component McrB"
                     /protein_id="Prokka:DMACINML_01296"
                     /translation="MSDLENSLKGFKDKDFGYYFGKDEKCYIYHTKFGRERNIEINES
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                     IVDNFSKTFGKEKIDEIPFDQGNFKKDIFEKWWDKSINSARMKGNATNLLKDKDKLIK
                     NLEKIKKAADESENLTKLFEKLKEVEGMKATARELAYFLQFNKDKDKFPLANDAMINI
                     AKYIFEILNENPTEIFDSSFDNKCKEEIYFDDVFGKLEIANDNLSEEIKEKIEHLPKY
                     YILDQFLNLIDKIKKSDLALITKDKLAKNDGSKDIKQSVYYKLYQAAYDFANLCGKAD
                     IKSNDLEGFKELLKTHKNIIFHGIPGTGKTYTIVNNIKNIIKNENQMLITQFHPSFSY
                     EDFIEGIKPTGIENGQLKLELKNGIFREFCNKAKEEEKEFLGELEKGNFNEALSDYGY
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                     DLDKSIDSFDLALRRRFIWQEMTCDYDVIKNEIYAKNIEEYAQACKKLNDKIKDIGEK
                     YQLGHSYFLKIEFKDDEIKNNDMKKLFSNRFEALLKEYLRSEYSEKDIQKHLDALKEL
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     gene            82470..83819
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                     component McrC"
                     /protein_id="Prokka:DMACINML_01297"
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                     FKGNIDMVEFIKHNIPLKAKVATKTREQIEDVHIINVLYKALQVIEKKNSSFLKNVKH
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                     DNYIVFDTKYKKMTMEGKSQNGMGDLDRNDLFQIHTYMGYYQKIGKVLLGGLLYPMQN
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     gene            complement(83824..84510)
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     gene            84749..86167
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     CDS             84749..86167
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                     EKDFKEDMENVIFTLNQYKTLLKWYLTDEFEAKDDVLKFLKENLEKTMTLYKYTKNKN
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     gene            complement(86173..87090)
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CDS             complement(86173..87090)
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gene            complement(87335..87784)
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CDS             complement(87335..87784)
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gene            complement(87910..89130)
                /gene="pgi"
                /locus_tag="DMACINML_01302"
CDS             complement(87910..89130)
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                KEGENLGIKCFFIPANVGGRFSILSAVGIVPLCFCGYNAKALLEGAKACFEDFFIHKK
                DEILQKAYHYCTHKSANINVLFSYSDAFKGFNEWYIQLIAESLGKKQGYKRIGLTPIA
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gene            complement(89124..89948)
                /gene="galU"
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CDS             complement(89124..89948)
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                     EVPKEQVSSYGVIAGNFVEEDLIMVNSMIEKPSPQEAPSNLAIIGRYILTPDIFGILE
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     CDS             complement(92168..93163)
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                     /protein_id="Prokka:DMACINML_01305"
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                     DKDTMILFKKAILYMQKTYKSGFLIASHDKNFLDSLAQKKYYLHAGEILEFENTNIFE
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     CDS             93934..94743
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                     QQSGQGMLASIKIAEEKKGVILTDRGTYIKYEANEKGNPNLVIVNEGDDNLKNFYSII
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                     /locus_tag="DMACINML_01307"
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     CDS             95278..97500
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                     DRKFIKFLTPASSTIIMNRFKFLELGGNDQEFVGHGYEDFDLMMRILKNCTDFEAIPT
                     NLEFDYRNWSFNDYKGFRALFSVVGNEACVHGIYLYHLWHAEPNQNGYLDNRELNHQK
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                     LPDSWFFDDKGFNYDSTSYDEKNWNKTLNEEQKIKTLTYIEEVLKGEKFLEKQGLSKG
                     SDNLKRKLGLRHKKIFFVPLQVKDDSVLKNFTYEPFSYENFLNILNELAKKLFIENIV
                     FVVKKHPLSLDLDKTTYDNLIFVPDDTNLNDLLGLCNAVLTLNSGVGVYAILAKKPCI
                     VCANAFYRFDNLNLQANNEKELFEHILNISQGNFNFNEEKALRFIHYLRYEFYSFGKS
                     YYKKSEENGRIYTKVYKIEFYSLILFGKKLLDFNSIKKQNYKLNSPIYKPYIYEIKEK
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                     HTNNYSAGIIVFNDNLKSSQKFYDFIYQFIAKNEDYFLEVKLGDQFLFSLYLLEKGLK
                     IYELNDNYYGNISWVKSKDASILHAWGQNNRFWNNKLCALAWPSWNVYYQKWLSLGGS
                     AYEKGFVSFLEVPQSGGEVFQYFERIVLAKRISQIKLEKQELIIDIDFSKKIKFHLAF
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     gene            complement(98941..99609)
                     /locus_tag="DMACINML_01311"
     CDS             complement(98941..99609)
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                     /product="2-amino-4-hydroxy-6-
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                     /translation="MENHYFFRSEKNLANALLLLTYFYTFMCIIFLALKNFYYELARV
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     gene            99826..100596
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gene            100618..101787
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CDS             100618..101787
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                /protein_id="Prokka:DMACINML_01313"
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                PPIGEALFRTFIPTQIDVISIVTLVGGTVGGYIVFSGAHRLIDAKLYGKENLNYINKA
                AVSGIIITGIMRVILFLAVLGVVSSGFILDKENPAGSVFHHALGDLGLKIFGIVLFLA
                AISSVIGAAYTSVSFIRSFHPWIEKYNRFVVIFFIIVSTLVFYILGKSPASILIIVGT
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gene            101789..102529
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CDS             101789..102529
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                /transl_table=11
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                /protein_id="Prokka:DMACINML_01314"
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                TKIEAGSVGIADKQTGVYPISSPGGWQIIARTPLEFFNKEDEKNPTLLKAGMFLKFKA
                ISKDEFYDIKEQVLKKVYQKEIYEYKSH"
gene            102510..103475
                /locus_tag="DMACINML_01315"
CDS             102510..103475
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                     NLSKRECENPVFQFAKEPTIRVVLGTNDDAFTQNGLNTFLNTSYKIGLKSDRMAIYAE
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                     /protein_id="Prokka:DMACINML_01316"
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     CDS             complement(104245..105144)
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     gene            complement(105278..105862)
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     CDS             complement(105278..105862)
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                /locus_tag="DMACINML_01319"
CDS             complement(105873..106307)
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                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:UniProtKB:Q9R381"
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                /protein_id="Prokka:DMACINML_01319"
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gene            complement(106315..107505)
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CDS             complement(106315..107505)
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gene            107636..108088
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CDS             107636..108088
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gene            complement(108085..108663)
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CDS             complement(108085..108663)
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                     RINKGIYNAWDNTQINKYIPEDERNIDFKHMVYLGDGETDIPAMKLLKDKGGLSIAVY
                     DPEHPKEKIDNVEILVDNERAHFVCEANYEENSSIDLIIKNYIDKIALETQFGKCRAK
                     QPSNDKNEVFKDDDDAKITPEDKINNALKLLEVDKISQNQEDNAIYLKASAYDDYGYQ
                     TSFYIWSGKKYIGFAKIAEKNQVENKHTSENLKKEFNKLDEKFISKITFKNNNLNKEQ
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     gene            complement(119824..120474)
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CDS             complement(119824..120474)
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gene            complement(120994..122109)
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CDS             complement(120994..122109)
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                /protein_id="Prokka:DMACINML_01334"
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                AHTLCDEIVRICKENGVYKIQTQNSSIQAKQILISAGSYVNEVLSVCEFDLPKVPVGI
                RRKVVNWFDTDSYKLSQGFPAFILEFEDDYFYGFPDFADGLKVGRDRVGEIISTREER
                VEFGSYEQDTLDIGKHIKEFFPDLKDFSKGSVCTYPLSPDDDFIIDFLDENLFFMGGL
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gene            complement(122347..122856)
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CDS             complement(122347..122856)
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                AISQNSGCS"
gene            122959..123858
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CDS             122959..123858
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gene                 123972..125375
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CDS                  123972..125375
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gene                 125386..127557
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CDS                  125386..127557
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gene                 complement(127601..127849)
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CDS                  complement(127601..127849)
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     CDS             complement(128349..129218)
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     sig_peptide     complement(129132..129218)
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                     /inference="ab initio prediction:SignalP:4.1"
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     CDS             complement(129230..129724)
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                     EARD"
     sig_peptide     complement(129671..129724)
                     /locus_tag="DMACINML_01342"
                     /inference="ab initio prediction:SignalP:4.1"
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CDS             complement(129733..130752)
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sig_peptide     complement(130681..130752)
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gene            130925..131680
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CDS             130925..131680
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gene            131670..132848
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CDS             131670..132848
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gene            complement(133027..133827)
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                     EENELYIIRIRAKGNKYRVVMIKKELIEHLLKDVRVNYLSEDGLLFVNRNGKALTQAY
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                     DLLRNDLSKLIVKNSMKTKLFKIQSYPTLHQMTSIIKGKLKKDIDYFQIFKALFPCGS
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                     MQGKISRLHLKKNAKKSLLFKGIENKSQICLYHSLHISKMPKSCEILALNDENIIMAI
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                     AFYSLGARKIIAKYGIFFVMGWSSLIASFILFGILEFKEGLVHYDFALNLYLAQAGII
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                     KELLDFKEFSVIPDRIEAGTYLCAGAITNSKITLKKVNAEHLGAVLAKLHQMGFETSV
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CDS             complement(39218..41539)
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                     IGNYYYAQANVKYLTNSKLLMNLFRITAVAMIFIGSQMNLKLAWSLADLTMAFMAITN
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     gene            complement(47413..48402)
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gene            complement(62905..63459)
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CDS             complement(62905..63459)
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gene            63629..64066
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gene            64066..64398
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CDS             67086..68189
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                DNEYVKILKDYANKNNHEVIKLCAKIEEELVGLSDEESAEFLSSLGVNESGLDQIIRT
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gene            complement(68195..69580)
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gene            complement(69590..71164)
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gene            complement(74353..75687)
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CDS             complement(74353..75687)
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                     AMTEFENLECLFTNDEEVGLMGANSLEHTLSSKMLLNLDHESDDEIMIGCAGGVDIEA
                     KLNFNTFKARGKIYELQAQNFQGGHSGINIIHNEKNSIKEMAKFIKENKGEIISFEGG
                     ERINSIPKHAKALVHFKNEVKGNEWIKCEFKEEGEFEICDQSKKLLNTINAFAHGVRA
                     YDKNLDIVQTSINLAILKMENQEIKFELFARSNILDGLKQIEFETLEFFKAFDYKVKS
                     FNFYPPWEGKANALSDKVLKALKKVSPNARVSTIHAGLECGIIEKKQELLCASIGPNI
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     gene            complement(82387..83634)
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                     /locus_tag="DMACINML_01429"
     CDS             complement(82387..83634)
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                     /locus_tag="DMACINML_01429"
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                     /product="putative MFS (Major Facilitator Superfamily)
                     transport protein"
                     /protein_id="Prokka:DMACINML_01429"
                     /translation="MQKKYKNIIYASLGGILEFYDFVLFAFFLDIFAKVFFPQNDTFW
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                     NLATLGIRSYFSVQEVEEYAWRIPFIIGGFFGFFALFLRTKLSETPEFERIKKENKLL
                     NFPLKDALKTYKTSMLVCFLMTVVLTSGVATLMILPKYFEELLSINKTSALWIQNFAI
                     LAVILGALIQGILASKWGSYRICSIFSIAFMFFGMLFSFYDANFLFYFLLACFAQGII
                     TFAPVFMTQIFKSELKFSGLSFAYNISYALLGFLTPFIVNAFYKEYIGVYLIVVGCCS
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     gene            complement(83681..84520)
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CDS             complement(83681..84520)
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                /product="putative amino-acid transporter periplasmic
                solute-binding protein"
                /protein_id="Prokka:DMACINML_01430"
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                AYFTKEYPDIKTLKYDQNTETFAALIDQRGDALSHDNTLLFAWVKEHPEFKMAIKELG
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                GKI"
sig_peptide     complement(84434..84520)
                /gene="cjaA"
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                /note="predicted cleavage at residue 29"
gene            84723..85826
                /locus_tag="DMACINML_01431"
CDS             84723..85826
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                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:CAL35101.1"
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                /transl_table=11
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                TGEEQGLISLKDYYDNLLSKNKNLKTNFTLEGFKLGEKVVSDITTSLSQSEPKIKDYI
                SKLSSGVFTISFENSLFMKNSDYNNNFNMKINNQDLNFDMNLNFDYKQSLLDFFEKAG
                IKYNTQTYAIDEKAVEELLDQRGFAQPIQESVTLNNFKINSSLDTQGVFENYITIAKG
                GLEALKIQSQNEEQTLLIDKALLALNEITKDTVYKLDLEAKFKPIALSDYPKEGINAV
                EKLTVNNQDFTETLKILFGFMMIPIMLGGATGF"
sig_peptide     84723..84782
                /locus_tag="DMACINML_01431"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 20"
gene            85941..86681
                /locus_tag="DMACINML_01432"
CDS             85941..86681
                /locus_tag="DMACINML_01432"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:ADT66289.1"
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                /codon_start=1
                /transl_table=11
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                /protein_id="Prokka:DMACINML_01432"
                /translation="MKILFSPSESKNDTCKEKPINKNSFIFENLFDFRMQVAKKYEEY
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                ELLDLRAGFYDKFYTPKRKFSTYKFIKKGKVVSHFAKAYRGILLALCAKIKAKNNTDI
                LNHLPSNLSLKEIQNKGLKEEIVLEILD"
gene            86879..87082
                /locus_tag="DMACINML_01433"
CDS             86879..87082
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                /note="conserved hypothetical protein"
                /codon_start=1
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                /product="hypothetical protein"
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                /translation="MQYFFVFLIIVFLFIVFMLIMRYEKKLELLNQSIQNIKEEVNGL
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gene            complement(87085..87825)
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CDS             complement(87085..87825)
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                /inference="similar to AA sequence:RefSeq:CAL35108.1"
                /note="hypothetical protein Cj0990c"
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                LLKFSDHSFEFDEILKCLYDEDEENTIIVEEIFTTSQTKQDGGVDLPPLVIKDDEALK
                NNIKFTPFNTFSRVFNKDRFIFIPNTCEQKESIRVEKNQKLNIFETLKITDLNTSFVK
                IEILDYDANNDSVNFDLDVFPSGASYKYGISQNTMYIILQGKMTSCLLLDFLKSFVYK
                NKKELACEKTFVLMLNHKLAYELKVFFV"
gene            complement(87826..89091)
                /locus_tag="DMACINML_01435"
CDS             complement(87826..89091)
                /locus_tag="DMACINML_01435"
                /inference="ab initio prediction:Prodigal:2.6"
                /inference="similar to AA sequence:RefSeq:CAL35109.1"
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                /transl_table=11
                /product="putative oxidoreductase ferredoxin-type electron
                transport protein"
                /protein_id="Prokka:DMACINML_01435"
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                EEKLELNKEAKKIFESCFLCTNCVEVCPSKLRVDNAIEEVRYDIAKKFGIAWYKKIIF
                FFLRRRKILDLAAKLGYVFQSCAFKIQGQGKNVGMKAKFSMPFVKKGRLLTSFNKKSF
                LNSNPDFINNGGEKTIGFFVGCLANYFYIDTANAVLKIAKEVKINVDLMKEQVCCGAP
                QFFTGDFKSVEILAKKNIEYFEKKLEKLDAIIIPEATCSAMLKIDLEHFFHMQNEPEW
                AKRAQKISSRIYMASEYFYKFTNLKELLESKKKLNYSITYHDPCHARKMQGVFKEPRE
                LLKANYHFVEMSNPNACCGFGGVSMQTDYYDRALSVGLKKASMIDESKACVVSAECSA
                CRMQISNALEQNSSKAIFASPLELIAKAL"
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     CDS             complement(89102..90457)
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                     oxidase"
                     /protein_id="Prokka:DMACINML_01436"
                     /translation="MRDYKAFVKYSKAGPRYTSYPTAVEFNTNFKYEEYIEILKKQNK
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                     HFGGGTPTFFSAKQLESLILKIKSIFGNFAKDAEISCEIDPRFLNEEQADVLTKNGFN
                     RISFGVQDFDEKVQKEIHRIQPFELTQNALKLVRDRGIKSVNMDLIYGLPFQSLQSFT
                     KTLEKAMLLNPDRLAIFNYAHVPWLKKNMRKFDENTLPSPDVKLEILEFCEKFLTQNG
                     YKMIGMDHFAKEEDELFKALENGTLHRNFQGYTTKGGADLIGIGLTSIGEGQSHYAQN
                     FKDMPSYEAAISEGRLPFERGVKLSYDDELRKAVIMDLMANFRLDIKAIEKEFKIDFK
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     gene            complement(90444..90935)
                     /locus_tag="DMACINML_01437"
     CDS             complement(90444..90935)
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                     PIDFSDVWIVAMDEIKRKAQEGIMEISIDLEKLLADIKKEHPNLFVDMQAMVERVKNN
                     ERL"
     gene            complement(90973..91896)
                     /gene="argF"
                     /locus_tag="DMACINML_01438"
     CDS             complement(90973..91896)
                     /gene="argF"
                     /locus_tag="DMACINML_01438"
                     /EC_number="2.1.3.3"
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                     /protein_id="Prokka:DMACINML_01438"
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                     WLITAAILGFDFSVALPKNYEINSEILEFAKEKAKISGAKILLTHDKFEAIKGKDVII
                     TDTWVSMGEESEKEKKIKDFDGFIIDEEAMSAANQDAILLHCLPAYRGYEVSEESFEK
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gene            complement(91893..92876)
                /gene="hemB"
                /locus_tag="DMACINML_01439"
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                /protein_id="Prokka:DMACINML_01439"
                /translation="MFKRFRRLRLNESLRAMVREHTLSVNDLIYPLFVVNGKGIKKEI
                SSMPDVFQMSLDEILKECKTISELGIKAIILFGVLENDKKDSCGSDAMDDEGLIARSI
                REIKKEFPNLFIISDLCFCEYTDHGHCGIIDPKTKSVDNDATLEISAKQALVHARAGV
                DMIAPSGMMDGIIETLRKALDEEGFENLPIMAYSTKFASSYYGPFRDVADSTPSYGDR
                KSYQMDFANGKEALEESLEDEAQGADILMVKPALAYLDVVKEISLHSNLPLCVYNVSG
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gene            92933..93493
                /gene="ribA_2"
                /locus_tag="DMACINML_01440"
CDS             92933..93493
                /gene="ribA_2"
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                /product="GTP cyclohydrolase II"
                /protein_id="Prokka:DMACINML_01440"
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                RIHSECLTGDALGSLKCDCGEQLEFSLKYIEKHGGMVIYLRQEGRGIGLFNKVNAYAL
                QDKGFDTIKANHQLGFKADERTYEIVEFILKHYKISKVNLLTNNPQKIHSIQDKIMAR
                VPILINPNRFNANYLEIKQNQMGHLL"
gene            93490..94089
                /locus_tag="DMACINML_01441"
CDS             93490..94089
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                KGSEVFDEVEGLKDYDIFENGLRRYCVLKNTQSGINTTS"
gene            complement(94090..94662)
                /locus_tag="DMACINML_01442"
CDS             complement(94090..94662)
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                /protein_id="Prokka:DMACINML_01442"
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                GEFKDVKYKFSKNTSTLANYLKGARAVVNPSSVFMGEGNEIITDNLAKVFFPSLLGNS
                DIKVVFKDVVAGENKGVISARVTIDKKSTLIPLSYTIENNKFVAKGQLDLHAFKNSSQ
                ALKALSDVAPGHGGISWPLVDIVFSADVVQ"
sig_peptide     complement(94594..94662)
                /locus_tag="DMACINML_01442"
                /inference="ab initio prediction:SignalP:4.1"
                /note="predicted cleavage at residue 23"
gene            complement(94754..95848)
                /locus_tag="DMACINML_01443"
CDS             complement(94754..95848)
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                /protein_id="Prokka:DMACINML_01443"
                /translation="MIKKIEHYKNILISNFKGLIFTACIVVFAMYLSSVQSIKDTTHL
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                KDMANFDQSASNIAIIIKMMRVILLVPFLLIVTYFFAKNQHSSSGKTAKSISIPYFAF
                IFLGVIVINTYLASKENFLGISTSDIISFGKLLCTLCIVFAMAALGLQIDFKKFLKSG
                SRVFGLAFVLGLVLVFGGYFLTLFFRGMLW"
gene            95993..96874
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CDS             95993..96874
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                /product="putative transcriptional regulator (LysR
                family)"
                /protein_id="Prokka:DMACINML_01444"
                /translation="MKIKDMEIFLDLLNTQSPTHTANNFAITQPNVSIIIKNLEQDLG
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                MQFWKKDELIVASSDKNLSQREFYIDELLDQKWILRETGSGLRDKFLNEIGNVSKKLK
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                NYNFNRALEKFEKIFQQ"
gene            96950..98815
                /gene="rpoD"
                /locus_tag="DMACINML_01445"
CDS             96950..98815
                /gene="rpoD"
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                     /inference="similar to AA sequence:RefSeq:CAL35119.1"
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                     /protein_id="Prokka:DMACINML_01445"
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                     DSPVRMYLREMGQIALLNKDEEIEISKKIELGEDIIIDAFCSVPYLIDFILDYREPLI
                     NRERRVKELFKSFDDEEKNDDKLDELEDEDEENDEELENEEETPKKTSKKEDERTLKV
                     IEKFKALEKAKKDWLKVSKDKESGDEILDKLGIAFKKNILKEKLMDLGPTSKLISEIV
                     KSMETALKSDEEFDKELKRLEYRLPMFSEELKSRHANILKDITKLSKEEITERALETT
                     MVSTYMEIKKLFQTKEASEKSFDLEKERLKEILEQIKRGKKISDEAKTRMAKSNLRLV
                     VSIAKRYTNRGLPFLDLIQEGNIGLMKAVDKFEYKRGYKFSTYATWWIRQAISRAIAD
                     QARTIRIPIHMIETINQINKIIREHLQKDGKEPDVSVIAKEVGLSVDKVKQVIKITKE
                     PISLEAPIGSEDDGKFGDFVEDRNSLSPMDHILKDDLKEQIDEVLDQLNDREKAVIRM
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     gene            complement(98816..99325)
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     CDS             complement(98816..99325)
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                     mutase"
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     gene            complement(99322..99840)
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     CDS             complement(99322..99840)
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                     /inference="ab initio prediction:Prodigal:2.6"
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                     /codon_start=1
                     /transl_table=11
                     /product="rhomboid family protein"
                     /protein_id="Prokka:DMACINML_01447"
                     /translation="MVVILLILINILFYFTIPYEYYSLLGLNILFFKGAYWQILSSMF
                     IHGNLTHLILNMIVLFQFGRILEPYLGAFRFFLLYIIGGIMCSILSAFYVYFSFNQLS
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                     CGYFLGKLRRKI"
     gene            99939..100355
                     /locus_tag="DMACINML_01448"
     CDS             99939..100355
                     /locus_tag="DMACINML_01448"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL35122.1"
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gene            complement(100451..102055)
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CDS             complement(100451..102055)
                /locus_tag="DMACINML_01449"
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                SELVDFLQNPKKYKEFGVKMPKGVLMVGPPGVGKTLIAKAVAGEAGVPFFYQSGSSFV
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gene            complement(102058..103308)
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CDS             complement(102058..103308)
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                     FPCILKPARLGSSIGISIAKNEKELDYAKDVGFEFDTDILVEDFKSDIKEYNLAGCMI
                     KDEFIFSIIEEPKKKEFLDFEQKYLSFSGHNELIEADLSEELKQKLKDNFAKIYNPLF
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     gene            17427..18158
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     CDS             17427..18158
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                     IAALLVLDFQKAQLVLLSNSGILAKKSFKVRFKIILFKFLKKLGLGKFYRYFASKDGA
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     CDS             18152..19579
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                     /transl_table=11
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                     /protein_id="Prokka:DMACINML_01480"
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                VKGDIDVITRFLEPQICIVGEIGNAHLEYFKNIENTRNTKLEALNSKRLEKAFLHTST
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gene            19750..23259
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CDS             19750..23259
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gene            complement(23337..24248)
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CDS             complement(23337..24248)
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                     RILRAVAFASRFDFKIADESLKLMQSMNIKDLSRDRINAELYKFFKSSKLEVGYKYLQ
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                     /gene="ygaZ"
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                     /product="Inner membrane protein YgaZ"
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gene            complement(28670..28846)
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gene            complement(28860..29195)
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gene            complement(30107..30628)
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                     (cytochrome C-type protein)"
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                     LVDASFTTLQPGESILFERSFENAPPLISHTIEDMLPITKDNNTCLTCHDKAIASDVG
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                     FILFCIDTFLSPRAICSHLCPLGAFYALISRFALLKIKHNHQNCTKCYKCIGICPEKQ
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                     ERTAKHAFLLPSVDHEVCVGCGLCELACITEKPAIRVLPREYVLGKAGSHYVKGWDQE
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CDS             complement(32168..34942)
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gene            complement(35847..36584)
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CDS             complement(35847..36584)
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                NSKIAIDEWNNNPNIDALIIWSHWAKALGDKALFIEDEKAVVYRSAEIIPTKKGLQNK
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sig_peptide     complement(36531..36584)
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gene            complement(36631..38661)
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CDS             complement(36631..38661)
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                SRSILALANKVILNNERLYPKELIVTRKDEFKAPSLLTFEELFDQYQNIAKMILTSGV
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                YKYYNFLTLGASEMSNGKGVNLLSVHASKGLEFDLVFVIDLAQGRFPNQKLMSMGGSL
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gene            38783..39715
                /locus_tag="DMACINML_01500"
CDS             38783..39715
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                SRLEPQLSTENMKVYVLDGKFLSDYRIKLLKDMLAIIEDNSKDYFLSVFVKMLPKGEM
                SLTIYNKDIIFSDMKKSYKYISMDKISPYIKTPEVLNQYVAREEIIERFKLQTKKEGK
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gene            39739..42351
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CDS             39739..42351
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                     RVAIARALTLNPKILLSDEATSALDPNTTKNILELIAKINAEFGITVVLVTHEMDVVK
                     DVAQKALLLEHGQIIGSGAIDELFLKPNEKMKEFLGESDFLPSTGLNIKLYFPKEVAQ
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     gene            43364..44269
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                     NPKKIKFVELKAAQLPRALNDVDFAVINSNYALSANLNPAQDGVFIEDKESPYANILV
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     gene            46066..46842
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     CDS             46066..46842
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                     KNPKNLKFIELKAAQLPRALNDVDLAVITTNYALGAGLNPLKDGIFIEDKDSLYAIVL
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gene            47579..48142
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gene            48182..48658
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gene            48649..49227
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                     NELEAIVDIAKERFKPKPNIGLRVRLHSAGVGIWAKSGGINSKFGLTSTELIEAVNLL
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                     FALTRVAGAYLGGDEKREMLTRIYGTAFADKESLKEHLRIIEEAKKRDHRKLGTELKL
                     FTFDDEIGGGLPIWLSNGARLRSKLEQMLYKIHRLRGYEPVRGPELLKADAWKISGHY
                     ANYKENMYFTQIDEQEYGIKPMNCVGHIKIYQSDVRSYRDLPLKFFEYGVVHRHEKSG
                     VLHGLFRVREFTQDDAHIFCMPSQIKEQVLEILAFVDNLMKLFDFSYEMEISTKPAKA
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                     FCRYLELYPQNPILLIDTYNYKQGLENAIKAFKKFKIKQCGVRIDSGNLEILSKEIRA
                     ILDKNDLKECKIIVSNSLNEKSIDKLLKNNAPIDAFGVGEKLITASSDPIFGCVYKLV
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                     YEELAGDVDDNKLLLAMVANQILEGVYFYSGFTAIYALARAGKMLGSAQMIRFIQRDE
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     CDS             complement(34561..35256)
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VERSION
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                     QAASGAGKEGMEELVRAMQSFFAFKLDEFEAQTFPHTLALNLIPQIDVFMDNGYTKEE
                     LKMINETQKILHKNLEISATCVRVPVLRSHSEAITMHFAKEVDVNKARDILQNAPSVI
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                regulator"
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                LSQEAQKALLEYNFPGNIRELISIVQRACILSEGLEISEQDLFLEARSVKKDVKNLEK
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sig_peptide     complement(14157..14237)
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                /note="predicted cleavage at residue 27"
gene            complement(14302..16872)
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CDS             complement(14302..16872)
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                /locus_tag="DMACINML_01639"
                /EC_number="5.99.1.3"
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                /product="DNA gyrase subunit A"
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                     EIARLDEILKSETLLENLIRDELKEIKNKFDVPRITQIEDDYDDIDIEDLIPNENMVV
                     TITHRGYIKRVPSKQYEKQKRGGKGKLAVTTYDDDFIESFFTANTHDTLMFVTDRGQL
                     YWLKVYKIPEGSRTAKGKAVVNLINLQADEKIMAIIPTTDFDENKSLCFFTKNGIVKR
                     TNLSEYQNIRSVGVKAINLDENDELVTAIIVQRDENEEIRLLDDDSLNDENINSDENL
                     IESIKGKMLFAVTKKGMCIKFPLAKVREIGRVSRGVTAIKFKEKNDELVGAVVIESDE
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                     phosphoribosyltransferase"
                     /protein_id="Prokka:DMACINML_01640"
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                     SSGSSLLEAKQFLEKNKISVLFAVVLADAKV"
     gene            complement(17484..18128)
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     CDS             complement(17484..18128)
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                     /translation="MNKKILFFIALALFLNACASKQNTFTQVNQLSKASECVPCESSS
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                     VGVLSLNDINRNKKFTLRTKQDVQGFENLKDISFYTHLLIKQMANKAASIISEL"
     sig_peptide     complement(18069..18128)
                     /gene="mapA"
                     /locus_tag="DMACINML_01641"
                     /inference="ab initio prediction:SignalP:4.1"
                     /note="predicted cleavage at residue 20"
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                     CVSAKTGVGIKELIETIITKIPAPKTDDEAPTKALIYDSWFDNYLGALALVRIYEGSI
                     TKNDEVLVMSTEKKHIVQDLFYPHPLSPIKTQSLQSGEVGVVVLGLKTVGDVQVGDTI
                     TLVKNKAKEAIGGFEKAKAFVFAGLYPIETDKFEDLRDALDKLKLNDSSITYEPETSL
                     ALGFGFRVGFLGLLHMEVIKERLEREFNLDLIATAPTVTYEIYQTDGELIKIQNPSEL
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     CDS             20141..21424
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                     (multidrug efflux system CmeDEF)"
                     /protein_id="Prokka:DMACINML_01643"
                     /translation="MFKKYLTLIHKAIILVFLPLSLSASNLREFIALSQTNEQYLIKQ
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                     ERLQKFHDAGLSPKDELESIKAKYHLSLLELSQNELKLTSIQKEIRILSNTNFTPSGN
                     AFLENPNQEKSQSYEVLIAKEQINLAKESVNLAKAEYFPKFYIQDNFGFYKNNYSPEI
                     PVYYQNVADRFLQKYSQNNQFILGVEWKIFDFNARAKEVEKERLNVQIANANARLSER
                     KNKEELNYINQSLKVLKQQIYTLNLSLNAANLAFESVDKKYQAGLVSYVEYLQALEAK
                     FKAQSDLELAHNEFEITKANYYFNAGIDLNSKVRE"
     gene            21421..22161
                     /gene="cmeE"
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     CDS             21421..22161
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                     (mutlidrug efflux system CmeDEF)"
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                     KTRKIYAEVETQNLTPGLFGEGRIITRD"
     gene            22165..25182
                     /gene="cmeF"
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                     VGKIEAKGFLEPQIRIELKPNELEKYNLNALEIANIIKNQNFKQALGELNNNQNNYII
                     KGYFEATNLEELANLRIKTGVFLSDIANISNLYEDEKQSAIYKNQEGVLLELGKITNF
                     NTLKMIQNVKNALPNLEKQISNDISIEVLYDKSLNIHKHLSQVIFDMVLGIFLTLVIV
                     FLFLRNLSATLIACIAIPTSIISTFFIIDLLGYDLNRLTFIALTLSIGIFIDDAIVVI
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                     SEVALHINREKAKLLDVDPEYIAGILGYSFAQLSIGSMDRGNSKDDIILSFAPQFKKD
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                     TLLLDNIDTILGENTNLNYTFSGFINLLDETVQGFIVAVILAFVLIYLVLAALYESFI
                     LPLIIMITMPLAFGGTSIGLFISGHNFSLFVLIAIILLFGMVGKNAILLVDVANKKCH
                     EGLDPDEALLIAGKSRLRAILMTTFAMIFAMLPLALSRGAGYEANSPMAIAVIFGLIS
                     STLLTLLVVPALFKFCFKLDTRLRKIYEREKIN"
     gene            complement(25203..26009)
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     CDS             complement(25203..26009)
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                     /protein_id="Prokka:DMACINML_01646"
                     /translation="MQIVQTLETINVNTDDINVFQYFKDLITKNFTKVVGRKNKIFSF
                     FEENEIPQRRYFLKVLDQKYRKSSNESIENLKDAHFKTFRLNFEQNNVLKPMLFIKVD
                     FAGDKILMKLSSNEKLFVTYMKNYFKEHCIEYNEMTRILILDYKNESTFEFFEAFADE
                     SEHLKYCVNFEVDRQEYKNFRQNIHNKENMKWKFNALAKLFSNYFNTLECTPQNDLSE
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     gene            complement(26011..26730)
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     CDS             complement(26011..26730)
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                     EDGISSIYCFYDPEFSHLSLGKFSLLNEIEIAKKEKLKYIYLGYFVKKCQSLSYKADY
                     TPNEILKGTRELFENEILWER"
     gene            complement(26730..26966)
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     CDS             complement(26730..26966)
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                     /translation="MDFFDSLKSIKKEMQTHSKEQKSPKNSNKKDMSHFNKEIKTQPQ
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     gene            complement(26966..28408)
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     CDS             complement(26966..28408)
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                     /product="acetyl-CoA carboxylase, biotin carboxylase"
                     /protein_id="Prokka:DMACINML_01649"
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                     FAIEARITAENVWKNFIPSPGKIGEYYPALGPSVRVDSHIYKDYTVPPYYDSMLAKLI
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                     biosynthesis protein"
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     CDS             29704..30720
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                     b-N-acetylglucosaminyltransferase"
                     /protein_id="Prokka:DMACINML_01651"
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                     KARIRKELKNIIFLGGSQGAKFINDLALNLAPELQKKGIGIIHQCGKNELEKYQQAYK
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                     ETMK"
     gene            complement(30710..31873)
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     CDS             complement(30710..31873)
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                     /translation="MLSFKKIFWLNVAIVIIVAFNLRAPITAIGPMIDIIQDEYNLNS
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                     MVFWSVFSFIALMIYYPQAKNGRFFRTKKKESKKINLLKNPTTWKITLFMGFQSFLAY
                     SLFFWYVQIIVEKGYDKDFATDMVLFSQLVAAPVSLFGPLLLGKLKKSLHTPYIAILC
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     gene            complement(31881..32735)
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                     ILKVELKN"
     gene            complement(32798..33688)
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     CDS             complement(32798..33688)
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                     FEEIFLHLLLNKNTYFIGFLAGILKEFRLDLSQLFEYCGREFVSVSEMADFAKLDFAT
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DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION     
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
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                     LKELLEYINETKEVDLKQKIFVLFKYVHGDIIKLIKAIEKSSVKKQEQADLILSTGHK
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gene            complement(12622..12697)
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sig_peptide     19076..19129
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CDS             complement(19589..20284)
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CDS             complement(20295..21638)
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                ELKIKIGARVIFCVNNWDKGYYNGEQGIIESITYEEDKTYIGIMKSNGVKIMLEPYVF
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     gene            complement(23957..24844)
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                     /transl_table=11
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                     AALVLIYFTNLHIIDAIFGIVVSLYTAFSAFKIIKKALAFLMDEALPKEQVSQICALI
                     SSNPEVVSYHELKTRKTPNCNYLSVHLVFCPIISLLSAHKVSDEIENGVREMFNGEKW
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     gene            complement(24841..25818)
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                     RNSHLDKSQIEARLKEIFGLKQIIWLENGFIKGDDTDHHIDTLARFIDKNTIAYSICE
                     DEEDEHYIPLQKMKKELEATGFDLVELPLPKPLYYEGRRLGATYANFVFVNDALIMPF
                     YKDENDEIIKQRLAKALPKRKIIGVDARVFLRQNGSLHCSCQNRFKGLR"
     gene            complement(25915..26352)
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     CDS             complement(25915..26352)
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     CDS             complement(26362..27954)
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                     YHSLENIEKDIAKTSRSYIVIFTIALIFTLIVVLFVLKIVVGNPIMELLSHAKELAQG
                     SGNLRARIRVKGRDEIAKACEYINQFIEKTQKTVSSASLNSKNVEKQSILLNSNAIEL
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                     KVSDLVQNENDLALKIENMVKYAQNIQKATQMMSEIADKTNLLSLNAGIESARAGSYG
                     KGFSVIAEDIRTLANNSEEFLHNVELIIKELLESIQEVAKELKENSHSIFSLNENTHL
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CDS             complement(28051..29583)
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gene            complement(30529..31299)
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CDS             complement(30529..31299)
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                KAFDIAKSELDNFIASISNLKSTKKELSLDEAYRILELSNNADLNAVKKQYRALAKKY
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CDS             complement(33493..34821)
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SOURCE      Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
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DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION     
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SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
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VERSION     
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SOURCE      Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
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ACCESSION
VERSION
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
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DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
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COMMENT     Annotated using prokka 1.13 from
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DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
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SOURCE      Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
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     2821 gggaatttgg ataattggga tatgtataat atcaattgct ttcgcactca aaaaggcaca
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     2941 ga
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LOCUS       DMACINML_24             2571 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
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            https://github.com/tseemann/prokka.
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     gene            992..1450
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                     /codon_start=1
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                     /codon_start=1
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     gene            2152..2382
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                     /codon_start=1
                     /transl_table=11
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     2161 ataataaaat attatgtaac aatttatata gatgagttat tagaaaatga aatgttaaag
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LOCUS       DMACINML_25             2204 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Ile(gat)"
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     tRNA            complement(86..161)
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                     /note="tRNA-Ala(tgc)"
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LOCUS       DMACINML_26             2132 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
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COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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     1321 atttataaga gcagtttcaa gattgattta attttagatg aaaactcttc ttttttttaaa
     1381 agggctacaa aatgtattat agctacaaaa gtcttaggag attttagcac aagtcaaatg
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     1621 ttgaaagctt ataaagaaaa ggaacagcaa aatattaccg ataaaatccc ttacaataaa
     1681 actattttg ttagagctta cttaaataat gaggagaaat ttttcttcga tgaggcaatt
     1741 aaatgggcat attgtataaa aaaagaagtg gaattggaag gcaatcaacc taaaattaat
     1801 attttagaaa atcttcaagg aaatgatata gcctttaata cttctatgct tttagcaagt
     1861 gatagggaaa agcttaatct tgcaaatgaa aaatatcaat taattttatt tgcctatttt
     1921 aacgcacctg catttaaaac aacacaagga ataacgcatt tagtgttaaa atgactaaag
     1981 atttaaacta tgcgaaaaaa gccattgaac ttaccctctc aaatataaaa gataaagaac
     2041 aaatttattt aaaagcccaa aaggattatg atgaattagt ccagcataat ttcactcaaa
     2101 gaattttaaa tgataaagat tctagggtag at
//
LOCUS       DMACINML_27             2132 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..2132
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            122..1123
                     /locus_tag="DMACINML_01829"
     CDS             122..1123
                     /locus_tag="DMACINML_01829"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:APA51640.1"
                     /codon_start=1
                     /transl_table=11
                     /product="mobilization protein"
                     /protein_id="Prokka:DMACINML_01829"
                     /translation="MNDLKNLSKHFQEKYGFQCYQIAIHRDEGHFNEQGEKLINHHAH
                     MEFITLDKETGKNNFRREKISPKVLREIQTEIAEILGMERGEDKRISGAKRIEPRAYA
                     ALKEKEKREKKRNINLEQEQEKEQFLNKSEYKKIIENFRKSQINQGLDKDFFKELSEL
                     KKNFQEIKEDNLSELLNDILREHLERIEKLKKENSILKAENELLKQKEQKNDKSIDQE
                     QKNASERNFEPKNDNNTEDKKIFFEKLATYRLNEGLSKIYSKPLKRIVEPETEAKKKE
                     RIKILTETMEKTEAYLPETLKKWLENNKDIDLKEILVAYQNTLSKELKQSKSIYKGR"
ORIGIN
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        1 aaataagata gtttcggaag cgaaagaagc ctatgaaaaa aataaaagcc ccaaagctcc
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      121 aatgaatgat ttaaaaaacc tttctaaaca ttttcaagaa aaatacggct ttcagtgcta
      181 tcaaatcgct atacaccgcg atgaagggca ttttaacgag caaggcgaaa agcttataaa
      241 ccaccacgca catatggaat ttatcactct tgacaaagaa acaggtaaaa acaactttag
      301 gcgtgaaaaa ataagcccaa aagtcttaag agaaattcaa accgaaatcg ctgaaatctt
      361 aggaatggag cgtggcgaag ataagagaat aagcggagca aaacgcatag agcctagagc
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      481 agagcaagaa aaagagcaat ttttaaataa aagcgagtat aaaaaaatca ttgaaaattt
      541 tagaaaaagt caaattaatc aagggcttga caaagatttc ttcaaagagt taagcgaact
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      661 aagagagcat ttagaacgca ttgaaaagtt aaaaaaagag aatagcattt taaaagccga
      721 aaatgagctt ttaaagcaaa aagagcaaaa aaacgataaa agtatcgacc aagagcaaaa
      781 aaacgcttca gaacgcaatt tcgagccgaa aaacgataat aatacagaag ataaaaaaat
      841 atttttcgaa aaattagcca cttacagact gaatgaagga ttaagtaaga tttattccaa
      901 gccccttaaa agaattgtgg agcctgaaac cgaagccaaa aagaaagaaa gaattaaaat
      961 tttaacagaa acaatggaaa aaacagaagc ttacctacct gaaactttaa aaaaatggct
     1021 tgaaaataac aaagatattg atttaaaaga aatacttgtc gcttatcaaa ataccottag
     1081 caaagaatta aaacagagca agagtattta caaaggcaga taaacacttt ctctcccttt
     1141 ttagcttagc aaatcgcacc tttggtgcta tgatttgcga taatcggggt gcgggggcgt
     1201 gaagttagcc tagagctaac gaacggacaa gccaccgccc taatgtatat catcaaaact
     1261 tttttgttt tctctctcgc gcgcgtacgc gtacgcgatt ttttttattt tttatatatt
     1321 ttttatattt ttagggggct ttctaagccc tatataatgg gggctagcga aatattaagg
     1381 gtagaaatct aaactattaa gggtagaaat ctaaactatt aagggtagaa atctaaacta
     1441 ttaagggtag aaatctaaac tattaagggg acaaaattct actattaagg gtagaaatat
     1501 attgacaacc tatccttaat atgctacaat aaaaaatccg ccttgagttt tcactcttgg
     1561 cggaaattta tcaatcaagg ctaactatga aacgacatag taagcgtttt gtgagattat
     1621 acctaaattt taggtttttt aagcttaaag ttgaagtatt tttctaacaa aaccgcaggg
     1681 gtagagaagc cccttgcctt gattgtctta ctttggatat gcaaatgagc gatatagtta
     1741 aataccataa tgattttaat aaaattcagt tgcctagttt tacagaaatc gaacaagatt
     1801 tattgtgtgg tttaatggta aaacttaaag aagaaaaagg caaagtaaca ttctatcctt
     1861 gggacttaag aaacattctc aaaagtagtt atgataataa tagtctaatg gaatttgcgt
     1921 cttctctaaa aaggaaattt ttcaaagctg actttacaat aattgaaaaa acaactaggg
     1981 gtgaaaaaga agttgaagca cacaaaacaa taaacctttt tacagaattt gcaatttatg
     2041 tttatgcaag ctcaaaagat ttagagagta tagaaataca agttaatccg caatttgaat
     2101 atattttaaa tcaactaacc gctaatttta ca
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LOCUS       DMACINML_28             2116 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..2116
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            50..126
                     /locus_tag="DMACINML_01830"
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     tRNA            50..126
                     /locus_tag="DMACINML_01830"
                     /product="tRNA-Ile"
                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Ile(gat)"
     gene            440..1039
                     /gene="rhtC"
                     /locus_tag="DMACINML_01831"
     CDS             440..1039
                     /gene="rhtC"
                     /locus_tag="DMACINML_01831"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:ABS43249.1"
                     /codon_start=1
                     /transl_table=11
                     /product="threonine efflux protein"
                     /protein_id="Prokka:DMACINML_01831"
                     /translation="MTFLFIFGIHLSALLTPGPDFFLVSAYALKFSFKEALKAAFGVS
                     LAILLWIIFSLTGLKILFDTFPFIQLVLSTLGAMYLFYLAYLLLKNISNEIHFTNSVK
                     ISQPFLGGFLTNITNAKAIFYFGSIFSSLNFTGDNFEIFLLVIILGLESLIYFIFIAF
                     LFSNLKIKMLYLNHHKKIDLFCAFIFISFACFTLATIYF"
     gene            1048..1308
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     CDS             1048..1308
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                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01832"
                     /translation="MLIQIKEINQQNITDILYGKPCFYSLGCIFDEKIINYWKQNILK
                     EKLGHYHNAPLIAKIGMAYYETINNEKLKKNILKMRNIGMIY"
     gene            1434..1829
                     /locus_tag="DMACINML_01833"
     CDS             1434..1829
                     /locus_tag="DMACINML_01833"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:SQE23465.1"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01833"
                     /translation="MLTENSSIEPHQDIFKRDDEITWNDNGQIKEQIAFNFFLDNAED
                     GGEMELWNWKPNDDEYRKFQHTNIKLNYGLDRSKISLPYTTYKPKLGEIVLFNPRYVH
                     AVKKANKGIRLTISCFLSVNKNEELVVWS"
ORIGIN
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       61 tcagctggtt agagtgcacc cctgataagg gtgaggtcac aagttcaagt cttgttaggc
      121 ccaccattag aatcagattt ggaatgatat taatttattt atatttctac ttgccttaat
      181 tatcctatat aaatcagtat tttattttta ttagtaaggt tttattaata ttttgaatta
      241 atattgattg tgttatatta aatcatataa aatgttttaa ataaggtgct aataaatgaa
      301 tttttaatta aataaagatt attaacattt tgtagcattt tgcaatatta ttttctatat
      361 ttgattgttt atatttttgt tttttataat tttttgagaa atttgcgata aaatcacaaa
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      421 aactacaaat ggaattctga tgactttttt atttattttt ggtattcatt tatctgcact
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      541 agaagcctta aaagcagcat ttggtgtaag tttggcaata ttgctttgga ttattttttc
      601 tttaactgga cttaaaattc tttttgatac ttttcctttt atccaacttg tattatctac
      661 tttaggagcc atgtatctgt tttatcttgc ttatttgctt ttgaaaaata tttccaatga
      721 aatacacttt acaaatagtg taaaaatttc acaaccgttt ttaggcggtt ttttgacaaa
      781 tattacaaat gctaaagcta ttttttattt tggaagtatt ttttctagct taaattttac
      841 aggagataat tttgaaatct ttttactagt tattatcctc ggtttagaat ctttaattta
      901 ttttattttc attgcttttt tattttcaaa tttaaaaatt aaaatgttat atctaaatca
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     1021 tgcaacaatt tatttttagg agcataaatg ttgatacaaa taaaagaaat taatcagcaa
     1081 aatattactg atattttata tggaaaacct tgtttttatt ctttaggttg tatatttgat
     1141 gaaaaaatta ttaactattg gaaacaaaat atacttaaag aaaaattggg gcattatcat
     1201 aatgcaccac tcattgcaaa gataggtatg gcttattatg aaactattaa taatgaaaag
     1261 ttaaaaaaga atattttgaa aatgcgaaat attggaatga tatattaaga aatgcttgtt
     1321 ttccttatat ttcaccaatt gattatatta tttctttatt tgatattatt tggaataaag
     1381 gttgcaagag agcggttttt aataatcgaa aaacatttgc agggctagta agagtgttaa
     1441 ctgaaaattc atcaattgag ccacatcaag atatttttaa aagagatgat gaaatcactt
     1501 ggaatgacaa tggtcaaatt aaggagcaaa tagcatttaa tttcttctta gataatgctg
     1561 aagatggtgg agaaatggaa ctatggaatt ggaagccaaa cgatgatgaa tatagaaaat
     1621 ttcagcatac taatattaaa ttgaattacg gattagatag aagtaaaatt tctttacctt
     1681 atactacata caaacctaaa ctcggcgaaa tagtattgtt taatcctaga tatgttcatg
     1741 ctgtaaaaaa agcaaacaaa ggtataaggc ttaccatatc ttgttttctt agtgttaata
     1801 aaaatgagga gcttgtagtt tggagttgag aaatcgccaa aatatttaca aggaaaagtt
     1861 taataagttg cacaattcaa gtttgctcaa ttttttgttt taatttaata tatttaataa
     1921 aattttaaga ttaattttgt ataatttcga ctttaacttc ttagaaaatt aaaagtcgtt
     1981 aaaaatattt tttaaaccta aatgttcttt ataattatca ttgttaagag tcacaagcaa
     2041 gttttaataa aaacaatttt acaggacttg ttaaaggata aaacccaatt atcttttctt
     2101 tggttttact tatatc
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LOCUS       DMACINML_29             1946 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION     
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..1946
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(120..437)
                     /locus_tag="DMACINML_01834"
     CDS             complement(120..437)
                     /locus_tag="DMACINML_01834"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01834"
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                     /translation="MKNSKGENIVKPKNTNTAYACAIQARFEQNKIVKIEPKYCISLI
                     NTCFDSKEITLDNDISRVGLNDALSKRTIDFVNRFKLLKHQPNTTNCLMKKQRKLRGV
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     CDS             complement(659..1261)
                     /locus_tag="DMACINML_01835"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01835"
                     /translation="MLEFFVNLLIFILIFFFFVFIFSIILYFIFKIFYKLKNKTKTIN
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                     FSNREKGNTMHDEKGEFFFNQKINKKIYFDFKKSESINVLQKNKFTLTEVTFEDCYDG
                     IHYSTHLSYIYNDYGIFLGGDEGAGFYFRYHKRLYCEDVR"
     gene            complement(1265..1711)
                     /locus_tag="DMACINML_01836"
     CDS             complement(1265..1711)
                     /locus_tag="DMACINML_01836"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01836"
                     /translation="MSKNIKTQEAKLDLIAKFLDYANVADASYAMLHWIDYVKKENDK
                     KHENGDTQKLGDKHNNQNSTYARAIQARFEQNKIVKIEPKYCISLINTCFDSKEITLD
                     NDISRVGLNDALSKRTIDFVNRFKLLKHQPNTTNCLMKKTDKIKRS"
ORIGIN
        1 agtttttgtt ttattttta ttttaaaaaa gactttaaag ataaaatata aaataataga
       61 aaatataaaa acaaaaaaga aaaatataag aataaatatt aaaagattaa caaagaattc
      121 tagcatttat taactcctct taattttctc tgtttttca taagacaatt tgtagtgttg
      181 ggctgatgtt ttaaaagttt aaatctattt acaaaatcaa tagttctttt actcagtgca
      241 tcatttaatc ctaccctact aatatcatta tccaatgtta tttctttact atcaaaacaa
      301 gtatttataa gagaaataca atatttaggt tctattttaa ctattttatt ttgttcaaaa
      361 cgagcttgta tagcacaagc ataagctgtg tttgtatttt taggttttac aatattttcc
      421 cctttactat ttttcataac aatatcttgc tttaatttat caccaaaagt ataaatatta
      481 ttcttttcat cttgctctat atttttccaa acatattaca acatcgcata actagcatct
      541 gcacaattag catagtctaa aaatttagtg attaagtcta atttagcttc ttgtgtttta
      601 atgtttttac tcatttgtta ttctaaaaat ctaaatctca aattatcttt ctaattttt
      661 atctaacatc ttcacaatac agtcttttat gatatctaaa atagaatcca gcaccctcat
      721 cacctcccaa aaatatacca taatcattat aaatataaga taagtgtgtt gaataatgaa
      781 taccatcata acaatcttca aatgtaactt ctgttaaagt aaatttattt ttttgcaaca
      841 cattaatgct ttctgatttt ttaaaatcaa aatatatttt tttatttatt ttttgattaa
      901 aaaagaattc tcctttttca tcatgcattg tatttccttt ttctctattg ctaaatattt
      961 cccaataagc tttattgtaa attattactt tattatctat atctttacac aaactcctaa
     1021 actcataata ctgcggatcc atatatttat aagaacatcc tcctactaag aataataaaa
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     1141 ttgttttatt ttttaattta taaaaaattt taaagataaa atataaaata atagaaaata
     1201 taaaaacaaa aaagaaaaat ataagaataa atattaaaag attaacaaag aattctagca
     1261 tttattaact cctcttaatt ttatctgttt ttttcataag acaatttgta gtgttgggct
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     1801 ccagcaccct catcgccttc taaaaatata ctataattat aatacaaata tcgtttaaat
     1861 tcttgatact taatgttatt tttatcatca atataccaag cttctatttc tttttctttt
     1921 acttttccta ttccaagttt aatttc
//
LOCUS       DMACINML_30             1741 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..1741
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(1357..1692)
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     CDS             complement(1357..1692)
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                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:EAQ72691.1"
                     /codon_start=1
                     /transl_table=11
                     /product="flagellin B"
                     /protein_id="Prokka:DMACINML_01837"
                     /translation="MKATALGSTDKTAGVTTLKGAMAVMDVAETAITNLDTIRADLGS
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                     QQNVLRLLQ"
ORIGIN
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       61 atagcatcag caatttgagc tgaaatttgt cccttagttt ctcttaaaga tactgaagat
      121 tgagaaatta tttgacctgt tccaaaacct actgctgaaa gtccagttcc tgaaatcgtt
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      241 aaaataccca tacttggagt aaagccactg actttaatac ctctaccctc tcttgaagta
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      481 acagtttgca cattaaaact agctctaacg cctgttttat cagcatattt attgatctct
      541 tcagccaaag ctccaagtcc tgttcctact gaagtagaaa taacaacgct ttgaaatgta
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      841 aaacgattga tatctgcttg aagcatagtt cttgttttta aactttgtcc atcttgagct
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     1141 actgaatttg catgtgcgtt taacgcaccg atgttggtgt ttattctaaa acccatttta
     1201 aatcctttca aaatattgca tcaaaaggac taaagcaaga agtgttccaa gttttgtttg
     1261 tgatttgatt tttaaataaa aaagctcggt atttctaccg agcttggatt tgtataaatt
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     1621 cacagccata gcacctttta gagttgtaac ccctgcagtt ttatccgttg aacctagcgc
     1681 agtagctttc atttgagcaa attgagattg tcctgatcca gcagaaaaac cactgccttc
     1741 a
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LOCUS       DMACINML_31             1671 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..1671
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(465..1109)
                     /locus_tag="DMACINML_01838"
     CDS             complement(465..1109)
                     /locus_tag="DMACINML_01838"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG87616.1"
                     /note="Domain of uncharacterised function (DUF1910)"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01838"
                     /translation="MVRDTSKDEAYFTKEIIESEEDIKESEKILLELPFGQRETCLFC
                     IEDRKFHLAMDKYSRGDDIDIVKKDLEAYILEKEKNRLEKGLDISWFDGNALELCVRV
                     LLDMDTACVLELIEEDERKRRDILNRDWFLHFIGSKGKNLNLERKCIRKEHELIKEFV
                     ATKDIEFLHQYMKKHTRLRDPLDTWDLEGAAIVKLMNLDKEEFKSYKYFPYDLI"
     gene            complement(1113..1493)
                     /locus_tag="DMACINML_01839"
     CDS             complement(1113..1493)
                     /locus_tag="DMACINML_01839"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG87598.1"
                     /codon_start=1
                     /transl_table=11
                     /product="methyltransferase small"
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                     /protein_id="Prokka:DMACINML_01839"
                     /translation="MQMDKYYKAKGYKRISLNKVKGLDDKIHHEMDGIYYNPDKNPKY
                     IIAEAKFGTSKLDRKTKQMSDEWLIKNKLKQLKDNVGEKQAKEIKKLLNSNEVRKDLF
                     HVDEGGKETIDYLDKDANKIKPKG"
ORIGIN
        1 tccacctaat tctaaacgat ttttttgtct taatagcata agtgcttcta aatctttttt
       61 aactagattt atatcatcac cacgagagta tttatccata gcaatacatt tttttctatc
      121 tgttatagaa aaaaaataat tttcccttct tgcatctcct agtggaagtt ctaagagtct
      181 tttttcatct tctttgattt ttttttcaca ctctattata tgtttcgtaa aatacgcttc
      241 atctctctta gtatctctta gcatttttta tccttttttat taagtttttg gtttttgcat
      301 ttttatctaa ttctttaata ctcacattgc cttttttatc aacatgaaat aaatcttttc
      361 tgacttcatt gctatttttt ttaagaagat ttgctatttt ttctctatct tttttatcta
      421 caataccaag tctatttcta ctctcttctg ttatccaaat aagattaaat taaatcataa
      481 ggaaaatatt tatagctttt aaattcttct ttatctaaat tcattagttt tacaattgct
      541 gcaccttcaa gatcccaagt atctagagga tctcttaatc ttgtatgttt tttcatatat
      601 tgatgtaaaa actcaatatc cttagtagct acaaattctt taataagctc gtgttctttg
      661 cgaatacatt tgcgttctaa atttaagttt ttacccttag atcctataaa atgtaaaaac
      721 caatctctat tgagaatatc tcttcttttt ctctcatctt cttctattaa ttctaataca
      781 caagcagtat ccatatctag taatactcta acacaaagtt caagagcatt tccatcaaac
      841 cagctaatat ccaatccttt ttctaaacga ttttttttctt tttctagtat gtatgcttct
      901 aaatcttttt taactatgtc tatatcatca ccacgagagt atttatccat agcaagatga
      961 aatttctat cttctataca aaaaagacaa gtttctcttt gtccaaaagg aagctctaaa
     1021 agtatttttt cggattcttt gatatcttct tcactttcta ttatctcttt agtaaaatac
     1081 gcttcatctt tactagtatc ccttaccatt ttctatcctt tgggttttat tttatttgca
     1141 tctttatcta aataatcaat agtttcttta cctccttcat caacatgaaa taaatctttt
     1201 ctgacttcat tgctattaag aagttttttt atttctttgg cctgttttc tcctacatta
     1261 tctttaagct gttttagttt attctttatt aaccattcat cactcatttg cttagttttt
     1321 ctatctaatt tgcttgttcc aaacttagct tctgcgatga tatattttgg gtttttatct
     1381 ggattataat aaattccatc catttcatga tgaattttat catcaagccc tttgacttta
     1441 tttaaactaa ttcttttata gcctttagct ttgtaatatt tatccatttg catttcagca
     1501 taattacctt tttgctgatt attttttggg tttttaaacc cactataaga ttaaattaaa
     1561 tcataaggaa aatatttata gcttttaaat tcttctttat ctaaattcat tagttttaca
     1621 attgctgcac cttcaagatc ccaagtatct agaggatctc ttaatcttgt a
//
LOCUS       DMACINML_32             1526 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..1526
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(92..1366)
                     /locus_tag="DMACINML_01840"
     CDS             complement(92..1366)
                     /locus_tag="DMACINML_01840"
                     /inference="ab initio prediction:Prodigal:2.6"
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                     /inference="similar to AA sequence:RefSeq:ALW35763.1"
                     /codon_start=1
                     /transl_table=11
                     /product="mobilization protein"
                     /protein_id="Prokka:DMACINML_01840"
                     /translation="MPKVAASHCNPKKQPALNHNDRTNDNAKTITKELTHLNEYSCTS
                     DEVRKNIEKLYKKAYENFYKYCENKNGLAKSGKPKGLQNFTKKEKCYHEFIYEIGENT
                     TMEQCQELTQKIAELTGFTPLQVVIHRDEVSENAKGEKQTHYHAHAVFFTLDNNGLQL
                     ARREASLNKGNLSKIQTLTAESLKMERGANRYENNEKQPQYIQDYKIYAQFKEQEKAL
                     LQRIQEQEHQLAQMALELKEKEKEIQDKAKELKSKENELQAKIEQYQKHIQTLELGHE
                     KALKELTQEFENRLSLWKNILTFGKHNAKVREDYQLTKKAFLVSTDESRREANKELEY
                     LKFEYRKVRDDRDNLRTLFETQKKKNDDLETRIKEIGKWCEKNLSVEQLKEIFPLKAE
                     RIEKELKYQRAFENSFEQVKTKRNDRGLGLSR"
ORIGIN
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       61 gtgcgatttg ctaaagcacc aaaaaagaaa attatctact aagccctaac cctctatcgt
      121 ttcttttagt ttttacttgt tcaaaagaat tttcaaaagc tctttgatat ttaagttctt
      181 tttctattct ttcagctttt aatggaaata tttcttttaa ttgctccacg ctcaaatttt
      241 tttcgcacca cttgcctatt tcttttatcc gagtttctaa atcatcattt ttcttttttt
      301 gtgtttcaaa caaagttctt aaattatctc tatcatctct gactttacga tattcaaatt
      361 ttaaatattc aagctcttta ttagcttctc tcctgctttc atctgtgctt actaaaaaag
      421 ctttttagt aagctgatag tcttctctta ctttagcatt gtgttttcca aaagttagaa
      481 tatttttcca taggcttagg cgattttcaa attcttgcgt aagttccttt aaggcttttt
      541 catgtcctag ctctaaagtt tgtatatgtt tttgatattg ctctattttt gcttgcaatt
      601 cgttttcttt cgattttagc tctttagcct tgtcttgtat ctctttttct ttttctttca
      661 attctagagc catctgtgct aattggtgtt cttgttcttg tattctttga agtaatgctt
      721 tttcttgttc tttaaattga gcataaattt tataatcttg tatatattgg ggttgctttt
      781 cgttattctc atagcgatta gctccacgct ccatttttaa actttctgca gttagggttt
      841 gaattttgct aagattgcct ttattcaaac ttgcttcacg cctagcaagc tgtaagccat
      901 tgttatcgag tgtaaaaaat accgcgtggg cgtgataatg ggtttgtttt tcccctttag
      961 cattctcgct tacttcatct ctatggatta caacttgtaa aggtgtaaat cctgtaagct
     1021 ctgcaatttt ttgcgtaagc tcttgacatt gttccattgt agtattttcg ccgatttcgt
     1081 atataaactc gtgatagcat ttttcttttt tagtaaaatt ttgaagtcct ttaggctttc
     1141 cgcttttagc taaaccattc ttattttcac aatatttata aaaattttca taagcttttt
     1201 tataaagctt ttctatgttc ttacgcactt catcgctagt gcaagaatat tcatttaaat
     1261 gcgtgagttc tttggtgatg gttttagcat tatcgttagt tctatcattg tgatttaacg
     1321 cgggttgttt tttaggattg caatgagagg cagcaacttt tggcattttt aaattctcct
     1381 tttggtgttt aaaaatgact aggcaaaaat caaaaaatct tttattgatt ttaattgatt
     1441 tttgctaggg agttaagggg tttaacccct tacaagctcg atacttggca caagtggcgg
     1501 atagcttgta tccttcaata atataa
//
LOCUS       DMACINML_33             1369 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..1369
                     /organism="Campylobacter species"
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                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            31..810
                     /locus_tag="DMACINML_01841"
     CDS             31..810
                     /locus_tag="DMACINML_01841"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG88098.1"
                     /note="Uncharacterized protein conserved in bacteria%2C
                     putative lipoprotein"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01841"
                     /translation="MLAISANAQSPKEAKPSFDCAKATTKVEKIICNDKSGELQKLDR
                     LYSKLYFSILKSIPKNTKEGQETKKQMQKFAKNFIDYRDNMRCFLLAKNDDEKEVEEV
                     FNKGRENGIMYENLDSVHFGFKPHHYKPCIARVYKMGILLLSTNTIIDTSFLIDKDTF
                     YTCKSNMILDIFSIKGLAKFRFYNKLFPQGYKETIIEASKALQELSSNGRYTQVCAFE
                     DEGFICTNGGCEFDLDEMQTRVIQPLDNFIQNIDFRKLNAN"
ORIGIN
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       61 ccaaaagaag ctaaacctag ctttgattgt gctaaggcaa ctacaaaagt tgaaaagata
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      181 ttttcaatac taaagagtat cccaaaaaac acaaaagagg ggcaagagac aaaaaaacaa
      241 atgcaaaaat ttgctaaaaa ttttatagat tatagagaca atatgcgttg ttttttattg
      301 gcaaaaaatg atgatgaaaa agaagtggaa gaagtattta acaaaggacg cgaaaatgga
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      421 tgtatagcaa gagtttataa aatgggaatt ttattgctta gcaccaatac tatcatagat
      481 acaagttttc tcatagacaa agatactttt tatacttgca agagcaatat gatactcgat
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      601 tataaagaaa ccattataga agcctccaaa gcattacagg aattaagctc aaatggtcgc
      661 tatactcaag tatgtgcgtt tgaagatgag ggatttatat gcacaaatgg agggtgtgag
      721 tttgatttag atgaaatgca aactagagtt attcagccac ttgataattt tattcaaaat
      781 atagatttta ggaaactaaa tgccaattaa gacaacaaat ttaagctatg aggaatttaa
      841 aagcttacaa ataaataaaa ttaatttcta tttaaaggag gtgttcttat gcaaaagttt
      901 ttaatagctt taggattgtg tttaatgtta gccattagtg ctaatgcaca atctctaaaa
      961 gaagctaaac ctagctttga ttgtgctaaa gcaagtacaa aagtagaaaa gatgatttgt
     1021 aatgataaaa gtggggagtt acaaaaactt gatagatata tggcaaagac atataaagaa
     1081 ctaagacaga atctaaacaa aaatgagcaa aataagcttt taacatcgca acgattatgg
     1141 cttcaaaccc taaatcaatg caaatctaaa gaatgtgtaa aagagctttt gcaaaataga
     1201 gttggagaat tgcaaaatta cacagcacac acgggcaatg tgtggcttgg gacttataca
     1261 ttacaagaaa atctttatat ggggagcttt acaataaaaa agtgtgataa gtttaatatt
     1321 tgtgaagcta gatatgaggc tatcctaaat aaaagtgaat ttaatgata
//
LOCUS       DMACINML_34             1070 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
```

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FEATURES             Location/Qualifiers
     source          1..1070
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            197..577
                     /locus_tag="DMACINML_01842"
     CDS             197..577
                     /locus_tag="DMACINML_01842"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:ABS43317.1"
                     /codon_start=1
                     /transl_table=11
                     /product="repeat motif-containing gene"
                     /protein_id="Prokka:DMACINML_01842"
                     /translation="MQGNIVKDCYISEGVKALFAVYFKDQTEESFFKALNEFAKENQI
                     ASQKIRDKTSREIKEELSKLVTSDLLNAKFDKVETRIDKFETSLNAKLDSFRTEVKTY
                     VIILAVLMFILQPTIFDFIISIFK"
     gene            697..1011
                     /locus_tag="DMACINML_01843"
     CDS             697..1011
                     /locus_tag="DMACINML_01843"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG85792.1"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01843"
                     /translation="MQKNIQDCVVNVHSYDPNSPSGYKQDLFDISSEDFVREYEFVDS
                     SDLDDMVKHKQSDEVFKVFYKKDGKIRLLRISNMQALNHFDHLKGVMTKIILDSGFKP
                     DE"
ORIGIN
        1 actaattcct attatttttg aaggaaagat aggcaaagat gcaataaact tttaaagaga
       61 aataggctgt catactttca aacataatag aatagcaaga atagtattag tggatatttg
      121 cataataaaa aaatgaaatt tttaaagaat tgaaatacta tatgcagtaa ttatgatata
      181 atgaaagaga aatacaatgc aaggtaatat agtgaaagat tgttatattt cagaaggtgt
      241 aaaagcttta tttgctgttt attttaaaga tcaaactgag gaaagtttct ttaaagctct
      301 taatgagttt gctaaagaaa atcaaatagc atctcaaaag ataagagata aaacctctag
      361 agaaattaaa gaagagcttt caaaattagt aacttcagat cttttaaatg ctaaatttga
      421 taaggttgaa actagaatcg ataagtttga aacctcattg aatgctaagc tagatagttt
      481 tagaacggaa gttaaaacat atgtaattat tcttgctgtt ttaatgttta ttttacagcc
      541 tacaattttt gattttatta tatctatttt taaataattt tttaaagaag caaggatttt
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      661 aaaaataaaa atttgtatta ttttaaagga tttaacatgc aaaaaaatat acaagactgt
      721 gtggttaatg ttcattctta tgatccaaat tcaccaagcg gttataagca agatttgttt
      781 gatatttcaa gtgaagattt tgttagagaa tatgaatttg tagatagttc tgatttggat
      841 gatatggtaa aacacaaaca aagtgatgaa gtttttaaag tgttttataa aaaagatggg
      901 aaaataagac ttcttagaat tagtaatatg caggctttaa atcattttga tcatcttaag
      961 ggtgtaatga caaaaataat tttagatagt ggttttaagc ctgatgaata gaaaagatta
     1021 atatgcgtaa agatcaagaa tatgcagaag aaaggtttta tgggcaaaaa
//
LOCUS       DMACINML_35              971 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
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VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..971
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            206..916
                     /locus_tag="DMACINML_01844"
     CDS             206..916
                     /locus_tag="DMACINML_01844"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:EAQ72616.1"
                     /codon_start=1
                     /transl_table=11
                     /product="methyl-accepting chemotaxis protein"
                     /protein_id="Prokka:DMACINML_01844"
                     /translation="MNAIHKIFEEYKSLDFRNKLDNASGNVEITTNALGDEIVKMLKQ
                     SSDFANHLASESSKLQSAVQNLTSSSNSQAASLEETAAALEEITSSMQNVSVKTSDVI
                     TQSEEIKNVTGIIGDIADQINLLALNAAIEAARAGEHGRGFAVVADEVRKLAERTQKS
                     LSEIEANTNLLVQSINDMAESIKEQTAGITQINESVAQIDQTTKDNVEIANESAIISN
                     TVSDIANNILEDVKKKRF"
ORIGIN
        1 catcaacgaa aacatccttg ctactaaaca aggtttagaa caagatgcta aagcagtaaa
       61 agaaagtgtt gaaaccgtag gagtagtaga aagtggtaat cttactgcaa gaattacagc
      121 taatcctaga aatccacaat taatagaact taaaaatgtt cttaatagac ttttagatgt
      181 tttacaaact aaagtaggat cagatatgaa tgctattcat aagatctttg aagaatataa
      241 atctttagac tttagaaata aacttgataa tgctagtggt aatgttgaaa tcactaccaa
      301 tgctttagga gatgaaatcg ttaagatgtt aaaacaaagt tctgactttg ctaatcactt
      361 agccagtgaa agttctaaac ttcaaagtgc agttcaaaac cttacttcat cttctaattc
      421 tcaagcagct tctttggaag aaacagctgc tgctttagaa gagattactt cttctatgca
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      661 gctagctgaa agaactcaaa agtctttatc tgaaatagaa gctaatacta atttattggt
      721 tcaatctatc aatgatatgg cagaatctat taaagagcaa actgcaggta ttactcaaat
      781 caatgagagt gtagctcaaa ttgatcaaac tactaaggat aatgtagaga ttgctaatga
      841 gtctgctatt atttctaata ctgtaagtga tatagctaat aatatacttg aagatgtgaa
      901 aaagaaaagg ttttaattag agactgatat ataaaattta gattgatatg cgagtatcaa
      961 tctaaagatt t
//
LOCUS       DMACINML_36              851 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
```

```
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..851
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            37..363
                     /locus_tag="DMACINML_01845"
     CDS             37..363
                     /locus_tag="DMACINML_01845"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01845"
                     /translation="MGSFTIKKCDKFNICEARYEAILNKSEFNDMHECDITLKLQIKS
                     QQEAIALNDDKDFANCKIYIRKNQQGIVFIRDEKVFNSPDYFCSTMCGNQTIFEWGDI
                     YKKEMQ"
ORIGIN
        1 tggcttggga cttatacatt acaagaaaat ctttatatgg ggagctttac aataaaaaag
       61 tgtgataagt ttaatatttg tgaagctaga tatgaggcta tcctaaataa aagtgaattt
      121 aatgatatgc acgaatgcga tataactttg aaattacaga taaaatctca acaagaagct
      181 atagctttaa atgatgataa ggattttgca aattgtaaaa tttatattag gaaaaatcaa
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      301 acaatgtgtg gcaaccaaac gatatttgag tggggagata tctataaaaa ggaaatgcaa
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      481 atgtaactat tggatatgga cttgatttaa agacaggaaa taatccaaag ttacttttag
      541 aagggtattt accagatgat tctaaaaaac ttaaaatagg agatgaagaa ttaacttttt
      601 atgaaattat agagaaatat agagccaata aggcaggttt tacagaccca aagatagtaa
      661 aaggttattt acaaaataaa gtgtttaatt tttcgcttac gcaagaacaa gcccaagaaa
      721 ttttggaaag aacctttgat tcatataaaa agtatatatc acaatatatt ggcgataact
      781 tgttggaata tagtcaagaa aaagcttcct tggtttcttt acattatcat ggcagattta
      841 ataatatcaa a
//
LOCUS       DMACINML_37              794 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..794
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            36..503
                     /locus_tag="DMACINML_01846"
     CDS             36..503
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                     /locus_tag="DMACINML_01846"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01846"
                     /translation="MIIWNMTFGWGWFVPYSLQPSYHEFKEMCKLNELPNDEHKYNKI
                     LSYFGLSLDTLDWENIKKNSTLLTQGYLEYNSQNDRYMYRYENKSDPRIRKVFFLFFN
                     DSIKLSNLYKIDFEVFWNDKRDYIHTKVTSYDTVIEENFRTCGYFSGYLKGIK"
ORIGIN
        1 ttctaaaaat atcaagtttt attctacttc ctttgatgat tatatggaat atgacatttg
       61 gttgggggtg gtttgtgcct tatagcctac aaccgagtta tcacgaattt aaagagatgt
      121 gtaagcttaa tgaacttcca aatgatgaac acaaatataa taagattcta agttattttg
      181 gattaagttt ggatacattg gattgggaaa atattaaaaa aaattcaaca ttattaacac
      241 aaggttattt agaatataat tcacaaaatg atagatatat gtatcgatat gaaaataaaa
      301 gtgatccaag aataagaaaa gtttttttct tattttttaa tgacagtata aagctaagca
      361 atctttataa aatagatttt gaagtatttt ggaatgataa aagagattat attcatacaa
      421 aagtaacttc ttatgatact gtaatagaag agaactttag aacttgtgga tattttagtg
      481 gatacttgaa aggaatcaaa taatgcacca taaacagcaa atacaaaagt ttagagataa
      541 cgcagaatta gcttgggcaa gttatggtta ttttgacttt atagacaagc aatatagctt
      601 tgatgaaaag gataaaaatg aatttaaaac tttatatgca aaaataaatg atatagatga
      661 aagtaacgaa aaagtgcaaa atgccaaagc tacctacacc gacattctca atatggaata
      721 taattcctta tttgatggcg acttctcccc actccaagct aaacaattct tttctcgcta
      781 tgatttatta aaac
//
LOCUS       DMACINML_38              783 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..783
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            121..564
                     /locus_tag="DMACINML_01847"
     CDS             121..564
                     /locus_tag="DMACINML_01847"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:AVS37499.1"
                     /codon_start=1
                     /transl_table=11
                     /product="ankyrin repeat domain-containing protein"
                     /protein_id="Prokka:DMACINML_01847"
                     /translation="MHEWILCGEEVKYLEEALKLGANPNMRSIKTENKSSFTNAGETL
                     LHQAAESDEKPIGACVEVLIKYGADVNAVNCGINKIEDGKISYYKPATPLDRANTYDI
                     SKNIKILKKAGAKTWKELVEEYNIDTSLERIEQIKMYEERRKDKK"
ORIGIN
```

```
        1 ggatacaatg cactcagtag atatatcgat agagatggaa aaaataaaga agtaatagag
       61 tattttttta aaaaaggatg cacatttgaa acttataatg aagaaagtgg cgatactcct
      121 ttgcatgaat ggatactatg tggcgaagaa gtgaagtatt tagaagaagc tttaaaacta
      181 ggagcaaatc ctaatatgag aagtattaaa acagaaaata aatcaagttt tactaatgca
      241 ggagaaaccc ttttacatca agctgcagaa tctgatgaga aacctatagg agcttgcgtg
      301 gaagtgctaa tcaaatatgg agctgatgtg aatgcagtta attgcggtat aaacaagatt
      361 gaagatggaa aaatcagcta ttataaacct gcaaccccat tggatagagc caacacctat
      421 gatataagca aaaatataaa aatcttaaaa aaagcaggag ctaagacttg gaaagaattg
      481 gttgaagaat acaatatcga tacaagctta gaaagaatag aacaaattaa aatgtatgaa
      541 gaaagaagaa aagataaaaa ataaaaggaa aaattatgga ttttaacaca gatattttag
      601 aaagcttaga taatttcaaa gcatttttag acacaaaacc tagcaaagaa cttttaaagg
      661 cagtaaaaaa ttatatagat gattttatgg aaggtgcgta tgataattta gatccagaaa
      721 actatgaagt tgcttttgaa gaagatactg gcatacctta tgatgaagca gatgaggatg
      781 aat
//
LOCUS       DMACINML_39              758 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..758
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            91..486
                     /locus_tag="DMACINML_01848"
     CDS             91..486
                     /locus_tag="DMACINML_01848"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01848"
                     /translation="MFLLPVYLLLFLAGGCSYKYMDPQYYEFRSLCYFNLGKVLIEDE
                     SIKNKTNIIVTPKSKQIKDRIVETRFERKNENQVVYYRINTYFYDNYGIFLKGDEGAG
                     LYFRYMEVLSCKNIDKKFKKDDWQVETLE"
     gene            490..630
                     /locus_tag="DMACINML_01849"
     CDS             490..630
                     /locus_tag="DMACINML_01849"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01849"
                     /translation="MSKNIKTQEAKLDLITKFLDYANIADASYAMLHLIDENDEKGFL
                     KG"
ORIGIN
```

```
        1 attattttat attttatctt taaaattttt tataaattaa aaaataaaac aaaaactata
       61 aattttaaaa caatatttaa aaaatttact ttgtttcttt tacctgtata tcttttatta
      121 ttcttagcag gaggatgttc ttataaatat atggatccgc agtattatga gtttaggagc
      181 ttgtgttatt ttaatttggg aaaagtgttg attgaggatg aatctataaa gaataaaacg
      241 aatataatag taacacctaa aagtaagcaa ataaaagata ggatagtgga aactagattt
      301 gaaagaaaaa atgaaaacca agtagtgtat tatcgtatta atacatattt ttatgataat
      361 tatggtatat tcttgaaagg cgatgagggt gctggattat attttagata tatggaagta
      421 ttaagttgta agaatattga caaaaaattt aagaaagatg actggcaagt tgaaactttg
      481 gaataacaaa tgagcaaaaa cattaaaaca caagaagcta aattagactt aatcactaaa
      541 tttttagact atgctaatat agctgatgca agttatgcga tgttgcattt aatcgatgag
      601 aatgatgaaa aaggtttttt aaaaggataa taatgctaga attctttgtt aatcttttaa
      661 tatttattct tatatttttc tttttgtttt ttatattttc tattatttta tattttatct
      721 ttaaagtctt ttttaaaata aaaaataaaa caaaaact
//
LOCUS       DMACINML_40              714 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..714
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gaatttaaag attggcaaag catatattta aaagatccca ttaaaggaag catagctcct
       61 tggactaaag cagaaaaagc ttattataaa tctttaaaaa ccaaaagaga aagatataaa
      121 tatctagtga ttagaagtgg tataagaagc actgttatag atataccctа tgatgcttat
      181 tgtaatgtag atgaaaaagg atatttaatc aatgaagaat acgcctatat ttatgatgaa
      241 gttaacaata ataaagaaac cctaaaatct tctcttttta gacaagaatg gggtatagca
      301 gcaggaatac taggaaaacc tgaatatttt gtgcgttcta aaaatcatgg ctttaatgcc
      361 agaatgatac aatgttttat tttatatatt caactcacag gtggaggata tgaagaatta
      421 ggtataaaaa gaggaattta taattatgct gataatcttt tagaaatagg tataggtatg
      481 gcagggatac ataaaaatcc tttaagggct aaattagtaa aagatttagc taaaactata
      541 cagcctgatg aatttggtat gctacctttt atagatgaga ttatgggagt agattgggtg
      601 attgatttaa ataaatatga ttttgcctat gatgaagaag gtagaatcat ttgggcttta
      661 tataatgata ttgaaaaagg taaattaaaa gatccaagag atgtggattc tact
//
LOCUS       DMACINML_41              641 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
```

```
     source          1..641
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(154..510)
                     /locus_tag="DMACINML_01850"
     CDS             complement(154..510)
                     /locus_tag="DMACINML_01850"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:APB39663.1"
                     /codon_start=1
                     /transl_table=11
                     /product="VgrG protein"
                     /protein_id="Prokka:DMACINML_01850"
                     /translation="MKGNKKEVVEGKLELHVNKGINYFTEEHFSMQTNNYIDIYTEQN
                     LSTQTKKQHTELAESKYSDFQTDCEVKAGNQILHQVGDTQIVTKKDCVIIKAGGVEVI
                     IDSNGLVVRGGELKAE"
ORIGIN
        1 tacatattat cttttcaact tttgtagttg ccttagcaca atcaaagcta ggtttagctt
       61 cttttgggga ttgtgcatta gcactaatgg ctaacattaa acacaatcct aaaactatta
      121 aaaacttttg cataagaact cctttaattt attttactct gccttaagct ctccacctct
      181 aaccacaagt ccattagagt ctataatcac ttctactcca cctgctttaa tgataacaca
      241 atctttctta gtaacaattt gagtatcacc tacttgatgg aggatttgat tgcctgcttt
      301 tacttcacaa tctgtttgaa agtcactata tttagattct gcaagttctg tatgttgttt
      361 tttggtttgc gtgcttaaat tttgttctgt gtatatatca atgtaattgt tagtttgcat
      421 actaaaatgt tcttccgtaa agtaatttat tcctttatta acatgaagct caagttttcc
      481 ctcaaccacc tcctttttat ttcccttcac atttcttatc tcatctttat ggataatagt
      541 attttgattt gcacctattt ctatatcttt gttttctcct acaaactcat gagagttttt
      601 agctattctt actttattat ctactcctac atttaaagta t
//
LOCUS       DMACINML_42              578 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..578
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            27..179
                     /locus_tag="DMACINML_01851"
     CDS             27..179
                     /locus_tag="DMACINML_01851"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG86653.1"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
```

```
                     /protein_id="Prokka:DMACINML_01851"
                     /translation="MYNINCFRTQKGTKYLNEILAPKFYNKYKDLEVEIDDKGNVLRW
                     IGEINR"
ORIGIN
        1 tttgggggaa tttggataat tgggatatgt ataatatcaa ttgctttcgc actcaaaaag
       61 gcacaaaata tctcaatgaa atcttagctc ctaaatttta taacaaatac aaagatttag
      121 aagtagagat tgatgataag ggtaatgtgc ttaggtggat tggagagatt aatagatgag
      181 tttatttgga ttttacattg gattttacaa aggataaata atgagcgaaa cttatgagat
      241 ttatacaccc aatgggttaa cattagatgt ggaaaaagat accaataaaa tactatttaa
      301 agaaaatatt aaacccacag gcaattatac tcaagaatat tccaaagcgg tttttgaatc
      361 ttattatatt atgaaaaact ccccctacaa agactataaa ccaatatatc tagatcctaa
      421 cttttataca ggagagaaat ccactctagt agaatttaaa gattggcaaa gcatatattt
      481 aaaagatccc attaaaggaa gcatagctcc ttggactaaa gcagaaaaag cttattataa
      541 atctttaaaa accaaaagag aaagatataa atatctag
//
LOCUS       DMACINML_43              572 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..572
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 aatgctagaa ttctttgtta atcttttaat atttattctt atatttttct tttttgtttt
       61 tatattttct attattttat attttatctt taaagtcttt tttaaaataa aaaataaaac
      121 aaaaactata aattttaaaa caatgtttaa aaaacttgct ttatttcttt tacctgtata
      181 tcttttatta ttcttagcag gaggatgttc ttataaatat atggatccgc aatattatga
      241 atttaagaag ttgtgtaaag ataatagtaa taaaatgata gtgtttaata aagattattt
      301 ggatttaaaa aaacaatttg ttcaagctat gacgaataat tctaatatta gaattaaaaa
      361 taatggtata aaatattttt ataatgaaaa attgaatttg gaaattcaac cttcaaattg
      421 gaaagaaata gaaactaaat cacgcgaaat taaacttgga ataggaaaag taaaagaaaa
      481 agaaatagaa gcttggtata ttgatgataa aaataacatt aagtatcaag aatttaaacg
      541 atatttgtat tataattata gtatattttt ag
//
LOCUS       DMACINML_44              564 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..564
```

```
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(129..554)
                     /locus_tag="DMACINML_01852"
     CDS             complement(129..554)
                     /locus_tag="DMACINML_01852"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG86435.1"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01852"
                     /translation="MQIPIYSKLKAKLESKGIDNISSGQIAWFVCSVGIFIIPMIYFY
                     ISNNYDQFTILFIMIFIFILNMFYTKNFFALLLLVILIFIYIKYHEFIYNFKILFFIF
                     APIILIFLRAWRILITFLCGYIFLVAMVYIFELLGGFYK"
ORIGIN
        1 atcaggactt ttgcctttgg caagtcctaa aaaggcatgg gtgaaatctt ctctttgcca
       61 ataacactga tttttaaaat ccaaaaaaca ttctaccaat ggatcaatat aaattgttac
      121 ataatatttc atttataaaa tcctcctaat aactcaaata tatataccat agccactaaa
      181 aaaatatatc cgcataaaaa agttattaga attctccaag cccttaaaaa gataagaatt
      241 ataggtgcaa aaataaaaaa taaaatttta aaattataga taaactcatg atattttata
      301 tatataaata tcaatattac aagtaataat aatgcaaaaa aatttttagt ataaaacata
      361 tttaatataa aaataaatat cataataaat aaaatagtga attgatcata attgttgctg
      421 atataaaaat atatcatagg aatgataaaa atacccacgc tacacacaaa ccaagcaatt
      481 tgcccacttg atatattgtc tattcctttg ctttctagtt ttgctttgag tttagaataa
      541 ataggaattt gcaaatttac tcct
//
LOCUS       DMACINML_45               563 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..563
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            137..511
                     /locus_tag="DMACINML_01853"
     CDS             137..511
                     /locus_tag="DMACINML_01853"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01853"
                     /translation="MTMQIIQDQIPQELSGRMTKQSLERLANHLHIATQNEMGDIPLW
                     LLWDLAITCKQLDLKENYQKVLIEIQMNLETQHKANLAEQRADLAEQRAEKAEQRAEK
```

```
                     AEQLYQQIKNFRISMMKKYQTN"
ORIGIN
        1 gagatgagta tgagaattta aactttggaa atcatatgca ctttaatgct aaaaatcaag
       61 agcagttttt taaaatgatt gaaaccttta gaaaaggtat cagataagcg aaaaagacaa
      121 aaacaggaga aagaaaatga caatgcaaat aatacaagat caaattccac aggaattgtc
      181 agggagaatg acaaaacaga gcctagagag attagcaaat catcttcaca tagcgaccca
      241 aaacgaaatg ggggatattc cactatggct actttgggac ttagcgataa cttgcaaaca
      301 attagattta aaagagaatt atcagaaagt cttaatagaa atacagatga acctagaaac
      361 acagcacaaa gcaaacttag cagagcagag agcagactta gcagagcaga gagcagagaa
      421 agcagagcag agagcagaga aagcggagca attatatcag caaataaaga atttcagaat
      481 atcaatgatg aaaaaatatc aaacaaatta aataaagaag aaagcaagga atttaatatc
      541 cccgctctaa gacggggcaa cct
//
LOCUS       DMACINML_46              559 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..559
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gatacttggg atcttgaagg tgcagcaatt gtaaaactaa tgaatttaga taaagaagaa
       61 tttaaaagct ataaatattt tccttatgat ttaatttaat cttatttgga taacagaaaa
      121 gagtagagat agacttggca ttgtagataa aaaagatagg gaaaaaatag aagaacttct
      181 tgaaaaaaat agcaatgaag tcagaaaaga tttatttcat gttgatgaag gaggtaaaga
      241 aactattgat tatttagata aagatgcaaa taaaataaaa cccaaaggat aaaaaatgct
      301 aagagatact aagagagatg aagcgtattt tacgaaacat ataatagagt gtgaagaaga
      361 aattaaagaa gatgaaaaaa tacttttaga gcttcctttt ggaaaaagag aaacttgtct
      421 tttttgtata gtagatagaa aaaaatgtat tgctatggat aaatactctc gtggtgatga
      481 tataaatcta gttaaaaaag atttagaagc acttatgcta ttaagacaaa aaaatcgttt
      541 agaattaggt ggatttgat
//
LOCUS       DMACINML_47              541 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..541
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
```

```
                     /strain="strain"
ORIGIN
        1 ttttttgatt ttgcggcatt taaatcaaca tcgccttttg cattaattgt tatgcgatca
       61 ccttttgctt caactccatt taaaacaata tttccttttg tactttctat atttaaatta
      121 ccgccagcat tcattttaga aatattttca ctagaatttt cgcttttatc gtggttaaat
      181 tttaatccca cagtttgttt agaatcagca ctgataaggt tgctcgtaaa tagatttcca
      241 gcattagcta aaacttgaga agctactatt ccataattta tgcctagatt ttgtttctca
      301 gcagctgcat tttgtactga ctgattaata acagacgcta taggactacc tgcttcgata
      361 acctctttag cgtataaact aaatcctgtg ctattttctg tcttaacatc ttcatattta
      421 gaactagcaa tgtcccctgc tttaagatta atatctttat ctgcttcaaa attagcacca
      481 cctatatcca aggtattatt tgccttgata ttaatatttg cacctttgat ggtgttagaa
      541 g
//
LOCUS       DMACINML_48              502 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..502
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 aaaaatataa aaatcttaaa aaaagcagga gctaagactt gggaagaatt ggttgaagaa
       61 tacaatatcg atacaagctt agaagaacca gaacaaatta aaatgtatga agaaagaaga
      121 aaagataaaa aataaaagga aaaacaatga aaacattaga agaattaata gctttagaag
      181 aaaaatatct aaaagaatta tgtttagaat tttatgatct tgtagaggct aacaaacttg
      241 aagaagttaa agaattttta aaagactatc ctgtacctga aatattcttt gaaaaatgct
      301 ataaagcata ttatgattat aaagaaagag ctattatcga tactgctatc actttagctt
      361 gtgcaggact tgcttatgat aaaagtaaaa gttttgaaat gatggagtat tttgaaagcc
      421 taggacttaa agctgatgaa gtacactttg gatacaatgc actcagtaga tatatcgata
      481 gagatggaaa aaataaagaa gt
//
LOCUS       DMACINML_49              499 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..499
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
```

```
ORIGIN
        1 gatacttggg atcttgaagg tgcagcaatt gtaaaactaa tgaatttaga taaagaagaa
       61 tttaaaagct ataaatattt tccttatgat ttaatttaat cttatttgga taacagaaaa
      121 gagtagaaat agacttggca ttgtagataa aaaacatagg gaaaaaatag aagaacttct
      181 tgaaaaaaat agcaatgaag tcagaaaaga tttatttcat gttgataaaa aaggcaatgt
      241 gagtattaaa gaattagata aaaatgcaaa aaccaaaaac ttaatagaaa ggatagaaaa
      301 tggtaaggga tactaagaga gatgaagcgt attttacgaa acatataata gagtgtgaag
      361 aagatatcaa agaatccgaa aaaatacttt tagagcttcc ttttggaaaa agagaaactt
      421 gtcttttttg tataacagat agaaaaaaat gtattgctat ggataaatac tctcgtggtg
      481 atgatataaa tctagttaa
//
LOCUS       DMACINML_50              495 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..495
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 aattcttccc aagtcttagc tcctgctttt tttaagattt ttatattttt atttatatcg
       61 taagtattag cttcatccaa tggagtagca ggatcataat attcaatttt cccatcttca
      121 atatcacata taccacaatt aactgcattt acatcagctc catatttgat tagcacttcc
      181 acacaagctc ctataggctt ttctttactt cttgcagctc tatgcaaaag ggtttctcct
      241 gcaccactaa agctaaattt attttctgtt ttaattcttc tcatattagg atttgctcct
      301 aattttaaag cttcttctaa atacttcact tcttcgccac atagtatcca ttcatgcaaa
      361 ggagtgctgc cacttttttc attataagtt tcaaatgtgc atcctttttt aaaaaaatac
      421 tctattactt ctttattttt tccatctcta tcgatatatc tactgagtgc attgtatcca
      481 aagtgtactt catca
//
LOCUS       DMACINML_51              494 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..494
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 cctaatacaa attcaggttt ttctgctact ttatttggag aaaaaagaaa acaaattgat
```

```
       61 agtaaaacta aagaaaaaag ctataccagt gaatatggct atatcaatta tattttagct
      121 attagaggaa cagaaatgag ttcttttaaa gatttgcttg tagctgatgc ttctttagcc
      181 ataggctcta tacctaaagc ccaatatgat gatatgataa acttttatga aacttgtatt
      241 aaagattatc cacaaatcaa agaaaaagac tctcttacca ttacaggaca ctctcttgga
      301 ggctgtcttg cacaactctt tgctttaagt atctgtgatg ataagaatag aaacaatatc
      361 aaagctttat atacttataa tgcacctgga gctagaaaga taatacctcc ttatgattat
      421 atagtcaaac tctttatatt tcacagtaaa gaacaacaag aaagatttat aaaagaagaa
      481 atagaaaata tagc
//
LOCUS       DMACINML_52              474 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..474
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 cctaaagagt gtcccactaa agtaatttta tcaaagcaaa attctttttt tattagcgta
       61 taaaatttca ataaagaatt gcattgtttt ttaggaattt ttccatttag aagtataaaa
      121 tcactgatca aatctccaaa atcaaatttt aaaggtctta aatcacttcc tgcgatagct
      181 aaaataaatt cttgattttc cttgttttga aataagcttg ccctaaatcc accttttgat
      241 tcaagacatt ctttattaat gtgagcaagt aaatcaaatc tcttgataaa atcaaatgcc
      301 atcaaaggtt caaattttcc tattgtaacg cattcttttt gaaaaatatt atgggttaaa
      361 accttaaaca atgtttttct atctatattt aaaaaaattg ttgtatttaa attaagataa
      421 gcagcatgag aaagcaaagt gtaatgatat aaatgcatta gagcattttt attt
//
LOCUS       DMACINML_53              470 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..470
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gtgtatggag gcgtgtttta ccgtggaaga taaaaaaatg ccgggttaac gaacccggca
       61 ttatcatcac tcttcgctgg attgctcctg catttttgta ccgcttggct tgcggcgctt
      121 accgatattt tttgtatcgc ggtgacgttt cttcacgcgc ggcttctctt tttctttctc
      181 ttttttcttc tcggcgcgtt tcgccagcac ttttttcgac ggtttgccgg tcagcttttc
```

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      241 gctgggcgca cgcgtggtcg ggcgaagctc atcaatgacg cgcgctttta gcggctcttc
      301 gatgtagcgg ccgattttca gcagcaacag atggtcgtgg gcttctacca gcgagattgc
      361 agtgcctttg cggccagcac ggcctgtacg accaatgcga tgcagatagg tatcgccact
      421 gcgcggcatg tcgaagttaa tgacgtggct gacgtcagga atatcaatcc
//
LOCUS       DMACINML_54              462 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..462
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gcgctggctg gtcggatgtg ggttcctggt cctcactttg ggatatatcg aataaagatc
       61 atcagagaaa tgttttaaaa ggagatatct tcgcacatgc ttgtaatgat aattacattt
      121 attccgaaga tatgtttata agtgcgattg gtgtaagcaa tcttgtcatt gttcaaacaa
      181 cagacgcttt actggtggct aataaagata cagtacaaga tgttaaaaaa attgtcgatt
      241 atttaaaacg gaatgatagg aacgaatata aacatcatca agaagttttc cgcccctggg
      301 gaaaatataa tgtgattgat agcggcaaaa attacctcgt tcgatgtatc actgttaagc
      361 cgggtgagaa atttgtggcg cagatgcatc accaccgggc tgagcattgg atagtattat
      421 ccgggactgc tcgtgttaca aagggagagc agatttatat gg
//
LOCUS       DMACINML_55              461 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..461
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ggcttcaacc gtttcttttt cgatcagcat atcgatagca tcggtcaact gaatttcatc
       61 cccggcgccc ggaggggttt tcgccagcaa cgcccagata tccgcgctca acacataacg
      121 cccgacaatc gcaaggttag acggcgcgac atccgctttt ggtttttcaa ccacgccaac
      181 catcggcaca ctttcgcccg gtgccagctc aacgccttta caatcgacca cgccgtatgc
      241 agtcacatct tctactggct caaccataat ctggctattg ccggtttcat cgaaacggcg
      301 gagcatttca gccaggttat cctgagacag gtcggactca tattcgtcaa gaataacgtc
      361 tggcagaata acagcgacag gttcgtttcc gacaacggga tgcgcgcaca atacggcatg
      421 gcccaggcct tttgccagcc cttgacgtac ctgcataata g
```

```
//
LOCUS       DMACINML_56              454 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..454
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gacaagttat cattaaagtt gatgaggtcc ttgaacagga aaaacctgaa gccatgttag
       61 ttcttggtga tactaactcc tgtatttcag caataccagc gaagcgtcgg agaattccga
      121 tcttccatat ggaggctggg aatcgttgtt ttgatcaacg cgtaccggaa gaaactaaca
      181 gaaaaatagt tgaccacacc gctgatatca atatgacata tagtgatatc gcgcgtgaat
      241 atcttctggc tgaaggtgta ccagccgata gaattattaa aaccggtagc ccaatgtttg
      301 aagtactcac tcattatatg ccgcagattg atggttctga tgtactttct cgcctgaatt
      361 taagacccgg gaatttcttt gtggtaagtg ctcacagaga agaaaatgtc gataccccta
      421 aacagcttgc gaaactggcg aatatactta atac
//
LOCUS       DMACINML_57              449 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..449
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(209..442)
                     /gene="apbC"
                     /locus_tag="DMACINML_01854"
     CDS             complement(209..442)
                     /gene="apbC"
                     /locus_tag="DMACINML_01854"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:UniProtKB:Q8ZNN5"
                     /codon_start=1
                     /transl_table=11
                     /product="Iron-sulfur cluster carrier protein"
                     /protein_id="Prokka:DMACINML_01854"
                     /translation="MQRHLTQKLAEKYHTQLLGQMPLHISLREDLDRGTPTVVSRPES
```

```
                     EFTAIYRELADRVAAQLYWQGEVIPGEIAFRAV"
ORIGIN
        1 tcgatacctt aaaaccaatt gaaaaaataa atcagtagga taggtatgat caattcaaat
       61 aatgtttttg ccgattattt cagataaaca cctgtctgtt taagcaggaa ttaacaatgc
      121 gggggctatt attttattaa tacattcact gcatcaatat atattaatgc agtgaatgtc
      181 atattctctt tggaatacgt caggaggatt acaccgcgcg gaaggcgatt tcacccggaa
      241 tcacttcacc ctgccagtaa agctgtgccg caacgcgatc ggccagttcg cgatagatcg
      301 cggtaaattc gctctccgga cggctaacca ccgtcggcgt accacgatcg agatcttcgc
      361 gcagactaat atgcagcggc atctgaccca gaagctgagt atggtatttt tccgccagct
      421 tctgggtcag atgccgctgc atattagtc
//
LOCUS       DMACINML_58              443 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..443
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 agatagaaaa aaatgtattg ctatggataa atactctcgt ggtgatgata taaatctagt
       61 taaaaaagat ttagaagcac ttatgctatt aagacaaaaa aatcgtttag aattaggtgg
      121 atttgatact agcgattata gaggaaatgc tattgaactt tgtgttagag tattattaga
      181 tatggatagt gcttgtgtat tagaattaat agaagaagat gagagaaaga aaaaagatat
      241 ttttaataga gattggtttt tacattttat gggttctaag ggtaagaatt taaatttaga
      301 acgcaaatgt aattgtaaag aacacgagct tattaaagaa tttgtagcta ctaaggatat
      361 tgagttttta catcaatata tgaaaaaaca tacaagatta agagatcctc tagatacttg
      421 ggatcttgaa ggtgcagcaa ttg
//
LOCUS       DMACINML_59              442 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..442
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gcacaagcct tacagcctat acacatactg tcttctacta tcactatgcc ccattttacc
       61 ttcatggttg cacccgttgg acacgctttc aagcaagatg ggttagaaca gtgattgcat
```

```
      121 gatatagaag tgtagtaagc aaaagcattt tgctcatagc ttccatcgtt tttgcaagtc
      181 cagtttcctc cttcggtttc aaatacacgg cggaaattaa cccctacagg catatcttta
      241 taatccttgc aagataatga gcaggttcta caacctacac acttgctttg atctaacata
      301 aagccaaatt gtgaattttc ttctaatttc atattatctc cttaagcttt tgcgatttca
      361 accaagatag aatgttgtcc attccctttg gatatagcag ttggttctaa acttgcaagt
      421 gaatttacac aagttcctac at
//
LOCUS       DMACINML_60              440 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..440
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 tccctggatt gtcctgcctc tccgacgcga gaatacgcat agcctatgaa gccaattttt
       61 agccgtggcc cgtcgctaca gattcgcctt attctggcgg tgctggtggc gctcggcgtt
      121 atcattgccg acagccgcct ggggacgttc agtcaaatcc gaacgtacat ggacactgcc
      181 gtcagtcctt tctattttat ttcaaacggc cctcgtgaac tgctcgacag cgtgtcgcaa
      241 acgctggctt ctcgcgacca gcttgagctg gaaaatcggg cgctgcgcca ggaattactg
      301 ctaaaaaaca gcgacctgct gatgctgggg cagtacaacc aggggaacgc gcggttgcgc
      361 gagctgctgg ggtcgccgct gcgtcaggac gagcagaaaa tggtgactca ggttatttca
      421 acggttaacg atccttacag
//
LOCUS       DMACINML_61              439 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..439
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gcttaatccc ggctgcaggg ttttggtgta acgtccaaag cgctccaccg tccactggta
       61 cccctgcgga acgattttga cgcccgcgcc gacgatcacc agcgcgacga aaatgagaat
      121 agggataaga atgagcatag ctaaacctcc tgttgcgttg tccataaacc gattttgctg
      181 acgaattaag cgaattatac ctgattcagt aaagcatgtt cccccttat taattacagg
      241 gatacactat cgctataaaa atatgaacaa cggatgcgca ataaatgaca gaacgtagca
      301 tgttgcttga gttaaagcag gtcggttacc ggactgcgac gacaaaaata gtgaataaca
```

```
      361 tcagttttac gctgcaacgc ggcgaattta agttaattac cggtccttct ggctgcggaa
      421 aaagtacgtt gttgaaaat
//
LOCUS       DMACINML_62              437 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..437
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 attttcttta gtatttttaa gtgcatgtgc ttttaaagaa aaaaaagcaa gtgaaataga
       61 aactcttgca agtaattatg gtggaattta tatctttgat aaaaaaataa gagaagagat
      121 attggaatta gagaaaaaaa gagaagaatt tcgtagtaag tatttgggta gtgaaattaa
      181 agtaggaaat gaaactcatt ttgtgaattt ttcttatttg aagaaaaaat tcccccaaat
      241 cctttctaat ggttgtaact attatcgtag tgattataga tataaaggca aggctaattt
      301 tggtttcaaa gataaacccg aatttgcata ctatgaagat caatttaaag catatatggg
      361 tgaagaaaac tataaaaaat taagacctta tttaggtatg acaacttatt atgtgtgtga
      421 gggtagaaaa tatcctg
//
LOCUS       DMACINML_63              418 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..418
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ttaaaatctt caggcaatcc tgcagctttg ttaaaatcac ttcccatata accatcttta
       61 tctacactat aaccataggc tgtattagta gaagtattac ttatatctac ttgtttatat
      121 tttagagtat aaatagagtt tttaaattca cttgatatat cataattagg agaacttgtc
      181 ttactactta tactaaaatt agtattattg ctagtatttg ttgtattagt agaatttaat
      241 acttcacttc ttgctagagt ttgtgaattt gcattttgaa tttcatttaa tttactagca
      301 ttttgtttta aaaaagcatt agcaaaactt attttagaat tttctttact ttctttatta
      361 gcttttgctt gtgaaagtat agaaccatag tttgagttat cattgatgct aaagatac
//
LOCUS       DMACINML_64              418 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
```

```
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..418
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gtccggatta tcgtcggtac tgccaatcac gtaccacggt ttgacctcta ccagccagtt
       61 accgttttcg gccatcagac gggtatacag acggttccag ctacgcgagg tggggtccga
      121 acgtccgtta gagtcatggt tgtagcccat ctctacgtcg cgcagcgtcc agccggcaaa
      181 gcgataatcg gtagcaaaac caagaaaaag ctgcggttcg tagttggttt cgcgaaacgg
      241 cgaagactct ttactgttgg aaagctgcca ccaggatttc tgcgtatagg aagcgcccag
      301 taccgagttc ggccccagta ttccgcgcca cagcggaaac gccaggctca actgaaattt
      361 cacttcatct ttacgtgcgt tttcagacca gttgtaggta cttatggcct ctttgttc
//
LOCUS       DMACINML_65              417 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..417
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            22..276
                     /locus_tag="DMACINML_01855"
     CDS             22..276
                     /locus_tag="DMACINML_01855"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CAL35035.1"
                     /codon_start=1
                     /transl_table=11
                     /product="putative hydrolase"
                     /protein_id="Prokka:DMACINML_01855"
                     /translation="MDKVVFKEPVFIGDIISCYSKVISVGNTSIGVEVEVTAQRVDSQ
                     GCTSCINVTSALVTYVSVTRDGKKKPISEELKRIHGFLNT"
ORIGIN
        1 gaacgcgttg taactatatc tatggataaa gtagtcttta aagaacctgt tttatagga
       61 gatattattt cttgctattc taaagttata agcgtgggaa atacttctat aggtgtagag
      121 gtagaagtta ctgctcaaag agtggattct caaggctgta cctcttgcat caatgtaact
      181 tctgctttag ttacttatgt cagtgttaca agggatggaa agaaaaaacc tatcagtgaa
```

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      241 gaattaaaga gaattcacgg atttttaaat acctaaaagc ttatttttgt atggtaaaaa
      301 ctttaccctc ttaagctcat cagcatttat ttaaaccgcc gctgttgtat tttttatcta
      361 aacactcctt gaaaaattct cctcttgttt ttggggtttt ttcaggatgt ttttgct
//
LOCUS       DMACINML_66              408 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..408
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ggttttaaag gcgcgcgcga tgtgcgattt gcgatgtggg tatcgatgct ggggatgtgg
       61 ggctgtcgcg ttgtggcagg gtatacgcct ggtattgtgc tgggtatggg ggttgtaggg
      121 gtttggctgg ggatgtttct tgactgggcc gtgcgcggcg cgctgtttta ctggcgtctg
      181 gtaagcgggc gctggctgtg gagatacccg cgcgtaaaga gggagtaagc gctttttgct
      241 gtgaatatca tcaggaaacg gtgaatttta accgaagtgt ggaataaagc agcaaacgaa
      301 cttttttgt gaaaacaggc tttgacaagc caggggcacc tcgttaatat tcgccccgtt
      361 cacacgattc ctctgtagtt cagtcggtag aacggcggac tgttaatc
//
LOCUS       DMACINML_67              407 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..407
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 tttcaatact cagtattttt tcaatatatt ttgaactttt aagctattca tagcattttt
       61 caattgcagc atggctctga atttctgagc ctaacaacca aatttatact atgtttggca
      121 acaaagtggg atattttgac ctcacaaggt tgatctctga gatgattctt cccttcccta
      181 cacacagaca gtttatcttt tctttgctaa tggtttttga actgccagtg atgtatacag
      241 atagcatata gtaagcaaac tgatagcaaa cagacacaag aacaggacta agttcaatta
      301 tagaaataat tctccataat tgttcaagtt ttatatttga atagcaacca caaatatagg
      361 acaacaagag tatcaaatat aattacagaa aattatcata tcatggc
//
LOCUS       DMACINML_68              395 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
```

```
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..395
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gacaaaacct ttatcctaat ccaaacaaga tcttttgtaa catcctcgcc ttggattaaa
       61 atttttaatc cactttcact atttttatca tcttcattcg catgctttaa aaaataatga
      121 tccgtattca tacgatcaag aaaaaatact tttccatcat aaattcccct gcccttaagc
      181 tcaacttttg cttttctaaa atcaaaatcc agattatcaa aaatagcctg ctttttatca
      241 aaaatggcaa atttaagtcc ggtgctttga gcgatattac tagcgctttc attcatgggg
      301 ataaagcgag aattgaggat atttataatg atatttctat ggctctccct taaaggagaa
      361 ccttttgtaa cgactaattc ctcatataat ttttg
//
LOCUS       DMACINML_69              395 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..395
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gcggagtgga tacaaacaca gatcgctacc ttaccgagta taaaacaagt actagcaata
       61 caatcataag agtagaaagt gttgaaatag acaaatccaa agccggagtt gatggaaaag
      121 atggcatagg ttacggcact atagttcaag atttaaatgg cgggaatgaa ataattaact
      181 caaccaataa aggaaatgat gcaacaaatg gtaccaaagg taccgatgct catctttacg
      241 gtaatggtgg taatggtggt aatggtgaaa gctttatcat cagcggtatg gtaggcagtg
      301 aagatacaaa gatctacgat cttaaccaaa atatcaccat ttcagctaca ggtggaaaag
      361 gtgccaatgg tgctgatggt ggctatgctg atggc
//
LOCUS       DMACINML_70              393 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
```

```
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..393
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 cttttgctct ttggataaat tcaagtatta attttgcttg ttctgctttg atagctgcac
       61 cctgagaagt caccgaaggg ctagttaaag caagagtttc aagctcttta agctgagcat
      121 taataagatc tttttgagtt ttagcaacac tttttctaaa aacttgcaaa gcattcatat
      181 ctgattgtcc atttgctacg atcagccttg aaacatcctc tagtgtcgtt ccttttcgaa
      241 ctactaaagt tttaagcccg ctatgttctc cattgactat tctgctgata ttttgcgaaa
      301 tgtattcggg actaagctgc acttcatcac ccgtttttaa taaaacttta gaaaattgca
      361 ttttattata ggcacttact tcaagtctat gat
//
LOCUS       DMACINML_71              391 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..391
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ctatcaaaac aagtatttat aagagaaata caatatttag gttctatttt aactatttta
       61 ttttgttcaa aacgagcttg tatagcacaa gcataagctg tgtttgtatt tttaggtttt
      121 acaatatctt ctcctttact atttttcata acaatatctt gctttaattt atcaccaaaa
      181 gtataaatat tattcttttc atcttgctct atattttccc aaacatatta caacatcgca
      241 taactagcat ctgctatatt agcatagtct ttgatttgag agataagttc tttaggattc
      301 atcagtaact ttgtcctgta tatttttcat cactttttat aaatttacca ttagtaaaat
      361 aatgaaaaga tccccctcct gcacttttac g
//
LOCUS       DMACINML_72              374 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..374
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
```

```
                     /strain="strain"
ORIGIN
        1 atattatgta acaatttata ttgatccatt ggtagaatgt tttttggatt ttaaaaatca
       61 gtgttattgg caaagagaag atttcaccca tgcctttta ggacttgcca aaggcaaaag
      121 tcctgataag ttagataaat atagatgaag aatcaaaaca aaaatttctt aaaaacaaag
      181 aatgggacaa gatagatcaa aaatggtatg aagctaaagg gcctaatgaa ttcaatgatg
      241 gtttttaggg ttttggaact ggagtttttt taactccttc taaaatgcaa aagattgatt
      301 ttgaaattgc aaaaggttta gatgagtggc ttgataatga aaatgtgtgt tgctttaatg
      361 tttatactaa agat
//
LOCUS       DMACINML_73              364 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..364
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(239..315)
                     /locus_tag="DMACINML_01856"
     tRNA            complement(239..315)
                     /locus_tag="DMACINML_01856"
                     /product="tRNA-Ile"
                     /inference="COORDINATES: profile:Aragorn:1.2"
                     /note="tRNA-Ile(gat)"
ORIGIN
        1 gatataagta aaaccaaaga aaagataatt gggttttatc ctttaacaag tcctgtaaaa
       61 ttgtttttat taaaacttgc ttgtgactct taacaatgat aattataaag aacatttagg
      121 tttaaaacct aaaggaagta tatgatatat caaagtatat ttataaaata tatacttgct
      181 ttagatttta aaacttgatt tcaaatcttg tttttatctt ttaagattga tatttctatg
      241 gtgggcctaa caagacttga acttgtgacc tcacccttat caggggtgca ctctaaccag
      301 ctgagctata ggcccttaat aatggtggag aatagcggga tcgaaccgct gacctcctgc
      361 gtgc
//
LOCUS       DMACINML_74              362 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..362
                     /organism="Campylobacter species"
```

```
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 taatagtatt ttgatttgca cctatttcta tatctttgtt ttctcctaca aactcatgag
       61 agtttttagc tattcttact ttattatcta ctcctacatt taaagtattg cttaatccta
      121 ctatagtgtc tttagataaa cctacattag ttaagtattc tcctcccaca ttgacatttt
      181 tagctaagtc tatggtttga gtatgaacct ttttaatcct ttcattataa attccatcta
      241 ccctagaatc tttatcattt aaaattcttt gagtgaaatt atgctggact aattcatcat
      301 aatccttttg ggcttttaaa taaatttgtt ctttatcttt tatatttgag agggtaagtt
      361 ca
//
LOCUS       DMACINML_75              357 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..357
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 atgataaaag caaaagtttt gaaatgatgg agtattttga aagcctagga cttaaagccg
       61 atgaagtaca ctttggatac aatgcactca gtagatatat cgatagagat ggaaaaaata
      121 aagaagtaat agagtatttt tttaaaaaag gatgcacatt tgaaacttat aatgaagaaa
      181 gtggtagcac tcctttgcat gaatggatac tatgtggcga agaagtgaag tatttagaag
      241 aagctttaaa actaggagca aatcctaata tgagaagtat taaaacagaa aatgaattta
      301 gctttagtgg tgcaggagaa acccttttgc atagagctgc aggaagtaaa gaaaagc
//
LOCUS       DMACINML_76              348 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..348
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 tttagagctt ccttttggaa aaagagaaac ttgtcttttt tgtataacag atagaaaaaa
       61 atgtattgct atggataaat actctcgtgg tgatgatata aatctagtta aaaaagattt
      121 agaagcatac gtattattaa aacaagaaca tcgtttagaa gtaggaattg atattggtta
      181 ttatagagga aatgctcttg aactttgcat tagagtatta ttagatatgg atactgcttg
```

```
      241 tgtattagaa ttaatagaag aagatgagag aaaaagaaga gatattctca atagagattg
      301 gtttttacat tttataggat ctaagggtaa aaacttaaat ttagaacg
//
LOCUS       DMACINML_77              333 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..333
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 agtagattgg gtgattgatt taaataaata tgattttgcc tatgatgaag aaggtagaat
       61 catttgggct ttatataatg atattgaaaa aggtaaatta aaagatccaa gagatgtgga
      121 ttctactcct gaaagtagaa atgaatttga tgatgctatg gatggatacg aaaatggaat
      181 ggtaactaga tttgatgtag atattagaaa cgaaagagat gagagatctg ctaaactgac
      241 tatggatacc ctagtattaa gtgccaaact cgcagccctc actcctcctc aaggctatcc
      301 taatgctcct tattatttta cacctgaaag att
//
LOCUS       DMACINML_78              300 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..300
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 taatttttag cttaattgtg ttgtctttgt gtttggttta taatttcatt gtatggtttt
       61 ttgggtggtg ttaagatatt gatttgctag gctggtaaat ttgtttgggt ttttttattg
      121 tttgaataca cttgctttat ttggtgggtt tattggttgt gagcttggtt ggttaagttg
      181 gactgatggt ttaatcattt ttaatctgtt tttagtttaa ttgttaaatt tggtgtttgc
      241 ttgtatattt ttatctatta aatttatttt ttgtatgcta attaaatatg tttttgtatt
//
LOCUS       DMACINML_79              296 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
```

```
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..296
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gcttttcttt acttcctgca gctctatgca aaagggtttc tcctgcacca ctaaagctaa
       61 attcattttc tgttttaatt cttctcatat taggatttgc tcctagtttt aaagcttctt
      121 ctaaataatt tgcatgattt agcaatatcc aaacatgcaa aggagtgctg ccactttctt
      181 cattataagt ttcaaatgtg catccttttt taaaaaaata ctctattact tctttatttt
      241 ttccatctct atcgatatat ctactgagtg cattgtatcc aaagtgtact tcatcg
//
LOCUS       DMACINML_80              294 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..294
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(116..268)
                     /locus_tag="DMACINML_01857"
     CDS             complement(116..268)
                     /locus_tag="DMACINML_01857"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /inference="similar to AA sequence:RefSeq:CKG86653.1"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01857"
                     /translation="MYNINCFRTQKGTKYLNEILAPKFYNKYKDLEVEIDDKGNILRW
                     IGKINR"
ORIGIN
        1 agtattttat tggtatcttt ttccacatct aatgttaacc cattgggtgt ataaatctca
       61 taagtttcgc tcattattta tcctttgtaa aatccaatgt aaaatccaaa taaactcatc
      121 tattaatttt tcctatccat ctaagtatat taccccttatc atcaatttct acttctaaat
      181 ctttgtattt gttataaaat ttaggagcta agatttcatt gagatatttt gtgccttttt
      241 gagtgcgaaa gcaattgata ttatacatat cccaattatc caaattcccc caaa
//
LOCUS       DMACINML_81              280 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
```

```
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..280
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 attcaaacaa taaaaaaacc caaacaaatt taccagccta gcaaatcaat atcttaacac
       61 cacccaaaaa accatacaat gaaattataa accaaacaca aagacaacac aattaagcta
      121 aaaattagat tcaataaata aaaaaggata attaatacaa aaacatattt aattagcata
      181 caaaaaataa atttaataga taaaaatata caagcaaaca ccaaatttaa caattaaact
      241 aaaaacagat taaaaatgat taaaccatca gtccaactta
//
LOCUS       DMACINML_82              273 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..273
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 atcataatat tcaattttcc catcttcaat atcacatatg cgacaattag ccgcatttac
       61 atcagctcca tatttgatta gcacttccac gcaagctcct ataggtttct catcagattc
      121 tgcagctcta tgcaaaaggg tttctcctgc accactaaag ctaaattcat tttctgtttt
      181 aatacttctc atattaggat ttgctcctag ttttaaagct tcttctaaat acttcacttc
      241 ttcgccacat agtatccatt catgcaaagg agt
//
LOCUS       DMACINML_83              273 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..273
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
```

```
                     /strain="strain"
ORIGIN
        1 ctagatattt atatctttct cttttggttt ttaaagattt ataataagct ttttctgctt
       61 tagtccaagg agctatgctt cctttaatgg gatcttttaa atatatgctt tgccaatctt
      121 taaattcaag caaagtggat ttttgccctg tataaaagtt aggatctaga tatattggtt
      181 tatagtcttt gtagggggag tttttcataa tataataaga ttcaaaaacc gctttggaat
      241 attcttgagt ataattgcct gtgggtttaa tat
//
LOCUS       DMACINML_84              271 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..271
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 tatttaaagt cttaaaatca ttaagaagtt ttaaataaag tcctaaattc attttaaaat
       61 ctaaatccat gtattgattt tcaatatttt gaatcttttt ttcatggata taaaaatgat
      121 tatccttttt tataatccca ttccaatctt tcaggtgtaa aataataagg agcattagga
      181 tagccttgag gaggagtgag ggctgcgagt ttggcactta atactagggt atccatagtc
      241 agtttagcag atctctcatc tctttcgttt c
//
LOCUS       DMACINML_85              258 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..258
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ccgatgaagt acactttgga tacaatgcac tcagtagata tatcgataga gatggaaaaa
       61 ataaagaagt aatagagtat ttttttaaaa aaggatgcac atttgaaact tataatgaag
      121 aaagtggtag cactcctttg catgaatgga tactatgtgg cgaagaagtg aagtatttag
      181 aagaagcttt aaaactagga gcaaatccta atatgagaag tattaaaaca gaaaatgaat
      241 ttagctttag tggtgcag
//
LOCUS       DMACINML_86              256 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
```

```
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..256
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ttaaattcta ctagagtgga tttctctcct gtataaaagt taggatctag atatattggt
       61 ttatagtctt tgtaggggga gtttttcata atataataag attcaaaaac cgctttggaa
      121 tattcttcgg tataattgcc tgtgggttta atattttctt taaatagtat tttattggta
      181 tctttttcca catctaatgt taacccattg ggtgtataaa tctcataagt ttcgctcatt
      241 atttatcctt tgtaaa
//
LOCUS       DMACINML_87              256 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..256
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ttatgatgaa gcagatgagg atgaatttga ggattggttt attaaaaatg tgctttatca
       61 tgatgattta agtgagattt ataaaatact aaaatcactt gttaaagatt aaaaactaaa
      121 tttacaaaga aagaaagaaa ggaaaaacaa tgaaaacatt agaagaatta atagctttag
      181 aagaaaaata tctaaaagaa ttatgtttag aattttatga tcttgtagag gctaacaaac
      241 ttgaagaagt taaaga
//
LOCUS       DMACINML_88              255 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..255
```

```
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gaattaaaac agaaaatgaa tttagcttta gtggtgcagg agaaaccctt ttgcatagag
       61 ctgcaggaag taaagaaaag cctataggag cttgcgtgga agtgctaatc aaatatggag
      121 ctgatgtgaa tgcagttaat tgtggtatat gtgatattga agatgggaaa attgaatatt
      181 atgatcctgc tactccattg gatgaagcta atacttacga tataaataaa aatataaaaa
      241 tcttaaaaaa agcag
//
LOCUS       DMACINML_89               255 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..255
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 gaattaaaac agaaaatgaa tttagcttta gtggtgcagg agaaaccctt ttgcatagag
       61 ctgcaggaag taaagaaaag cctataggag cttgcgtgga agtgctaatc aaatatggag
      121 ctgatgtaaa tgcagttaat tgtggtatat gtgatattga agatgggaaa attgaatatt
      181 atgatcctgc tactccattg gatgaagcta atacttacga tataaataaa aatataaaaa
      241 tcttaaaaaa agcag
//
LOCUS       DMACINML_90               255 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..255
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
     gene            complement(74..238)
                     /locus_tag="DMACINML_01858"
     CDS             complement(74..238)
                     /locus_tag="DMACINML_01858"
                     /inference="ab initio prediction:Prodigal:2.6"
                     /codon_start=1
                     /transl_table=11
```

```
                     /product="hypothetical protein"
                     /protein_id="Prokka:DMACINML_01858"
                     /translation="MDEANTYDINKNIKILKKAGAKTWEELVEEYNIDTSLEEPEQIK
                     MYEERRKDKK"
ORIGIN
        1 tttgtgtcta aaaatgcttt gaaattatct aagctttcta aaatatctgt gttaaaatcc
       61 ataatttttc cttttatttt ttatcttttc ttctttcttc atacatttta atttgttctg
      121 gttcttccaa gcttgtatcg atattgtatt cttcaaccaa ttcttcccaa gtcttagctc
      181 ctgctttttt taagattttt atatttttat ttatatcgta agtattagct tcatccaatg
      241 gagtagcagg atcat
//
LOCUS       DMACINML_91              255 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..255
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 ctctaatagc taaaatataa ttgatatagc catattcact ggtatagctt ttttctttag
       61 ttttactatc aatttgtttt cttttttctc caaataaagt agcagaaaaa cctgaatttg
      121 tattagggca atgttttaat aaatcatagc gagaaaagaa ttgtttagct tggagtgggg
      181 agaagtcgcc atcaaataag gaattatatt ccatattgag aatgtcggtg taggtagctt
      241 tggcattttg cactt
//
LOCUS       DMACINML_92              255 bp    DNA     linear       16-DEC-2020
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
  ORGANISM  Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.13 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
     source          1..255
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
ORIGIN
        1 tctttaactt cttcaagttt gttagcctct acaagatcat aaaattctaa acataattct
       61 tttagatatt tttcttctaa agctattaat tcttctaatg ttttcattgt ttttcctttc
      121 tttctttata aatttagttt ttaatcttta acaagtgatt ttagtatttt ataaatctca
      181 cttaaatcat catgataaag cacattttta ataaaccaat cctcaaattc atcctcatct
      241 gcttcatcat aaggt
```

//