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DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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/inference="similar to AA sequence:RefSeq:AAW35443.1"
/note="conserved domain protein"
/codon_start=1
/transl_table=11
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ORIGIN

1 aaaaagtcag acaagaatat agttttattg gcaaaggtga attaaatgga gaatttggag 41 aattacaagc tagaaatatc tctcaagtct ttttttattg gcaaaggtga attaaatgga gaatttggag 81 aattacaagc tagaaatatc tctcaagtct ttttttattg gcaaaggtga attaaatgga gaatttggag 121 taagtggctt tagtgcatt ttgattttatg atgagattaa attccatccttggctattttgaattttttattg 161 taagtgcatt ttgattttatg atgagattaa attccatccttggctattttgaattttttattg 201 taagtgcatt ttgattttatg atgagattaa attccatccttggctattttgaattttttattg 241 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 281 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 321 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 361 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 401 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 441 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 481 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 521 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 561 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 601 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 641 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 681 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 721 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 761 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 801 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 841 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 881 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 921 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 961 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 1001 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 1041 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg 1081 ctttgcttgg ataatatcctt aaagagattt ctttattttgctattttgaattttttattg
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LOCUS       DODKMMJL_5              1234 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
          Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..1234
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/mol_type="genomic DNA"
/strain="strain"
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181 ttagaaaaat ctttaaatat caaattagaa tgcttaagca agcaaagctt agaatataa
241 gatttattt tttacttattt tttataactaa aaactacatc aagtagatc aaacaacta
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421 gaaatgtatt tattaaacct tagtatagta gctttgtccta ataccatagc aatgtaag
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661 ttaggagaac aagttatataa tttataataagat taatataatg ctttaaatag ccattctatatttaa
721 aagatgtgata ctttccaaac aagataaatg cttatattct tctttatatg atacatgaa
781 aaaaaaagac aagataaggc tttaatagaa ttaaatagag aacaaagaga ataaagagat
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901 aaaaaatttcttta ttaaagatatgttt tcatttactt tataaatctt taatcataactt tcttttttaaaacataa
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1021 gggtattttta cacagctacc taagatctta aacattatcta aacacttgttta aagtagatgg
1081 aagatagataa acatagatcc tttataacagc ttagcttctc cacaaatag aatattatg
1141 tttcaaatcag cacaagattg aagataaatg ttaagagatg aagatagaa aacaaacagt
1201 tatgtttgtta ggttttggga gttt

LOCUS       DODKMMJL_6               654 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
          Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..654
/organism="Campylobacter species"
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>>BfR-CA-15829_min_cov_30 putative plasmid location

LOCUS   FAFJHLOP_1        3230 bp    DNA    linear       12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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/strain="strain"
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/locus_tag="FAFJHLOP_00001"
  CDS             complement(443..1720)
/gene="trxB_1"
/locus_tag="FAFJHLOP_00001"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86610.1"
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/transl_table=11
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/protein_id="Prokka:FAFJHLOP_00001"
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complement(1792..3069)
/gene="trxB_2"
/locus_tag="FAFJHLOP_00002"

CDS
complement(1792..3069)
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/locus_tag="FAFJHLOP_00002"
/inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CKG86610.1"
/codon_start=1
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LDELIGVWID
VKNYQFAYDEKGRVNDLKDDEVGKILKDPRIDSTPEFRWDFKEMAYKNGMR
TRF
DGNPNWHSKEQFERNDTILCAALTPQPGPNNPYYSPEREIYKXKLDR
LEDPRIPIAUYRFPPRELRAKILFGEENIKD"

ORIGIN
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241 tctcaacattg cttatttttt ctatatctat aaaaagttttt atatctttttt ctattttttt
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1741 cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt cttttttttt
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LOCUS       FAFJHLOP_2              1016 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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/mol_type="genomic DNA"
/strain="strain"
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/gene="trxB_3"
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CDS             complement(447..944)
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/inference="similar to AA sequence:RefSeq:CKG87041.1"
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LOCUS       FAFJHLOP_3               958 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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        /mol_type="genomic DNA"
        /strain="strain"
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LOCUS FAFJHLOP_3 958 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
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LOCUS       FAFJHLOP_5               702 bp    DNA     linear       12-APR-2021  
DEFINITION  Campylobacter species strain strain.  
VERSION     
KEYWORDS    .  
SOURCE      Campylobacter species  
ORGANISM   Campylobacter species  
Unclassified.  
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.  
FEATURES             Location/Qualifiers  
source          1..702  
/organism="Campylobacter species"  
/mol_type="genomic DNA"  
/strain="strain"  
ORIGIN

LOCUS       FAFJHLOP_6               664 bp    DNA     linear       12-APR-2021  
DEFINITION  Campylobacter species strain strain.  
VERSION     
KEYWORDS    .  
SOURCE      Campylobacter species  
ORGANISM   Campylobacter species  
Unclassified.  
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.  
FEATURES             Location/Qualifiers  
source          1..664  
/organism="Campylobacter species"  
/mol_type="genomic DNA"  
/strain="strain"  
ORIGIN
SVKALDEKVRQGKLKDPRVDSTPESRKEFDEEANAYTFGNRMNFSSDIRDSRSKESA
RLFDDLLILHAKLAALTTPQGYPNAPYYFSPEQLEDFYKRVQVLDANKLDPRIPAIYRYN
FPRELRALKILPGEENSIKD

ORIGIN
1 ccatttttca tgattatagt ggtggctagt ctgcctaatg gcgtctttta atcttttaatg
61 ctattttctct ccctgggtaa attatatcct cccctttgga atatatctca
taatatagcg gatctcgtct atcaagttta gctctctcct gtttctttta gagctctcttct
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481 aatgtgattaa cttattataat cttattataat cttattataat cttattataat cttattataat
541 agcatttaca cttattataat cttattataat cttattataat cttattataat cttattataat

//
LOCUS FAFJHLOP_10 554 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..554
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN
1 taaaaatcct ttaagagagc aacaaattaa aaccttagct aagactttaa aacctgatga
61 attttactgg cttctctttta tagatgagat tatgggagta gattgggtga ttttatttaaa
taatatatagc cctatattgc gtagttatg tctgtcttct gtttctttta gagctctcttct
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121 taatatagcg gatctcgtct atcaagttta gctctctcct gtttctttta gagctctcttct
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241 gctgccagtt tggcatgaag tatcagaagtg tctcctcttct gtttctttta gagctctcttct
301 ctatctatgcc gaattacag gcgaagttct attctttacc aagaagttct attctttacc
361 tctctctctcct gcctctctct gcctctctct gcctctctct gcctctctct gcctctctct
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taatatatagc cctatattgc gtagttatg tctgtcttct gtttctttta gagctctcttct
481 aatgtgattaa cttattataat cttattataat cttattataat cttattataat cttattataat
541 agcatttaca cttattataat cttattataat cttattataat cttattataat cttattataat

//
LOCUS FAFJHLOP_11 535 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..535
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
ORGIGIN

1 atacataaaa atccttaaat gtaaaagatt tagctaaac tatacagcct
gatgaatttg gtatgctacc ttttatagat gagattatgg ggtgattgat
ttaaatcagt atcaatttgc gtatgacggt aaaggtgatt ctacttgggc tttatatgat
181 gatattgaa aagtaaat aaagatctaa agagatgtgg attcctctt tgaacacgg
241 aaagaatttg atgaagaaac tttatatgat gagattatgg ggtgattgat
ttaaatcagt atcaatttgc gtatgacggt aaaggtgatt ctacttgggc tttatatgat
301 gatattgaa aagtaaat aaagatctaa agagatgtgg attcctctt tgaacacgg
361 taatatcagt atcaatttgc gtatgacggt aaaggtgatt ctacttgggc tttatatgat
421 taatatcagt atcaatttgc gtatgacggt aaaggtgatt ctacttgggc tttatatgat
481 taatatcagt atcaatttgc gtatgacggt aaaggtgatt ctacttgggc tttatatgat

//

>>BfR-CA-15831_min_cov_30 putative plasmid location

LOCUS       EDCPFOPP_1              2138 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
          Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..2138
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"

    gene 345..647
        /locus_tag="EDCPFOPP_00001"

    CDS 345..647
        /locus_tag="EDCPFOPP_00001"
        /inference="ab initio prediction:Prodigal:002006"
        /codon_start=1
        /transl_table=11
        /product="hypothetical protein"
        /protein_id="Prokka:EDCPFOPP_00001"
        /translation="MILCIFSSFYLSLACCPAKLTPSVPTT
APTTVPITGKLEPTAAPVAPPAAREMPSGMDTPCNAIAIAATLAVAVEATLL""

    gene 714..932
        /locus_tag="EDCPFOPP_00002"

    CDS 714..932
        /locus_tag="EDCPFOPP_00002"
        /inference="ab initio prediction:Prodigal:002006"
        /codon_start=1
        /transl_table=11
        /product="hypothetical protein"
        /protein_id="Prokka:EDCPFOPP_00002"
        /translation="MIIVILTPTLVSVKALTLDFPSALARKKFNIPKFIIILECIILA
ICELSMPNFTISFSKALVAKPSVMPKA""

    gene complement(1026..1664)
/locus_tag="EDCPFOPP_00003"
CDS
complement(1026..1664)
/locus_tag="EDCPFOPP_00003"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:EDCPFOPP_00003"
/translation="MSEINNNTEIKEQDTQDEIIWEGKKHIPSFLLWITYVLLCFA
LYLFPRNPSKEIDYKWIFVFFTLVIYALAOQIKYRMANIKRIYITKEKLVIEYII
KNDLVFPLGTFFVVYRRLSFVLTGHIYITFGDKVEYLEEPGLFSGDDPTKDFER
INAIKPHVMPYLLSLSDEEFEIKIFHVSGFSEIDTTLKEAMELREKKDE"

gene
complement(1715..2107)
CDS
complement(1715..2107)
inference="ab initio prediction:Prodigal:002006"
codon_start=1
transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:EDCPFOPP_00004"
/translation="MANIKRIYITKEKLVIEYIKNDLVFPLGTFFVVYRKYISYLSLP
GHIVIYTFGDGKVEYLEEPLSFDGDPTKCFERINAIKPHVMPYLLSLSDEEFEKI
FFHVNSKIFDTTLKEAMELREKKDE"

ORIGIN

1 attcatcctc atctgcttca tcataaggta tgccagtatc ttcttcaaaa gcaacttcat
61  agttttctgg atctaaatta tcatacgcac cttccataaa atcatctata taatttttta
121  ctgccttatt agctatgggt tgtattctga ttatagttgg atttttttct tgagcttctt
181  tataactttg ctcatcttta tctaaataat aaggaaaact tagcatcaaa agaatggttt
241  taaataaagc actattaata tcactttattp cttttcactg tcatcttcat
301  ttaacactct taattctata tactgatgag tgatgagata attgatgatt ttatgcattt
361  tttcatctaa tttttcctct aaatattttt ctttggcttc ttgttttttt aattcctcat
421  cttcatcgcc aaaaattaag tcattaaaaa aacctgctac aagtgttccc accactgcac
481  cccacacctgt cccaacaata ggaaagctcg accctacagc tgctccagtt gctgcacctg
541  cggcaatacg agaaagtatg gatacgccag ctctagctgc gatattagat gctactcttg
601  agctagctat cttggttgcg gcattagaag caaccctgct ggtttgagtt aaggtttgtt
661  tggcaacatg ttcgctacct ttttctattg ttgctccaat aggagtttca ttcatgatta
721  tagtgatact aacaccaacg cttgtttcag tcaaagctct tacattggat tttccctctg
781  ctttagccag aaaaaaaatc aatattccaa aattcattat tattttagaa tgcatcattc
841  tcgcaaatatg cgaatattct tcttggccaa actctcact tctttttttt tcttttctga
LOCUS  EDCPFOPP_2               863 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

ORIGIN

1 caatatatgt tatccaaaaa agaaaaacag aaggtatatg cttttttcct tcccaatgta
ttcctttgag ggtgtccttg tctttgtatt gtattttcct cttttatatg
tatccacttc tgccttaacc tctccacctt taaccacaag tccattagag tctataatca
cattctactc acctgcttta attataacac aatctttctt ggtaaacaat tgaatgagct
cattccactc acctgcttta attataacac aatctttctt ggtaaacaat tgaatgagct
dttaaatagtt gttatcttgt atatgggcgg ataaattttg atgaacatta aggaaaaatt
cattctactc acctgcttta attataacac aatctttctt ggtaaacaat tgaatgagct
dttaaatagtt gttatcttgt atatgggcgg ataaattttg atgaacatta aggaaaaatt

gene    complement(125..670)
//
| LOCUS         | FDNNOFDK_1 | 3982 bp | DNA | linear | 12-APR-2021 |
|--------------|------------|---------|-----|--------|-------------|
| DEFINITION   | Campylobacter species strain strain. |
| ACCESSION    | .          |
| VERSION      | .          |
| KEYWORDS     | .          |
| SOURCE       | Campylobacter species |
| ORGANISM     | Campylobacter species |
| Unclassified.|
| COMMENT      | Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka. |
| FEATURES     | Location/Qualifiers |
|              | source 1..3982 |
|              | /organism="Campylobacter species" |
|              | /mol_type="genomic DNA" |
|              | /strain="strain" |
| gene 49..1071|            |
| /locus_tag="FDNNOFDK_00001" | |
| CDS 49..1071 |            |
| /locus_tag="FDNNOFDK_00001" | |
| /inference="ab initio prediction:Prodigal:002006" |
| /inference="similar to AA sequence:RefSeq:APB38683.1" |
| /codon_start=1 |
| /transl_table=11 |
| /product="replication initiation protein" |
| /protein_id="Prokka:FDNNOFDK_00001" |
| /translation="MSDIVKYHNDNFKNIQIQLEIQDLCLGLMVKLKEEKGKTVFY PWDLRNILKSYDNNSLMEFASSLKRRKFKADFTIEETRGEKEVEAHKTINLTFEF AIYYASSKIDLEIESIEIQNVPMQPQFEYILNQLTANFTAFESEIALSGKTYTKTLRLLQ YRTTGKARFWHEEEFCRVMISIPQYRSAIDKWKPAIKELSKNLFQVRMPQFKNL AYEKKEAKGSGRRGKGVSGITFTFKPENIEMQKLENSQMEQKILESQKILNLNLNLN QVRFVYNKLWQFNDDFNEFKIIAVELQDTEYLNLFGNHMMHFAKNAKQEQQFMMET FRKGI" |
| gene 1101..1475 | |
| /locus_tag="FDNNOFDK_00002" | |
| CDS 1101..1475 |            |
| /locus_tag="FDNNOFDK_00002" | |
| /inference="ab initio prediction:Prodigal:002006" |
| /codon_start=1 |
| /transl_table=11 |
| /product="hypothetical protein" |
| /protein_id="Prokka:FDNNOFDK_00002" |
| /translation="MTMQIIQDQIPQELSGRMKQSLERLANHLHATQNEAPMDDIVALW LLLWDALTCKQDLKLYNQKVLIEIQMNLETQHKANLAEQRADLAEQRAEKAQRAEK AEQLYQIQKNFRRSMMKSQTYN" |
| gene 1806..1970 | |
| /locus_tag="FDNNOFDK_00003" | |
| CDS 1806..1970 |            |
| /locus_tag="FDNNOFDK_00003" | |
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:FDNNOFDK_00003"
/transl="MDYEKYSKMLRQLINAYNAEKKEKTLDDFQKLDENKLNME FLKTTIKESL"
gene
1974..3302
/locus_tag="FDNNOFDK_00004"
CDS
1974..3302
/locus_tag="FDNNOFDK_00004"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:APA51640.1"
/codon_start=1
/transl_table=11
/product="mobilization protein"
/protein_id="Prokka:FDNNOFDK_00004"
translation="MSYDEIEKVRSAYTKTASESTKRNYISSGNFKSTSFQVFHNA NVRPDYAIggELVFDLGGYEAELEKLKNIVISEAEKAYENK5PKPFKAKKSYEWSSLV NIKPDSMNDLNKLHKFQEGYGFCQYQIAIHRDEGHNFEQGKLEILNHAYHMEFITLD KETGKNNFRREKISRKVLREIITEIAEGICMERGKLKISGAKIKFRAAYAEEKK REKKRNINLEEQCEOQFLNKSEYYKKEIFRNSIQINGLQDKDFKELSEKLNKFNQEI KEDNLELNdLREHLREIEKLKKEILKKEILKQEEOKNDKVQONDQEQKNSQER NFEPKDNNTNEDKKIEFEKLATYLRNEGLISYKPLKRIVEPETEAKKERIKILTE TMKTEAFLPETLKKWENKDIKEILVEYQNTLSKELQKSIYKGR"

ORIGIN

    1 aggggtagag aagcccccttgccttgag ttaccttgttgg ctgactttgtt ctttttagga acttctgctt atatatagttt ctttaatagttt gttacttttg gtttttagtt cttatctatt ctatctgctt ctatgcnttt gttttagttt ctttttagga ctatcgtgacttt ctttatctatt gttttttaatag ttactcttta attctttgartt tatttcttttt tatttcttttt tctttttttattctttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
LOCUS       FDNNOFDK_2              2761 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES              Location/Qualifiers
source          1..2761
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           /mol_type="genomic DNA"
gene

23..1219

/locus_tag="FDNNOFDK_00005"

/CDS

23..1219

/locus_tag="FDNNOFDK_00005"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:EAQ72546.1"
/codon_start=1
/transl_table=11
/product="putative sugar transferase"
/protein_id="Prokka:FDNNOFDK_00005"
/transl_email="MLDPPKLLNMDTEKINYKNTAEALAWEMNLPLPDKYDGFIFISSHG
TGEKAFQEMLARCDBGKLQKNNKWDNGKDRYRAFYYKDLVIDCTAKKCIPICENFLY
YGKYLMHFQGKVPILCIVRDPMSAVSONYKIVDKQKLHFSKNKKNNEVMFNYFYT
TTTSKSIIDNLEKLKKRIILHRITISNMRFTYIAKTHIQNLKMDKYYIDSSIESASK
AYLKLKGEIDVYGFSVPEFNLKINISFHTHLFYIDPIIPIDYTHQIPDNLNQIF
FHMYQQTEDQDITHLFLNQQDSSMHNFICTQTQDVYIDIIHDEKIYYEIRDNLNFF
NKINNHIAILRKEAIASEEDILKIIYKEDKQTSDAFKCLIIEDEFKDVEKESMLKKKW
HLYLFIKL"

gene

1243..2631

/locus_tag="FDNNOFDK_00006"

/CDS

1243..2631

/locus_tag="FDNNOFDK_00006"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AHY40622.1"
/codon_start=1
/transl_table=11
/product="putative sugar transferase"
/protein_id="Prokka:FDNNOFDK_00006"
/transl_email="MYIVLAVSNYKYVGVLSSIIKNTKENDNFANEKYIFHVILT
SISLNLNQKQLTLDVLYSNYPCELKIHDIDQSFHEFKAWHNHAYYRFIEIANI
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NFDPJYVAGIMIDLNKWRQCDIKKCIQAFLDDHGLADQSYNLALKDSIYKYL
PLGWNLIAPEYVLQGyrHYVQKCLDEGDKNAYTYRFKESQALNEEKIVHFCAAK
WWNLYVKKNERDFNERKJHWDIAINMEGFKEFRYLYRLNLELWLRKINSIASNGIK
HVTKIIIQVNHNAKSRQINQLSYKLQGIIALINSKISLGCLMPVYIIISTTVHQCQKK
YHNAIHKDKPSLLPLEQYPDYNNEAIKLKQHFSYKLGSVMSLKYWYLGGILALPFR
VFKLYKHNKKKI"

ORIGIN

1 ggaaacat ccttatcct ctttgcttga tctaaaaag ttaaataatg atactgaaaa
61 aattaattat cagccgaact gcgtcgggaa atgaatttac ctttcgcaaa
121 taagttagat tttatatta taagtagtca tgcgaatgc gaataagctt ttaaagataat
181 gctgacctgt tttttagttt ctaaagcag caaaaaaat attgtgtatg atagaagaa
241 atgatatagag cctctctctt atataatatc tgaataggctg tttattactg aatatgaat
301 cctactactt ggagagagct gaaatcagttg cttgaaatg ataatag
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tatttttagtttttt tatttttagtttttt tatttttagtttttt tatttttagtttttt
841 aatatttata tttcatatgt atcaaaactgc atcatctg ctgtatgtga
CDS complement(376..2841) /locus_tag="OIDGCHHC_00001" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:ASI88309.1" /codon_start=1 /transl_table=11 /product="IncP-type conjugative transfer protein TrbE" /protein_id="Prokka:OIDGCHHC_00001" /translation="MLALKFRSKAKAFTPDLNYASFIDEGILLNKDKSLTAGFYVRA GDISSMTINERTLSARINSVLKTLNGWAVHIDCSRIK TERNYIDGGDFYKNNAIQIL ENERKHYFDNVHFNLFMTIFTYLPHPKSINKITDLMIDETKRNQGDKILEYFKNL TLFKLEDLSNYIKIERMLPRAIDEYNVEYILDMLEYIFICGREGQKIILPNAPMF FLDCLLLGRHFGEHGPRDINQYIGIAIEGFPSIESYPNLNAITELNFDYRFNTRFI FLDDFEAQNSLNKRYKQWQKTGWDQLLDRPARKQDDHAVLVMQELDSALSESKG MIGGYGYTANTIVFDRYESLEYKLDIRKVLNENGLFSRTEINSEAVYLGTLPGV FYPLRRPILNLNLTHLPLASIWAGDKYNSSERFPNNSPLPMQVTSNGTPFRLNH VSDLGHTLIGFPQGSGLSTLLANIFLAVQKYPNAAKYYAFDKQGSSLALLPLATLGGHIGH YVAGDHSSLAFPLANIKTDAAIAWAEFIEETCLKLQNVNTPQKKLIHEALISHINT NSTSLTEFVSALQSDRLDALOGYTSTGGFLFDPSEEDKLSSISITTFIEEELMLNL GDQYIIPALLFYFRIEKGLDGSPTLILIDEAWLKHAPFADKIVNWLKVRKANAV IMATGQSGAKSGLD1QYECPTKIFLNPNEAYKKGSENVLAPYDFYKIFGLNVDQ SIISINAIQKREYYTSPALTFLRNLALGKTNLAFATTDKVSVRQRQLEYKHKENW AYKWLEEEIN VRKFDNSQKEEA"

gene complement(2845..3132)
CDS complement(2845..3132) /locus_tag="OIDGCHHC_00002" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:ASI88308.1" /codon_start=1 /transl_table=11 /product="IncP-type conjugative transfer protein TrbD" /protein_id="Prokka:OIDGCHHC_00002" /translation="MEELOQSDIYSLNKNPGLFGADRELIMVNGVISFALIFTGATL LTSISIGFLUFFCNMLLRLMKSOLMRQIIFLRQIKYKYYAIASTPSKID"

gene complement(3132..3428)
CDS complement(3132..3428) /locus_tag="OIDGCHHC_00003" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:ASI88307.1" /codon_start=1 /transl_table=11 /product="Conjugative transfer protein TrbC" /protein_id="Prokka:OIDGCHHC_00003" /translation="MKKFLLIFLFLAFLSYEAFASSTTGALPGWEGPLEQKASGVPVAF VISILAILGAGGLNGGELSGFKTFLYIVLIALVGANSFMSLFS TGALI"

gene complement(3438..4376)
CDS complement(3438..4376) /locus_tag="OIDGCHHC_00004" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:ASI88306.1" /codon_start=1
Conjugative transfer protein TrbB

Product: MSNLFEQARINEKIKREFDGILTHLEDKETIELMLNSDGKLWLE
KLQGDICLGEFSEARAKITTAISTLDTTNAOPELPLDSRFEPALLPPIV
AKPFTIRKAKVIFTLGDYVDSNIITPQNKEVLNAIERRQNILVVGTTGSGKTTFS
NAIIDISKITPDHRIVIIEDTAELQCASENKVILRATDKVDMRLKATAMRLRPDI
IVGETRGEALDLKAWNTGPQGATIACAIANSANGGLTRMEQISEATSKMGLIAE
AVNLIVFSKSeqTRKVEIIKVIDYENDKYITQIT

Gene complement(4916..5656)

CDS complement(4916..5656)
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

Product: hypothetical protein
/protein_id="Prokka:OIDGCHHC_00005"

Translation: MLFYEIINCKPNNTMNKRTYKVIRCIFKNTDEASKYYQQA
WLAKQVNPKLANDSTQRDKERLILDALGIGALAYGWFFYKRNFGDIVNTEFSS
IGQIDDLNNGKTLEREVSPPNRQFINAFICNAYNFKNICKYDNLKYPNEMDKDFAC
VLFEFTKQOMVKADEFIIFLYIGGSTRKMMNLTISYTDNLTAEDDLIQQKTYNVI
RVLNALDIEFKEYMTELELYPKILNDQTF

Gene complement(5646..6563)

CDS complement(5646..6563)
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11

Product: hypothetical protein
/protein_id="Prokka:OIDGCHHC_00006"

Translation: MNKNSSSKLNAKNKNDQFYQYEDINKNELNFYKNAFKDRIVY
CNCDDPQSNFTKFKLNFRLKLKLKSSTNFOVGSNKGWIFIGIFIIEKNKPY QGGLENNG
DFRSDETIKLKNESSIIVNPPFSLFREDILISQNOQDLFLIGNANAISYKNCNFYM
MKNKRWLGQVCRWNTSGKVALVEGARSWFSFNNQKRNKSKISLKNRKNQNYQDIYD
YNNAIEISKSKDIPSYTGIMVPFTFLDKYNPQFEIIIGADYQVNNSGELIYIKRNDW
NGKTDRAINGKRLYSRIFIKHRGNNAI

Gene complement(6586..6999)

CDS complement(6586..6999)
/inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:ABS43377.1"
/note="conserved hypothetical protein"
/codon_start=1
/transl_table=11

Product: hypothetical protein
/protein_id="Prokka:OIDGCHHC_00007"

Translation: MKKVYLDTNIFLDYFNTERTYHNEAKQOLMYYLTTNQIVFSED
MISTIAYLKKENLNNFTHFLKLDISLEKNNFTSFVGVSISVMAZCAYEKYRGDFEDYL
QVFCAEKEGCSAIAYMDKFPNLIPIKRYGEIDI

Gene complement(6996..7910)

CDS complement(6996..7910)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ABS43377.1"
/note="conserved hypothetical protein"
/codon_start=1
/transl_table=11

Product: hypothetical protein
/protein_id="Prokka:OIDGCHHC_00008"

Translation: MKKVKLYNTNLKFKFNTERTYHNEAKQNQIVFSED
MISTIAYLKKENLNNFTHFLKLDISLEKNNFTSFVGVSISVMAZCAYEKYRGDFEDYL
QVFCAEKEGCSAIAYMDKFPNLIPIKRYGEIDI

Gene complement(7916..8916)

CDS complement(7916..8916)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ABS43377.1"
/note="conserved hypothetical protein"
/codon_start=1
/transl_table=11

Product: hypothetical protein
/protein_id="Prokka:OIDGCHHC_00009"

Translation: MKKVKLYNTNLKFKFNTERTYHNEAKQNQIVFSED
MISTIAYLKKENLNNFTHFLKLDISLEKNNFTSFVGVSISVMAZCAYEKYRGDFEDYL
QVFCAEKEGCSAIAYMDKFPNLIPIKRYGEIDI

Gene complement(8916..9916)

CDS complement(8916..9916)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ABS43377.1"
/note="conserved hypothetical protein"
/codon_start=1
/transl_table=11

Product: hypothetical protein
/protein_id="Prokka:OIDGCHHC_00010"
CDS complement(6996..7910)
/locus_tag="OIDGCHHC_00008"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86570.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00008"
/translation="MSNEIEIKDLNEINKKNKQVYVRRDKLSTDYITGEVENQII
VKKVQTKEFILKFLTDYINLESQEKTLFFTLLSSVDYKNVRFDKSMKQNYIVLD
KVLSRAGMYRALGIEKKVIFKINREFVKSAGVGSDDCFLFNPNLVGRGSSWNLKN
LRHITITRWDENFENLEIIEEELGFDEIRNNQKQQYQVREINQEHNETTQKVNT
IVIEEKNNSINQYSFDKKEEPSINKVLISNDTQPSLFDENQKEARELFIEKYAGI
LTGAYDSTKSAEMKRELDDKLEEGRI"

CDS complement(8181..8534)
/locus_tag="OIDGCHHC_00009"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/protein_id="Prokka:OIDGCHHC_00009"
/translation="MGCGVCSRLERQTNLTPYYCCKKSKRRLVSSNLQMSVSEICCKK
FFVFKSRLRRRKLLKNAFYKRYNSALIRFLIFPPVGGKLLVVGKLFLEKFIFPNKLGK
NYFFCLNMYHFLGKS"

gene 8971..9414
/locus_tag="OIDGCHHC_00010"
/CDS complement(8971..9414)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ADN91794.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00010"
/translation="MKKLALVLAALVALNVSAFAGVIITHNSNLVKSDDIYAKAA
LEDAKEDMRQFNTDNLEIYAIIESIHKKDPHEYDVLRQDGLKIERENMAKGKTVYNYI
FLVVDKNTWNASTWKECDHDRPIKLSNGKCKAGIYINRYNFK"

gene complement(9443..9691)
/locus_tag="OIDGCHHC_00011"
/CDS complement(9443..9691)
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00011"
/translation="MFSAEQFGGLKAAGSEPMAWMLIELAKGLLLKVFAYIASAYVMWK
TILGGPDWTRLMSGNSASDVTEDVGRMMENKTFCMV"

gene complement(9914..11008)
/locus_tag="OIDGCHHC_00012"
/CDS complement(9914..11008)
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00012"
/translation="MFSAEQFGGLKAAGSEPMAWMLIELAKGLLLKVFAYIASAYVMWK
TILGGPDWTRLMSGNSASDVTEDVGRMMENKTFCMV"
gene complement(12958..13173) /locus_tag="OIDGCHHC_00016" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00016" /translation="MAKTINRDILNSISKSAEMQENKTFEGKNFTIFSKVSQYNS LKEHCEKNSMGKLIKDLLKEKKNL"

gene complement(13200..13403) /locus_tag="OIDGCHHC_00017" CDS complement(13200..13403) /locus_tag="OIDGCHHC_00017" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00017" /translation="MLLIIDNITSQIDNCKHFSIAKNIIRDRIIFKNLSLAGKILEVLDSKGASDLKAKEELNSLKFENL"

gene 13914..14108 /locus_tag="OIDGCHHC_00018" CDS 13914..14108 /locus_tag="OIDGCHHC_00018" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00018" /translation="MNKDKKYLNFSEYYEVRDFLELYPEKDRENIENILMTIGENKKS KNLSFELDFKELGFKES"

gene complement(14122..14451) /locus_tag="OIDGCHHC_00019" CDS complement(14122..14451) /locus_tag="OIDGCHHC_00019" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00019" /translation="MQRGEAKIEFYSNINYLKKEFENGCVSKFLYDKALKEKNEKMT YKQFNKBFNDEFKWNKIKIKETIQEDNQLQSLVLRKIKPLKLKINTSSKVFDAKFKGD IKEEDDLL"

gene complement(14465..14914) /locus_tag="OIDGCHHC_00020" CDS complement(14465..14914) /locus_tag="OIDGCHHC_00020" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00020" /translation="MDIKIATFEDIEFIKYCFLEFKNKLEKNEKMT VSGGIFIKDFGTEKAGFACGKSKGSLNIEYINMIYILEKFRNKLATNFYKMK"
gene 15124..15507
/locus_tag="OIDGCHHC_00021"
CDS 15124..15507
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/translation="hypothetical protein"
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00021"
/translation="MRKDKIAIRLSDEYKHIMQKAQNHWGLTISRYLRLSMNYPIT CIVDQKAHNVLNIAIGD1GRLGGLFHKLVRNEDNKVNSKRTYNDIDEIVDQILD LQILLKEQAIRIIQNDNQKDSQKA""
gene complement(20601..20996) /locus_tag="OIDGCHHC_00029" CDS complement(20601..20996) /locus_tag="OIDGCHHC_00029" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00029" /translation="MNKKELIEEIAKKHIILDEMDAVSIEIIFDDFLEKIDL LFTKYKTLESYKFNIFINEIREYSKSNQAEALKDITQVQAQNTIKPSQEKTETKKE KNTNIFWIAIAASQIIIFLLVGLLIGIII"

gene complement(21062..21529) /locus_tag="OIDGCHHC_00030" CDS complement(21062..21529) /locus_tag="OIDGCHHC_00030" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:OIDGCHHC_00030" /translation="MRKTIAIFAFSFAFISILYSYLIFGGFHFYNTPSMPLGLYKEI NSSTFNKNDIVLKLIPKEIKLLKIANVSDAEVEVTQGVFINESLPPPNSKIFSDS EGNLEEFKPFKRLKENELFVMGENIKSYDSRFYGVNONLQNEVKKVKLMISF"

gene complement(21534..22196) /locus_tag="OIDGCHHC_00031" CDS complement(21534..22196) /locus_tag="OIDGCHHC_00031" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:ASI88290.1" /codon_start=1 /transl_table=11 /product="Cell filamentation protein" /protein_id="Prokka:OIDGCHHC_00031" /translation="MWDSQENLSEFDKFLIKTNKIGAISDELFRKERDITNAKALEL SKPNIKGNTFYQHLNINHKIYIFQDVFHDWAGKDRMEVLGHLNGFYQAPGSTTINVFPGK DLNATAPQIETFNLKEDNLYNKSDLNDFAKLNFARNLNALHPRENGRTQRIFLNL ELAKSHORTKLDSLIPKDTIMASVESQSLKLAGKLEAIKTNLKSRQNLDEQNKIGSL"

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ORIGIN

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 gene complement(1756..3051)
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// gene="thioredoxin reductase"
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 gene complement(3069..6566)
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ACCESSION

OIDGCHHC_3

DEFINITION
Campylobacter species strain.

VERSION

6566 bp DNA linear 12-APR-2021

KEYWORDS

SOURCE
Campylobacter species

ORGANISM
Campylobacter species

Unclassified.

COMMENT
Annotated using prokka 1.14.6 from

https://github.com/tseemann/prokka.

FEATURES
Location/Qualifiers

//

LOCUS
OIDDHCCHC_3 6566 bp DNA linear 12-APR-2021

DEFINITION
Campylobacter species strain.

ACCESSION

OIDGCHHC_3

VERSION

6566 bp DNA linear 12-APR-2021

KEYWORDS

SOURCE
Campylobacter species

ORGANISM
Campylobacter species

Unclassified.

COMMENT
Annotated using prokka 1.14.6 from

https://github.com/tseemann/prokka.

FEATURES
Location/Qualifiers

//

LOCUS
OIDDHCCHC_3 6566 bp DNA linear 12-APR-2021

DEFINITION
Campylobacter species strain.

ACCESSION

OIDGCHHC_3

VERSION

6566 bp DNA linear 12-APR-2021

KEYWORDS

SOURCE
Campylobacter species

ORGANISM
Campylobacter species

Unclassified.

COMMENT
Annotated using prokka 1.14.6 from

https://github.com/tseemann/prokka.

FEATURES
Location/Qualifiers

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ORGANISM     Campylobacter species Unclassified.
COMMENT      Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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ORIGIN

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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 1.14.6 from https://github.com/tseemann/prokka.
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3961 aaaaaataaa gaaatttatg tttataatca tcgctttgat agagtagtaa caaaagctat
4021 aaaaaataaa gaaatttatg tttataatca tcgctttgat agagtagtaa caaaagctat
4081 aaaaaataaa gaaatttatg tttataatca tcgctttgat agagtagtaa caaaagctat
4141 aaaaaataaa gaaatttatg tttataatca tcgctttgat agagtagtaa caaaagctat
SOURCE: Campylobacter species

ORGANISM: Campylobacter species

Unclassified.

COMMENT: Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES: Location/Qualifiers

- **source**: 1..3545
  - /organism="Campylobacter species"
  - /mol_type="genomic DNA"
  - /strain="strain"

- **gene**: 62..955
  - /gene="tssI1"
  - /locus_tag="OIDGCHHC_00077"

- **CDS**: 62..955
  - /gene="tssI1"
  - /locus_tag="OIDGCHHC_00077"
  - /inference="ab initio prediction:Prodigal:002006"
  - /inference="similar to AA sequence:RefSeq:AOH52008.1"
  - /codon_start=1
  - /transl_table=11
  - /product="type VI secretion system, secreted protein"
  - /protein_id="Prokka:OIDGCHHC_00077"
  - /translation="MIVSFLDDDIDKPYVSSSSLYNGTNPSLVLNPFDHDQTSLSKTI
  GVNEEGYNELTLSNIKKEQYILKAQKYDLVQHNFTQRILNDKSDSVDGTYNIERIK
  KVHTQTDLAKNANVVGEGYLTNVGLSNDTVIGLSNTLNVDNVRIVAKNSHEFVGEM
  KDIEGQANQNTIDIKKEIKNMKLLIEKSLTXIEKKEFFLNVQHNLSAIKDNTS
  LKSNSMQTKIEEQYSESENTETFDFQTDCEVKAGQILHQVGDTQIVTKDCVIKAG
  GVEVIIIDNSGLVVKGGELKAE"

- **gene**: 966..1781
  - /locus_tag="OIDGCHHC_00078"

- **CDS**: 966..1781
  - /locus_tag="OIDGCHHC_00078"
  - /inference="ab initio prediction:Prodigal:002006"
  - /codon_start=1
  - /transl_table=11
  - /product="hypothetical protein"
  - /protein_id="Prokka:OIDGCHHC_00078"
  - /translation="MKKPFYKLKRFYIPCIIIIIIFAVLAKLLYSPLYTIYWGMYHYP
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  DRYFEAFIKSCAGNNFVLHKGKEQIYFNLYNLFISGNSTNEQKYNLRASTRDLERQ
  IFEELKFKIHYEEFYDLEGVYDLKGTEYIGTAIFSFKTQLQNVFLSNAQLCSFED
  RNLMEFMKMKENIEFKNLDVKNIDDLKRNITYKIKLIDMENLNETQKALDECK"

- **gene**: 1768..1896
  - /locus_tag="OIDGCHHC_00079"

- **CDS**: 1768..1896
  - /locus_tag="OIDGCHHC_00079"
  - /inference="ab initio prediction:Prodigal:002006"
  - /codon_start=1
  - /transl_table=11
  - /product="hypothetical protein"
  - /protein_id="Prokka:OIDGCHHC_00079"
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361 gaataaatag ctttctgtaa ttgataaatt aattatatgag aagttgtggtatatggattttg
421 tatttttagtt aatttattag aatttttattatatatgaaatttttaggtatatggattttg
481 gaataatggaag aaataataggt ttgathaatttagtaaatttagtagatttgaatgtaaattttg
541 cttaaatagtag atatatataaaa ttagttgataatacactacatatgtaaaatttttaggtatatggattttg
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661 gattgatttgg tgtcatattttta ttaggataatgatttgaatgtaaattttttaggtatatggattttg
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841 tgataactataaa gaaataataggt gtgataaatttagttagttatatggattttg
901 tagttaaatag aactattttgaa atttaataatgatttgaatgtaaattttttaggtatatggattttg
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1021 agctataataaa ggaagtagtttatatttttaggtatatggattttg
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3061 ctttaaatagaa atacacagtttatattttttaggtatatggattttg
3121 aaagaaaaataatgtaaa atatatttttaggtatatggattttg
Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

**Features**

**source**

- /organism="Campylobacter species"
- /mol_type="genomic DNA"
- /strain="strain"

**gene**

- complement(77..217)
- /locus_tag="OIDGCHHC_00082"
- /inference="ab initio prediction:Prodigal:002006"
- /inference="similar to AA sequence:RefSeq:CKG86746.1"
- /codon_start=1
- /transl_table=11
- /product="hypothetical protein"
- /protein_id="Prokka:OIDGCHHC_00082"
- /translation="MRCIKIFKDYQKFPYGLDKLYSKDFITKLDFKDKAYNVLYNTGV"

**CDS**

- complement(77..217)
- /locus_tag="OIDGCHHC_00082"
- /inference="ab initio prediction:Prodigal:002006"
- /inference="similar to AA sequence:RefSeq:CKG86746.1"
- /codon_start=1
- /transl_table=11
- /product="hypothetical protein"
- /protein_id="Prokka:OIDGCHHC_00082"
- /translation="MRCIKIFKDYQKFPYGLDKLYSKDFITKLDFKDKAYNVLYNTGV"

**gene**

- complement(204..698)
- /locus_tag="OIDGCHHC_00083"
- /inference="ab initio prediction:Prodigal:002006"
- /inference="similar to AA sequence:RefSeq:CKG86821.1"
- /codon_start=1
- /transl_table=11
- /product="hypothetical protein"
- /protein_id="Prokka:OIDGCHHC_00083"
- /translation="MGDSIMLSTSLGLVGIFIFARFTNIKFLYLTLSVILVFSILNYWIKINIKEVKSIFSIYIIFTAIIVVYYLYTYGIESYDKLALLSSLEAEKLSIPQEYKARNYFGFLCTMTMFLVITFILLPCQLQAYLFCYSTEERKKSWSIFGVCNIFILLIASVYAMY"

**CDS**

- complement(204..698)
- /locus_tag="OIDGCHHC_00083"
- /inference="ab initio prediction:Prodigal:002006"
- /inference="similar to AA sequence:RefSeq:CKG86821.1"
- /codon_start=1
- /transl_table=11
- /product="hypothetical protein"
- /protein_id="Prokka:OIDGCHHC_00083"
- /translation="MGDSIMLSTSLGLVGIFIFARFTNIKFLYLTLSVILVFSILNYWIKINIKEVKSIFSIYIIFTAIIVVYYLYTYGIESYDKLALLSSLEAEKLSIPQEYKARNYFGFLCTMTMFLVITFILLPCQLQAYLFCYSTEERKKSWSIFGVCNIFILLIASVYAMY"

**gene**

- complement(699..2234)
- /locus_tag="OIDGCHHC_00084"
- /inference="ab initio prediction:Prodigal:002006"
- /inference="similar to AA sequence:RefSeq:CKG86849.1"
- /codon_start=1
- /transl_table=11
- /product="hypothetical protein"
- /protein_id="Prokka:OIDGCHHC_00084"
- /translation="MDEGLFENLVLVTEYIGAMQEKSNEFSNNSIFRSLEYDATVLPAAELECCYEFKHYKQSNNEAALGWAASYQLQALWQNSPKIDTIQNYHLPIKQKNPNPQAQERKLEIQNQLQSKGIEPLI1HTYPPPNDQSYEMKQRQNEFSRHRDNKTN EVREEEKSKFYTTLDWDFKFYSHFPIIKRSLKFFHTKEDIYTNQFTQIEILQKTHN ITLKLNLSQGEYKFDFAIDIKENDSKKEEYIIKENDEMPKDKYVRKLACKPYELDTLNQYIQAGDDEFFRRQIMENLRQDFIEFSWLIKTYLRFNP6TRKHMTLYDTFEIGKQTYDELMQDLSYACSGKFSNVPSKLSIKKEIYGDFREKVLYRVDMLVY"
//
LOCUS   OIDGCHHC_10   2521 bp   DNA   linear   12-APR-2021
DEFINITION Campylobacter species strain strain.

ACCESSION .
VERSION .
KEYWORDS .
SOURCE   Campylobacter species
ORGANISM Campylobacter species
   Unclassified.
COMMENT Annotated using prokka 1.14.6 from
   https://github.com/tseemann/prokka.

FEATURES   Location/Qualifiers
   source          1..2521
      /organism="Campylobacter species"
      /mol_type="genomic DNA"
      /strain="strain"
   gene            74..571
      /gene="trxB_3"
      /locus_tag="OIDGCHHC_00086"
   CDS             74..571
      /gene="trxB_3"
      /locus_tag="OIDGCHHC_00086"
      /inference="ab initio prediction:Prodigal:002006"
      /inference="similar to AA sequence:RefSeq:CKG87041.1"
      /codon_start=1
      /transl_table=11
      /product="thioredoxin reductase"
      /protein_id="Prokka:OIDGCHHC_00086"
      /translation="MLPFIDEMGVDWIDLNRKYKALDEEGRIIWLTYDEIYGKLYKLPDRVDSTSESREKFHDHYMDGKYNMVFTRFVDIRNERDERSAKALTDFLVSRAKLAALTPQQGYPNAPRYPYSPLEIIYKRKLKLLDPRIPAIYRNYFPRELRALKFGEENGIKD"
   gene            complement(576..1475)
      /locus_tag="OIDGCHHC_00087"
   CDS             complement(576..1475)
      /locus_tag="OIDGCHHC_00087"
      /inference="ab initio prediction:Prodigal:002006"
      /inference="similar to AA sequence:RefSeq:CKG87069.1"
      /note="Uncharacterized conserved protein%2C contains FHA domain"
      /codon_start=1
      /transl_table=11
      /product="hypothetical protein"
      /protein_id="Prokka:OIDGCHHC_00087"
      /translation="MIEKEELGITIENYDECISGSKAFVFDTKGGTGSGDCTFRIQ"
> locus_tag="OIDGCHHC_00090"
> /inference="ab initio prediction:Prodigal:002006"
> /inference="similar to AA sequence:RefSeq:CKG86610.1"
> /codon_start=1
> /transl_table=11
> /product="thioredoxin reductase"
> /protein_id="Prokka:OIDGCHHC_00090"
> /translation="MLKDFSKNFPMLDPFMNVQTETIQGILNMMDMDFMTQSEAYILAIATMDEYPVQFLEQGIEYTVLAEKR"
LOCUS       OIDGCHHC_12             2262 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

SOURCE      Campylobacter species
ORGANISM    Campylobacter species
            Unclassified.

COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES             Location/Qualifiers
  source          1..2262
      /organism="Campylobacter species"
      /mol_type="genomic DNA"
      /strain="strain"
  gene            370..510
      /locus_tag="OIDGCHHC_00091"
  CDS             370..510
      /locus_tag="OIDGCHHC_00091"
      /inference="ab initio prediction:Prodigal:002006"
      /inference="similar to AA sequence:RefSeq:CKG86746.1"
      /codon_start=1
      /transl_table=11
      /product="hypothetical protein"
      /protein_id="Prokka:OIDGCHHC_00091"
      /translation="MRCIKIFKYQKFTPYGLDFKLYSKDFITKLDFKDKAYNVLYDT"
      /translation="GV"
  gene            511..1020
      /locus_tag="OIDGCHHC_00092"
  CDS             511..1020
      /locus_tag="OIDGCHHC_00092"
      /inference="ab initio prediction:Prodigal:002006"
      /inference="similar to AA sequence:RefSeq:CKG86768.1"
      /codon_start=1
      /transl_table=11
      /product="hypothetical protein"
      /protein_id="Prokka:OIDGCHHC_00092"
      /translation="MGEDITLSIFWGLVGIFIFRVTIDTILTIALSVLIVFSIINIYW"
      /translation="IKINIEFKYSVYFLYFIIFFTAIIIFYLYSYLETSRGYVMLGPEVEELSPQEVIV"
      /translation="YKCSKFLIFINIFITITIFIPCLLQAYLFKRYSTEERKRLASWFIGFLCNIILIA"
      /translation="SAYLMYIFI"
  gene            1139..1645
      /locus_tag="OIDGCHHC_00093"
  CDS             1139..1645
      /locus_tag="OIDGCHHC_00093"
      /inference="ab initio prediction:Prodigal:002006"
      /inference="similar to AA sequence:RefSeq:CKG86719.1"
      /codon_start=1
      /transl_table=11
      /product="hypothetical protein"
      /protein_id="Prokka:OIDGCHHC_00093"
      /translation="MGDSITLSIMGMLFLYFVIFIKNYIIIALIVLIVFSIINIYW"
      /translation="IKINIEFKYSVYFLISFIIFTAIVIVFYLYDLETSGRLVLLGPPEIEELSPQEVIV"
DEFINITION Campylobacter species strain strain.

ACCESSION 
VERSION 
KEYWORDS .

SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers
  source 1..2057
            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
  gene 130..768
            /locus_tag="OIDGCHHC_00095"
  CDS 130..768
            /locus_tag="OIDGCHHC_00095"
            /inference="ab initio prediction:Prodigal:002006"
            /codon_start=1
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            /product="hypothetical protein"
            /protein_id="Prokka:OIDGCHHC_00095"
            /translation="MSEINNNAEIKEQDTEIIWEGKKIHPFLLFWITYIVLLCLFLYLFPLRNPSKEIDYKWIFVFTFLLIGYAFARAIYKMANIKRITKEKLVIYEYIKNPLVPLGTTFFIYRRQISYSPGHIIVHTFVDKAKLEYLPGFSDGDPTKGCFEKINAIKPVHMPYSSLSEEFKEFFHVNTTSEIDTTFLKEAMELRKEKKDE"
  gene 761..913
            /locus_tag="OIDGCHHC_00096"
  CDS 761..913
            /locus_tag="OIDGCHHC_00096"
            /inference="ab initio prediction:Prodigal:002006"
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            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:OIDGCHHC_00096"
            /translation="MNENIYGSLELYSKETQSTPSDKRLGVFGDLAPYALQVLRLLLRGLYK"
  gene 910..1527
            /locus_tag="OIDGCHHC_00097"
  CDS 910..1527
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            /inference="ab initio prediction:Prodigal:002006"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:OIDGCHHC_00097"
            /translation="MNENIYGSLELYSKETQSTPSDKRLGVFGDLAPYALQVLRLLLRGLYK"
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
COMMENT
FEATURES

LOCUS OIDGCHHC_14   1994 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.

source 1..1994
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene 96..239
/locus_tag="OIDGCHHC_00098"

CDS 96..239
/locus_tag="OIDGCHHC_00098"
inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00098"
/translation="MAQAQLLEDLSQKFIRSEKENIISSLKVAYPEKIDKIFVGK VYE"

gene 232..1485
/locus_tag="OIDGCHHC_00099"
CDS 232..1485
/locus_tag="OIDGCHHC_00099"
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inference="similar to AA sequence:RefSeq:CKG88360.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00099"
/translation="MNKTLIFHENSEINDLNASFAPGTYEILQLEKEDKLTNWSYVEC NSEKKMYLLDTDCHIEAKDLKFIDSFKGNCIGFHLIPRDNDEPTKDKIDYKYYYY IV FAYDEKIAIPSLEDHVIDMSFMRVGVGKDESEESKPRNDFNSDIQTCIFSVFEC VEFLKACQSFKEKNEIDNYVFKNQPAGKIAYYYYFLDANEFFIKSVSNDGNKLYK EREKYYKVASVYKINPDKMEFKKLQNOVDDIAKFLDFKARKLIDEKVLPI VGYNPQGDSGTYDVNTLDLNPASVYDFIDITIEHFRFHYICYKSNKSNIEKDDL YLDNVQFYIPWNFYKIFNSYDKKCLILYDNEDETKKLCLKNRTYGSWKFLNPTLDLPPS PLYYLQPSELDSRIMAYYFRKEIKL"

ORIGIN

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1621  tttgaaaatt  aataaagag  ggttttaaat  tttgataattc  tataattttt
1681  accttggcaaa  aatttttttt  gataaaaaag  acacacacac  catccccaaa  tatatttttt
LOCUS       OIDGCHHC_15             1445 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..1445
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene            76..855
/locus_tag="OIDGCHHC_00100"
CDS             76..855
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG88360.1"
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/transl_table=11
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/transl_table=11
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KQGLYNNSSYTVISNVMNIVKTQIETKIVHEIRHAYMQQKLLNDALQRMYFTYK
KYVFNAEQYLDENKDVYVQFQSETEARAIENIIKIEQ"
ORIGIN
1 tattatatta tagtttttgc ttatgatgaa aaaaaggcta tacctagttt agaagagat
61 catatagga tagatagag ctttagagta ggttagggga aagatgagag tgtgaaagga
121 agtaagctat ctagttttg aataatctgat accgatttta tagagaaag gaaaagagta
181 aatattagag ctgatttttata tagtttttgc ttatgatgaa aaaaaggcta tacctagttt
241 aatgagctat ctagttttg aataatctgat accgatttta tagagaaag gaaaagagta
301 attttttag aatattagag ctgatttttata tagtttttgc ttatgatgaa aaaaaggcta
tacctagttt agaagagtattt ctggtagtaaat ggttagggga aagatgagag tgtgaaagga
361 aatgagctat ctagttttg aataatctgat accgatttta tagagaaag gaaaagagta
421 aatgagctat ctagttttg aataatctgat accgatttta tagagaaag gaaaagagta
481 tagtttttata tagtttttata tagtttttata tagtttttata tagtttttata tagtttttata
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LOCUS       OIDGCHHC_16             1355 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..1355
/ororganism="Campylobacter species"
/mol_type="genomic DNA"
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ORIGIN
1 tctcactcta aaaacctaaa ccatatctc ttagaaaaa aagataaaaaa taaagaaatttt
   61 atcttttttaa ataatgcttc atcgatgtca aatttaatcc atattatatg taatcattgt
  121 gatgtattta ttaaaaatga ttctttgctt gatattaaaaa gaatagaaaaa agaatatgat
  181 attaaatatt aagaattttt tttgctttt aatactttt ttttatttaa
  241 aaagaaaaat atgaattttt aaagataatat attatatattt tttatatattt
  301 taccatatag aggatttaag tctttttaaa gattttaaattt aataaatattt
  361 gcaaggattt aagaatatctctt ccatagtaaaa aagagaaaaat aaaaagttaaatt
  421 gagcctaaaaa aagaaagtgc ctaacacatt cgaaggattaataaacttttc aaaaagaactt
  481 ttaaaacaatt cctcattcct tcatatagaa ccctgctttt tctatatattt tctataaagat
  541 gcccaacatat ccattctgtt gactcttaa atacatattatc caccatctttaatgataacat
  601 gctctttagag tagttattttt aaaaagagct aacgccttta ttaagatgtaa gatattggtta
  661 aaagaaaaagt atttttagg ttttttatttattttaaagatattgtagt atttttattttatttt
  721 tattttcta cctcctattct tatactattttaa atatatatttttatattatttatt
  781 gttggatcttt tattataatt tttatgatgg tttttgatatatttttatttttatttttattttt
  841 tatttttaaa cagtttattttt ttttttattttt ttttttttttatttttatttttatttttattttt
  901 gcaagcatcct tataaaaaaa cgggagccatatc tttttttttt atttttttttttttttttttt
  961 gataaaatga aagcggaaag gcgttattttt tcacattatctgatgttctgca cagagttatc
 1021 ttgggccttt tctctgaggg agagttataaatattttattttttatagagattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
    source 1..1314
        /organism="Campylobacter species"
        /mol_type="genomic DNA"
        /strain="strain"

ORIGIN
1 aaaaagataa aaaaagacaa acgataataa aagataatct atatctttttt acatcaataac
61 aaaaagagaga gtttgctgagt agtgtaggtg tagtttgatc ttcatgaaag
121 atttaagcaag cgaagcttag aatgggaaag ggattctgaa ttctttattag
181 tagatgttcc taagcagag aaataaatag taatatttcat aaaaagaaata gaagtgaagac
241 tcgtgtaga agagatgtg gtaagctcttg aaaaaagatct aaggtgattt ttctctcttag
301 agccaaaaat tgcaccaggg accttttagg aatgggaaag ggattctgaa ttctttattag
361 ttaaatctag tcgagttctat acataatctg aatggagaca taatataagtt tttatagttt
421 aagaatgaca ggtgtagtatg ttctctctct ttcagtttatt ttctttttatct aatcgtaaag
481 tctatgagtt ctggcaataa taataatgtc aatgggaaag ggattctgaa ttctttattag
541 ttggtcctat cttcagctag gttataatag taatataagtt tttatagttt tttatagttt
601 tctggtttaga agatagaaat gaaatataaa gactctctaa tttatagttt tttatagttt
661 tcatagatataagagatgc ttttggctctgt gcgtagagag agatagaaat gaaatataaa gactctctaa
721 caaagagaggg gactatcagct aaatgtagttttt aatcgtaaag
781 ctaatgtagtttt ttcagtttatt tttatagttt tttatagttt tttatagttt
841 ttaaatctag tcgagttctat acataatctg aatgggaaag ggattctgaa ttctttattag
901 aggataaatct tagttttagtct gtagagatga tagggtgaaa gcattgtagg
961 ctagataattact tagatcagctaa tagatcagctaa tagatcagctaa tagatcagctaa
1021 atcagttcctttt tttatagttt tttatagttt tttatagttt tttatagttt
1081 gagatgagag atcatcctag ctaatgtagtttt aatcgtaaag
1141 ttaaatctag tcgagttctat acataatctg aatgggaaag ggattctgaa ttctttattag
1201 ttggtcctat cttcagctag gttataatag taatataagtt tttatagttt tttatagttt
1261 aagaatgaca ggtgtagtatg ttctctctct ttcagtttatt ttctttttatct aatcgtaaag

//
LOCUS OIDGCHHC_18 132 bp DNA linear 2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
    gene 40..393
        /gene="trxB_6"
        /locus_tag="OIDGCHHC_00101"
    CDS 40..393
        /gene="trxB_6"
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// LOCUS      OIDGCHHC_19  1037 bp  DNA  linear  12-APR-2021
// DEFINITION Campylobacter species strain strain.
// ACCESSION
// VERSION
// KEYWORDS
// SOURCE      Campylobacter species
// ORGANISM   Campylobacter species
// Unclassified.
// COMMENT    Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
// FEATURES
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//          1..1037
//          /organism="Campylobacter species"
//          /mol_type="genomic DNA"
//          /strain="strain"
//          1..954
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// gene     Location/Qualifiers
//          1..954
//          /locus_tag=OIDGCHHC_00102
//          /inference="ab initio prediction:Prodigal:002006"
//          /inference="similar to AA sequence:RefSeq:AVS37497.1"
//          /codon_start=1
//          /transl_table=11
// CDS       Location/Qualifiers
//          1..954
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//          /codon_start=1
//          /transl_table=11
/product="type VI secretion protein VgrG"
/protein_id="Prokka:OIDGCHHC_00102"
/translation="MPQYNYPRYKREIATNALSYLSVAPAMIDKGLDTLKLQENTDYE
LSSINHYLTLANSTIGVDNADARARNEITLKNKDKEEIYILAQKDYEKKEIEGNNYEQ
TIKNNKTESEVGALTLGHSQNNIIIFGFKNVNGAETYLENEYLLSVDNTVGNGLNNTLVN
GISNEVNIQONHEEKIGNDKRIVINNNLEQDINFDIQRIGHKNKETIKGYSVLQTNQ
SIFKFSQKOLSEITNDFKAEDTFVSFKAKKNCSFTADEVYTMANKESFLTAQKQIV
SRVNGNTTIQTDKIIILQVGTQVIIIDSKGLRVQGDLRAD"

ORIGIN

1 atgccccaat ataattatcc aagatacaaa agagaaatcg ctacaaatgc attgagctat
61 ttaagcgtag ctcctgctat gattgataaa ggtttagata cattaaaact tcaagaaat
121 actgattagt attaagctc tataaacaat cattatctta ctattagcaaa ttctacaata
181 ggagttagata atgccgatgc aagagcaagg aatgaaatta ccctaaaaaa gcacaagac
241 aagaagaaga tttatatcct acgcacaaaaa gattataaag aagaaatagg taaaatttac
301 gagcacaacca taataaatatataaa tactctca gaagtgggag cccttataac cgaattatac
361 actttaggac atatgcaaaa taaaataaata taataacttca gaagtgggag ccttatatac cgaattatac
421 ttagaaatata ccttgctttc taagatgactaatgtgggtt taaatataac ttttggttgtg
481 gaagcagctga atgaagcagc tcctggcaca accacagaa aaagatctag aggctgtaaa
541 agagtaataa tcaataacac cctatacaca aatatcataa aatgtgttat tccaaaagaaatctgtaa
601 ggacataataa aaaaatagcaag ccctaaaaaat ccttcagtgc tcttattttc tcttacacaaac
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781 actatgcccc caaattgctaa tttatttttactttttaaac cgaacaaaaa aatattgggtg taggtgagaa
841 aataataactc tcaaaatataa aataaatgactaatgtgggtt taaatataac ttttggttgtg
901 attataataataaatgctaa aagatgctag ggtgaggcg gaaagatcgaa taaaaatatc tttttttttaa
961 ttttttttttaaataaatgctaa aagatgctag ggtgaggcg gaaagatcgaa taaaaatatc tttttttttaa
1021 atgaaatataataaatgctaa aagatgctag ggtgaggcg gaaagatcgaa taaaaatatc tttttttttaa

//
LOCUS OIDGCHHC_20 1028 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain.
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
  source 1..1028
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
  gene complement(554..910)
/locus_tag="OIDGCHHC_00103"
CDS complement(554..910)
/locus_tag="OIDGCHHC_00103"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:APB39663.1"
/codon_start=1
/transl_table=11
/product="VgrG protein"
/protein_id="Prokka:OIDGCHHC_00103"
/translation="MKGNKKEVVEGKLEHVNKGINYFTEEHFSMQUITDQYMNYYIDYTFEQN"
LOCUS       OIDGCHHC_21             1005 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..1005
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN
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121 ctttaaccgc ggtcattgctt ccctacttaat tttctgtactt ggtcattgctt fttctacttt  
181 ttgatcttctgcc ggtcattgctt ccctacttaat tttctgtactt ggtcattgctt fttctacttt  
241 tataactactc ctccttttttc ttcttttttt ctttaatacg tcaaatgatttctaatgtt  
301 gatagatatttttacttttttttttttcttttttt ttctttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
LOCUS       OIDGCHHC_22              961 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
          source          1..961
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
          gene          120..620
/locus_tag="OIDGCHHC_00104"
/CDS          120..620
/locus_tag="OIDGCHHC_00104"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86719.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00104"
/translation="MGDSITYLFILGLGFISVFTFARTYFITLAVFIIFSINYWMR INIKEFKVSYFLIFFWIFADITYGFYFGYFNENPAKFTSLFEVKQLPSEELYLVFSC LAFLIIMEFIITFFILPCLLQAYFKCYFSTGEKRKKLSWFIGFACNIFLLIVSFY KLYENL"
          gene          607..738
/locus_tag="OIDGCHHC_00105"
/CDS          607..738
/locus_tag="OIDGCHHC_00105"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86746.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00105"
/translation="MKIFKDYQKFTPYGLDFKLYSKDFITKLDFRDKAYNVLYDIGV"

ORIGIN

1 aagactatca aaattcact ccttatggtt tggattttaa actttatagt aaagatttta
61 tcataaaact tgatattttaa gataaagctt ataattgtct ttataataca ggggtttaaa
121 tggggagatag cattacactt tataatatt ttggcctttta gggatttatt agtttcctta
181 ctttttcgaag aaccttaattt ataattcttaa ttgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgatgat
LOCUS       OIDGCHHC_23              932 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM    Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
  source          1..932
                     /organism="Campylobacter species"
                     /mol_type="genomic DNA"
                     /strain="strain"
  gene            126..539
                     /locus_tag="OIDGCHHC_00106"
  CDS             126..539
                     /locus_tag="OIDGCHHC_00106"
                     /inference="ab initio prediction:Prodigal:002006"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:OIDGCHHC_00106"
                     /translation="MFKKLALFLPVYLLFLAGGSYKMDPQYYEFKSLCYFNGLK
VLIEDESIKNTNIVTPK5QIKDRIVETRFRKENQVYYINTYFYDNYGFLK
GDEGAGLYFRYMEVL5CKNIDDKKFKDDWQVETLE"
  gene            543..683
                     /locus_tag="OIDGCHHC_00107"
  CDS             543..683
                     /locus_tag="OIDGCHHC_00107"
                     /inference="ab initio prediction:Prodigal:002006"
                     /codon_start=1
                     /transl_table=11
                     /product="hypothetical protein"
                     /protein_id="Prokka:OIDGCHHC_00107"
                     /translation="MNKNIKTQEAKLDLITKFLYANCADASYAMLHLIDENDEKGFL
KG"
ORIGIN

1 ttaatctttt aatatttttt cttatatatttt tcttttttttt ttatatatttt tttatatatttt ttatatatttt
61 tatatattttttttt atatatattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
gene 49..222
/locus_tag="OIDGCHHC_00108"
CDS 49..222
/locus_tag="OIDGCHHC_00108"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:OIDGCHHC_00108"
/translation="MDNALKTNMQMSLHKIVDMHPYWNTRYVLEGNENMNFE FIEDELACGNLYQ"

gene 394..609
/locus_tag="OIDGCHHC_00109"
CDS 394..609
/locus_tag="OIDGCHHC_00109"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86895.1"
/codon_start=1
/transl_table=11
/product="methyltransferase small"
/protein_id="Prokka:OIDGCHHC_00109"
/translation="MDYFKALHDEYGNLVDSLFFYAKLNGDFRELQARNFSQRYE IKFQSNTTSGFSTALSYEKTEKIKRS"

ORIGIN
1 tacgatgata cttacaaaac tcttttaaat tttaagagag aagataagac ggataaatatt
61 gcaatattatat tttataaat gctaatgatag gctataggtag aagctttggag
121 ccatattgga atactagaag gtatgtgtta gaaggcaatg agggtaatat gaattttgag
181 ttatagagg atagctctcg tttgtgccaa atttatcaat aatattatat ggaataaata
241 atgaccaata aagacatttt aacatttttt cattttttgt gtagctttag
301 tatattttttt ttgatttttt tgaagagag aagcttttag gatatttttt actattaaact
361 agatttttta aagataagag tgaattagaa aaattggact attttaaagc attacatgag
421 gaatatttttt ttttatttttt ttgtttatttt aagcttttag gatatttttt actattaaact
481 gatttttagg aattttacgt tagatttttttt tctttaagag atgagctttgc atcttttgttgc aagcttttag gatatttttt actattaaact
541 tccacacacta caagttggttt tagactctgct ttgcttttag agaagactg caagcttttag gatatttttt actattaaact
601 aggagttaat aatgtcatag tagtttttttt ttttattttttt tattttttttt tattttttttt tattttttttt tattttttttt tattttttttt
661 ttttttttttt ttttatttttt tattttttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt
721 ttttttttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt ttttatttttt

//
//
LOCUS OIDGCHHC_26 730 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES source 1..730
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
LOCUS       OIDGCHHC_28              639 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

FEATURES             Location/Qualifiers
source          1..639
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
gene            complement(20..562)
    /gene="trxB_7"
    /locus_tag="OIDGCHHC_00111"
CDS             complement(20..562)
    /gene="trxB_7"
    /locus_tag=" OIDGCHHC_00111"
    /inference="ab initio prediction:Prodigal:002006"
    /inference="similar to AA sequence:RefSeq:CKG87041.1"
    /codon_start=1
    /transl_table=11
    /product="thioredoxin reductase"
    /protein_id="Prokka:OIDGCHHC_00111"
    /translation="MLKDFSKNPPYDEMGMLPFLDELIGVDWVIDPNRYRFAEDEKGR
VNDALKDDVEKILKDPREDSTSESRLFEYKLDAYRNGMKTRFDGDNPNAWSKEQV
ERFNTDLILCAKLAALTPQGTYNAPYYSPERLEFIYKNHNLKDLDPRAIPAIYR
FPRELRAKILKFGENGIKD"

ORIGIN
1 gtctgcctat gaggttactt taatctttaa tgccattttc ttcgccaaat ttgagtatct
61 tagctctaag ttctcttggg aaattatatc tataaatagc agggattctt ggatcaagga
121 gtttatctaa attatgattt ttgtaaataa actctaatct ttcaggagag taataataag
181 gtgcattagt atagccttga ggaggaatga gggtcgcag tttgccacat aataaatcag
241 tatcattaaa tctttctact tgctctttac tccaatgatt tggattatct ccatcaaatc
301 tagttttcct tccattttta taacgtctca attatatag cttccagcct tacctcttg
361 aagtagaattc tatatccttt ggtatatgta gttatctttta tcaacatcaca tctttttag
421 catcattacc tctcttttct ctctcctctg cattacctga ctcttctctg cttaccccc
481 aatcctattc ttaagatgct taagactgcag ggaaggagtg aatcctattc ttaagagagat
541 ttttagaaaa gcgctttgctc attgagcctc taagagggtt tttgtgatag ccatctgtta
601 aatcttatg agctatagaa tcataaagac ttttaaac

LOCUS       OIDGCHHC_29              629 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
ORGANISM  Campylobacter species
Unclassified.

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES  Location/Qualifiers
source  1..629
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene  complement(50..616)
/locus_tag="OIDGCHHC_00112"

CDS  complement(50..616)
/locus_tag="OIDGCHHC_00112"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG88165.1"
/codon_start=1
/transl_table=11
/product="ribosomal protein L7/L12"
/protein_id="Prokka:OIDGCHHC_00112"
/translation="MAKNVNVGEYLTNGSKDLKVTGGLNTAVDKNKVRKAVKNSH" "

//

ORIGIN

1 tatataaaat cttttaagtt tgttaaaagg ttttttcatt gcttatcctt tactctgcct
tytttcatt gttttcatt tactctgcct
61 taagctctccaccttaacc acaagtccat tagagtctat aatcacttct actccacctg
tcaagtctat aatcacttct actccacctg
121 ctttatagat aacacaatca ggttttgcgt taataatttg tttttctacc tgtatagtct
181 cttcgctatc ggcttttaac tcatgaatag tttttgcgta agtttgata tttacagct
241 ccatttgcgtg tttttataatca gtttaattct cttttttctctt gccgtaatgc
301 tgtctttttct tttatatcct actcttttct tgtcttttct tttttttctct tttttttctct
361 taatctactagccttacctaatccatactactataatccatactactactataatccatactacta
421 cttatatgtg tattagcttctt gcgtatatct tattacattct tattacattct tattacattct
481 actcatgaga gttttttagcc actctttactt actattattct actattattct actattattct actattattct
541 ttaatctact ctactaatat gttttttagcc actctttactt actattattct actattattct actattattct actattattct
601 tattactattactatagcttat gcttatcctt tactctgcct


//

LOCUS  OIDGCHHC_30 587 bp DNA linear 12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS  .
SOURCE  Campylobacter species
ORGANISM  Campylobacter species
Unclassified.

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES  Location/Qualifiers
source  1..587
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN

1 atgagtttct gtaagattac aaatctatta tttctttct tttgagataa ggagccttta
ttttctttct tttgagataa ggagccttta
tttatgatg tattagcttctt gcgtatatct tattacattct tattacattct tattacattct tattacattct tattacattct
tattactattactatagcttat gcttatcctt tactctgcct
| Source | CDS           |
|--------|--------------|
| gene   | 218..316     |
| /locus_tag="OIDGCHHC_00113" |
| CDS    | 218..316     |
| /locus_tag="OIDGCHHC_00113" |
| /inference="ab initio prediction:Prodigal:002006" |
| /codon_start=1 |
| /transl_table=11 |
| /product="hypothetical protein" |
| /protein_id="Prokka:OIDGCHHC_00113" |
| /translation="MSKNIKTQEAKLDSLKFLDNYANADASLYAM" |

**ORIGIN**

| ORIGIN | 584 bp |
|--------|--------|
| LOCUS  | OIDGCHHC_31 |
| DEFINITION | Campylobacter species strain strain. |
| ACCESSION | . |
| VERSION | . |
| KEYWORDS | . |
| SOURCE | Campylobacter species |
| ORGANISM | Campylobacter species |
| Unclassified. |
| COMMENT | Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka. |

**ORIGIN**

| ORIGIN | 517 bp |
|--------|--------|
| LOCUS  | OIDGCHHC_32 |
| DEFINITION | Campylobacter species strain strain. |
| ACCESSION | . |
| VERSION | . |
| KEYWORDS | . |
| SOURCE | Campylobacter species |
| ORGANISM | Campylobacter species |
| Unclassified. |
LOCUS       BKOFBKEE_1              7180 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM    Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
                      source          1..7180
                      /organism="Campylobacter species"
                      /mol_type="genomic DNA"
                      /strain="strain"
                      gene            348..851
                      /locus_tag="BKOFBKEE_00001"
                      CDS             348..851
                      /locus_tag="BKOFBKEE_00001"
                      /inference="ab initio prediction:Prodigal:002006"
                      /codon_start=1
                      /transl_table=11
                      /product="hypothetical protein"
                      /protein_id="Prokka:BKOFBKEE_00001"
                      /translation="MKILEKDFDICKIYIQKWEKNINKKFDSSRGVNFPCISEPV
                      CYAFLNYWNNNETGDATSDSGLIEIKATSNNFSDLSSFSNTKFDKLFVRLDGQR
                      DLYYDIKELENEEQFQILEVNKEKTVDQQKKQSNRRPLSLIYQQIEKEKIEPLYYVDFI
                      KKVITKN"
                      gene            921..1844
                      /locus_tag="BKOFBKEE_00002"
                      CDS             921..1844
                      /locus_tag="BKOFBKEE_00002"
                      /inference="ab initio prediction:Prodigal:002006"
                      /inference="similar to AA sequence:RefSeq:ASE91810.1"
                      /codon_start=1
                      /transl_table=11
                      /product="DNA (cytosine-5-)-methyltransferase"
                      /protein_id="Prokka:BKOFBKEE_00002"
                      /translation="MKVASFFAVGVIDLAFSNHIVYLVNEIDKNATKTFKNFDEV
                      DCRDIQTVNEKELPDFICTLGGFPQCSAFLAVYGKFLNSRGNLFFDIIRAEKCPK
                      IIFLENVKNLSVSHCGRKFIKLSLGSYYVYDVNLAMHGYGTNPQRERIYIVCF
                      KNKGYKDFNPNPPFLLNKNIDIVFNLKVDLKFFVPTEKKNFHLYMLQNTKNNVI
                      YQWRRKYYRNKNSYCPTTLANMGTGVMVPLVTGHIRKLTPECFMFQGFPNSYK
                      LPIADNHSNLKQAGNVSVCVKVQRIADRSN"
                      gene            complement(2128..2328)
                      /locus_tag="BKOFBKEE_00003"
                      CDS             complement(2128..2328)
                      /locus_tag="BKOFBKEE_00003"
                      /inference="ab initio prediction:Prodigal:002006"
                      /codon_start=1
| gene        | complement(2329..3009) | /transl_table=11 | /product="hypothetical protein" | /product_id="Prokka:BKOFBKEE_00003" | /translation="MGFKNINTEKASINFANNARGDKINTQKRDILVSFTQDEYDVKESALIQMGVQYIRYKLFI" |
|------------|------------------------|------------------|----------------------------------|--------------------------------------|--------------------------------------------------------------------------------|

| CDS        | complement(2329..3009) | /locus_tag="BKOFBKEE_00004" | /inference="ab initio prediction:Prodigal:002006" | /inference="similar to AA sequence:RefSeq:ASI88294.1" | /codon_start=1 |
|------------|------------------------|-----------------------------|--------------------------------------------------|--------------------------------------------------|------------------|

| gene        | complement(23589..4917) | /transl_table=11 | /product="Plasmid partitioning protein ParA" | /product_id="Prokka:BKOFBKEE_00004" | /translation="MIISICNEKGGSKSTLAVNLSSRLTEDGDSILLFDPQRSVEFNINRNNSNLKQNFKSDFINLNSGFKNELNYDIAITDGGGRDSREMRAKAMLLSNNVIIIPASQYDVSDLHMLNITYEYVRFKLNIILLILINVSPCPFLIKELNNLIDYTHEKEVNLNDVFLESVLYERQAYIIKRAVIEGKSIIEEECSDKNDKALKDFEKFYYQEIFQILKNNKD" |
|------------|------------------------|------------------|---------------------------------|----------------------------------|------------------------------------------------------------------|

| CDS        | complement(23589..4917) | /locus_tag="BKOFBKEE_00005" | /inference="ab initio prediction:Prodigal:002006" | /inference="similar to AA sequence:RefSeq:APA51640.1" | /codon_start=1 |
|------------|------------------------|-----------------------------|--------------------------------------------------|--------------------------------------------------|------------------|

| gene        | complement(24921..5085) | /transl_table=11 | /product="mobilization protein" | /product_id="Prokka:BKOFBKEE_00005" | /translation="MSYDEIEKVKRSAYTKTASESTKRNYISSGNFKKSTSFQVFHNA NVRPDAIGGELVFDLLGGYEALELKHKIVSEAKEAYKNSPKAKFKSASLYWESLVVNIKPDSTMNDLKNLSKHFEKYGFQCYQIAIHRDEGFHNFQEGKLNHHAMFETILD KETGKNFRRFREPKSVLRIETQTEIAEILGMERGEDKFRGSKRINPRAYAALKEKKREKRRKINLEQEQQIEQKEQFLKSNSEYKIIENFRKSOQQNGQGLDFDKFKESELKFNFOEQI KEDNLSELNDLIRHLEIREKIKSKENILKAELELLKQEPKDNDNIDQEQKNASER NEFKNKDNTEDKIFKEKLATLAEKNLSKYYKPSKPKRLKIREPETAEKIKKIKLITE TMEKTEAYLPETLKKWWNLNDKIDLKEILVAYQNTLSKELKQSKSIYKGR" |
|------------|------------------------|------------------|---------------------------------|----------------------------------|------------------------------------------------------------------|

| CDS        | complement(24921..5085) | /locus_tag="BKOFBKEE_00006" | /inference="ab initio prediction:Prodigal:002006" | /inference="similar to AA sequence:RefSeq:AS188294.1" | /codon_start=1 |
|------------|------------------------|-----------------------------|--------------------------------------------------|--------------------------------------------------|------------------|

| gene        | complement(5488..5823) | /transl_table=11 | /product="hypothetical protein" | /product_id="Prokka:BKOFBKEE_00006" | /translation="MDYEKYSKMNLRQLINAYTNAEKKKEKRLIDDFQKLDENKLIMEME FLKTIKESL" |
|------------|------------------------|------------------|---------------------------------|----------------------------------|------------------------------------------------------------------|

| CDS        | complement(5488..5823) | /locus_tag="BKOFBKEE_00007" | /inference="ab initio prediction:Prodigal:002006" | /inference="similar to AA sequence:RefSeq:APA51640.1" | /codon_start=1 |
|------------|------------------------|-----------------------------|--------------------------------------------------|--------------------------------------------------|------------------|
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene
complement(117..386)
/locus_tag="HKBNLMBC_00001"

CDS
complement(117..386)
/locus_tag="HKBNLMBC_00001"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AMK28635.1"
/codon_start=1
/transl_table=11
/product="addiction module toxin RelE"
/protein_id="Prokka:HKBNLMBC_00001"
/transl="MKYNIKYSSKFKHYYKKNLTDQKEEQKTIIERALGPLEPKYKH
HALKDGLFRECHIIPDLILIYQKQDQKILYCFDQSHSELF"

locus_tag="HKBNLMBC_00001"

CDS
complement(386..700)
/locus_tag="HKBNLMBC_00002"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:HKBNLMBC_00002"
/transl="MLAQEKDNDSGYIYTEKLTKSERQLKVMLDTLEKTIQAEK
AKLESLKDCDKGKFKVQDLMKLKWRTPSAELAMQELKNGGTLCSMEFDRQMAE"

locus_tag="HKBNLMBC_00002"

CDS
complement(871..1971)
/locus_tag="HKBNLMBC_00003"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:HKBNLMBC_00003"
/transl="MAKNTDIVELKEGFRNQSVSNVSNIANARTKMTALEKTYQVS
TLQMDTEFKEYEISVSDFQLKALNISDQREQVQKLCRRLIRQVEFIQENQGEYIAY
TIFSORMNYKHEEQXISMKFNEEFPRFLEELKQFTKIQKVYIKSKFQSKSYFQYALK
DYRKMOSQDFKNLENIFNIFELPKTYNTRKYQYVLKPAIDEINAKDSLWSEQEIIGK
KGKKTIDIRLYFQNKNEKMSDFTEKELIKQYNKFSNFVNFAVCRLAGDFNTINDLMK
ITRIESTKNTYFYRHNSGFEESCIIGTPKNDLNSLANGIYRAINLIYEKEKKKQA
LPTMQWQDDKDKLFKSKILKLEQENPEAKIY"

locus_tag="HKBNLMBC_00003"

CDS
complement(2315..2965)
/locus_tag="HKBNLMBC_00004"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:HKBNLMBC_00004"
/transl="MNNIDDIRIKEKDYDITIKYIEWCNELKNKNEILQDKIVMTIST
ALFGRIVNLDSLLLYTHWTKLIFITLLINSVTIIFLLISLKMANKSIENDIESV"
YNNTIKRKYFYIAKWTQYIYLLSFAFVTIIFCIILCIVSYKELTMDKKQENNIIHMCN
ESYLGTSKPIFSDYLSKQNNQENNKKINSNNTDNSSTLNLNNIQSSTLENEKEKD"
gene complement(2962..4677)
/locus_tag="HKBNLMBC_00005"
CDS complement(2962..4677)
/locus_tag="HKBNLMBC_00005"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=1
/product="hypothetical protein"
/protein_id="Prokka:HKBNLMBC_00005"
/translation="MGAISSINFKKSNAIQTRHNDRLPPNYLGIDCECNTHKEAL
TLKNQIIKGYITEGTGFKQAQYSWEYSNIEKPTDMQDLERIALFLNKKGFY
CYQIANHRDEGHINEQGKEINHHAHELITNLKENGRMWRRELITPKVLRQMQSEV
AEILGMRQGQDKRTKRIEPRKQAQMEKADKDIQELQSELAAKEIERLEAKAWI
LEKNTAKEEYKALKELNKNYTKEDEIONLKEKSLASDEENRNLENLKQEO
MGLNEVNILAFPPFSFDKFTKLISVEYQNHXKFNSYFDEKEKFKSNRRFLDKVFQDN
GNSIALNNSNNQMSKEVSLMKMAMVKGWDLNLIKGSDFKAEYCQYIAEQKNK
IKELENSLNEKQKDEHNEKNDKLKPISDQTNDKELEAKIEEINENKKEK
LLLNGRNLNLYFVKELGDNYSSLNDFDMKNEKISEDFINNYGIESLWDLRDIKILKYCKIY
TYLKDLPFFNPQYEAYENKLSTISLLEQRRKXNNPKNLQDFTNQTRKND
QGFSR"

ORIGIN
1 cgtgcgatta cattcacaat cggcccaaat taagtaatta ggcggtaaat ctctgtcatt
61 atgccttgtt tgaatagcat cgccaccaat taagtaatta ggcggtaaat ctctgtcatt
121 aataactcgc tattgagcc tatatcaaaa caataaagaa ttatttttatc atcttgtttt
181 aataactcgc tattgagcc tatatcaaaa caataaagaa ttatttttatc atcttgtttt
241 ttttaaggct gatctttgta ttttggttcc aaaggcccat cattagctaa acgctcaata
301 attgtctttg tttcttgttg ttctttggtg tttagcttct tgtaatgcta tttaaattta
361 gaagaatatt tgatattgta tttcattaat cttccgccat ttgtctgtca aattcttcca
421 ttagtctaca aagctttcaa cggccatttt ttaactcttg ccatagcttct aaattcttcca
481 cacaggtgtt tgcgcttttt ttcattaaag catcttttac aaagtgccct ttttttaattt
541 tgtcttttag tttgcttttt agctttgctt tttctgcttt tttctgcttt tttctgcttt
601 ctataactcgc aacgttggta tttctgtttt cttctgtttt cattagcttt cattagcttt
661 agatatattg agatattgta tttcattaat cttccgccat ttgtctgtca aattcttcca
721 atatatattg gattagtttc atatcttattg atatcttattg atatcttattg
781 taataatttct gatattgact cattactttt ttaataaaac aataaagctt tttttatttt
841 ctgctttatt tttttatttt tttttatttt tttttatttt tttttatttt tttttatttt
901 cctatttttt cattcttttt taatttttttt ttttttttttt ttttttttttt ttttttttttt
961 tgttagttat ttgctttttt tttttttttt tttttttttt tttttttttt tttttttttt
1021 atggctttta gaaatttaaaa aatcatcttt attttctttc atttttttttt tttttttttt
1081 accaaaaact ttagatattg aagcttttaa ttttcttttt ttttcttttt ttttcttttt
1141 tattttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1201 cagctttattt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1261 cccctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1321 tctctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1381 ggtgtttttt ggtgtttttt ggtgtttttt ggtgtttttt ggtgtttttt ggtgtttttt
1441 attaaaaata aataaagctt tttttttttt tttttttttt tttttttttt tttttttttt
1501 ggctttttttt ggtgtttttt ggtgtttttt ggtgtttttt ggtgtttttt ggtgtttttt
1561 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1621 aatctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1681 gccttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1741 ttgctttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1801 atactttttt ttggcttttt tttttttttt tttttttttt tttttttttt tttttttttt
NMKLNOQRNFNYNDKLWQFNDFDNEFKIIAVELQREDYENLNFANHMHFNAKQEQFF

KMDTFRNGIR"
/codon_start=1
/transl_table=11
/product="Ssb"
/transl_table=11
/product_id="Prokka:BDFFJJMB_00002"
/product="DNA topoisomerase III"
/product_id="Prokka:BDFFJJMB_00003"
/product="cpp47"
/product_id="Prokka:BDFFJJMB_00005"
/gene complement(3612..5654)
/locus_tag="BDFFJJMB_00003"
/CDS complement(3612..5654)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:APA82025.1"
/codon_start=1
/transl_table=11
/product="DNA topoisomerase III"
/product_id="Prokka:BDFFJJMB_00003"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ADT73517.1"
/codon_start=1
/transl_table=11
/product="Hypothetical Protein"
/product_id="Prokka:BDFFJJMB_00004"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:EAQ71790.1"
/codon_start=1
/transl_table=11
/product="Hypothetical Protein"
/product_id="Prokka:BDFFJJMB_00004"
/translation="MAFIKLSNGSNPRLMVDVNNALNYKDAQTGEIKQRQVATALVDV IEEAGKVAGMDQGAVTASFKINNEWKNYFVNRKDSHNIVLMPTDAKERSNRDNHVFI NNHNKESKRVHAINDKREAGK ALIEGIGISEFQNGSDKSYLFYLDTHIKLSNWEK ALEKTKEKGGDYLAVNRNGGFEIKNEVEKMKEQSKQQDGFSKEETIGQTQEIKEPEKT QNQEFGR"

gene complement(7146..8027)
/locus_tag="BDDFFJMB_00006"
/CDS complement(7146..8027)
/locus_tag="BDDFFJMB_00006"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:EAQ71821.1"
/codon_start=1
/transl_table=11
/product="cpp46"
/protein_id="Prokka:BDDFFJMB_00006"
/translation="MMAEENQNLFDDEIQENENESNSLFEVEIKICNYQEIEQIK ILEILNINIGILNTDENTKEGIFIKDLEQNFNFKLNTNIKTLISFYKNPSQEELEI INKTLLMKELETLLNSSFLNLKIEDFAQQTQLRALLNDLNFLVNDNTLLESLNSALT GDDNLKDFKEEKIELRLLSSLQTYDQFLKLFEKKAILDSFQISTSRTIKNIKRAI STLIFFTFFGIFSFGVSYIVLYKYEDYKKITHNAQKLSSIVKENKDSSLTSFPKNKT ILNKDENGHITLQGGE"

gene complement(8027..8785)
/locus_tag="BDDFFJMB_00007"
/CDS complement(8027..8785)
/locus_tag="BDDFFJMB_00007"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ADT73520.1"
/codon_start=1
/transl_table=11
/product="YggA-like protein"
/protein_id="Prokka:BDDFFJMB_00007"
/translation="MKKIFATILFFGVSSSSNIAKIDVLTGDKLACEAMLLASPV KPPCGAALARYFSIDARKWADVIARKRSFLNLCPVDASSPEMYKYKNDILVHDGE CTIPVNLKRIEIVLTERTINCSHDGCTCIEITHGYRINPQLTNSGCRASSKTY DHLKYLTNCNFYKEDWQRYEKQESYNIPLISEQKEQGEKLVPSYAEFVRLP VNKRRQIGFKGYYRIDIAFYQIKIIIKDCWNEK"

gene complement(8782..9213)
/locus_tag="BDDFFJMB_00008"
/CDS complement(8782..9213)
/locus_tag="BDDFFJMB_00008"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:EAQ71817.1"
/codon_start=1
/transl_table=11
/product="cpp44"
/protein_id="Prokka:BDDFFJMB_00008"
/translation="MKKTLSFLLLTSIVFTGCAVSAKPKKLEGSSKLQLNSLLEER YKFVPDKSRLSNMDWYQLELAKNEGLLSNEQVVKTFILLAHAKNRIILGEKNVIQE YNEYFKKNGVQAEILQLPNIIIKGNKNTNMLFFHAKGENK"

gene complement(9197..10993)
/locus_tag="BDDFFJMB_00009"
/CDS complement(9197..10993)
/locus_tag="BDDFFJMB_00009"
/inference="ab initio prediction:Prodigal:002006"
gene complement(10990..12003)  
/locus_tag="BDFFJJMB_00010"

CDS complement(10990..12003)  
/locus_tag="BDFFJJMB_00010"

/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:EAQ71814.1"
/codon_start=1
/transl_table=11
/product="cmgD4"
/protein_id="Prokka:BDFFJJMB_00009"
/transl_table=11
/codon_start=1
/product="virB11"
/protein_id="Prokka:BDFFJJMB_00010"
/transl_table=11
/codon_start=1
/product="P-type DNA transfer ATPase VirB11"
/protein_id="Prokka:BDFFJJMB_00011"
/transl_table=11
/codon_start=1
/product="virB9"
/protein_id="Prokka:BDFFJJMB_00011"
/transl_table=11
/codon_start=1
/product="virB9"
/locus_tag="BDFFJJMB_00012"
CDS complement(13163..14056)
/gene="virB9"
/locus_tag="BDFFJJMB_00012"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ATG66341.1"
/codon_start=1
/transl_table=11
/product="P-type conjugative transfer protein VirB9"
/protein_id="Prokka:BDFFJJMB_00012"
/transl_table=11
/translation="MKNITLISLSLFPLASTAFALNEPQKSEYDQRIAHAEYNSKDVFKMIARNGPSVIEPGDDEIIINTATGFAEGWLIEKNNFLFIFPKAYKTTLFVENDPY
NQSSQKEMIVDPNPRDWKTNLIVTNLKYIFDLUHNLNDSKQATYKLSNFYSDDIKLQK
ESEIIKELEKIKIIEELKNIVRNPWDFLMKANKGSEDIAPNYAYDDGFTYLFNDFNT
KTIFSVIDYENGKMIILNHIRDGKYDVLVQKIAKQILRSVGKVGIFVNGFKN
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41289..42497
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61 atacctttaa cccatatctt aatcttgatt ttactataag gaaacgcgca ccatttgggt
121 tcgatatttg tccatatcat attgtctca ttggagaaat ggtttaggtggt
181 gaacaggtag tataaaacca taatgtagcc aataatctgc ctctggctt tataatctg
241 atcctataat gaaaaatgtga tggatattcttt ttttatttgatt tataatctg
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421 cttcaatatttt gttcagcctg acgtcgggtg tttttagctat tattttttgt
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//

>>BfR-CA-15843_min_cov_30 putative plasmid location
| Feature | Location/Qualifiers | Description |
|---------|---------------------|-------------|
| source  | 1..19540            | Linear DNA  |
| gene    | 51..251             | Campylobacter species strain strain. |
| CDS     | 51..251             | Protein product: hypothetical protein |
| gene    | 522..872            | Protein product: hypothetical protein |
| CDS     | 522..872            | Protein product: hypothetical protein |
| gene    | 969..1529           | Protein product: hypothetical protein |
| CDS     | 969..1529           | Protein product: hypothetical protein |

**Comment:** Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
gene 1548..1853  
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CDS 1548..1853  
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gene 3235..3561  
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gene 3571..4017  
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CDS 3571..4017  
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gene 8908..9597
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gene 9879..9983
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/translation="MGVNPSSYIMDASKGNELEAKEAQQGLFDMRKK"

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gene complement(11080..11412)
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RREVYPIV"

gene 11879..12379
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gene complement(12538..12981)
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CDS complement(13574..14446)
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/note="Domain of uncharacterised function (DUF3825)"
codon_start=1
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gene complement(14582..15013)
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gene complement(15026..15808)
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CDS complement(15026..15808)
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ENMAAAGAVAGATGAAAGSYNGGAGGMAAGAGALGVLGLKIDTDIWQMVDI
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gene complement(16351..17010)
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LOCUS       IKNDEOKD_3              4643 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM    Campylobacter species
             Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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CDS
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LOCUS    IKNDEOKD_4              1042 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
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CDS             77..589
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DIDIDPYPVVSSLNYGNTTMMQPQNYPRKREIATNALSYLSVAPAMIDGLDSTL
KLEENTDYELSSINNHYLTLANSTIGDNARNEITLKNKDKKEEIYILAQDYKEEII
EGINMYEQTIKNTSEVGALYTEFITLEHGMONIIFFKVNMEAYLENTPLSADTKN
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GSYVLQTQSIKFSQSDLSSITNDCFCAEADTFVFSFKKNCSCADDEVYTMANKE
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gene  7477..8346
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FFVGGINSYSFDELLQNIQLNFLKHEYIKNQFIVKFDALKLKELEYINETKEVLQKI
FVLFKYVHGIKLKIKAIEKSSVQKVQADQADLILSTGHSKGLMWNVNEIIIDFLNIKQ
ELEERDTQITAIKEELNNLYVAVITRAKNSLSISKDYLEKEFQGENLERIIIE""

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| /protein_id="Prokka:IHOPMAOI_00021" |
| /translation="MKIIKKLQKDGSLKKQVYYSVQEVSQMHSVTHVTVRLWSRGIL
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| CDS             | 16701..17621 |
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| /transl_table=11 |
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FEYYIYCYQFQIDKESLFFGNYELVFCFLYYRALNNKNNTQKVAKIINVIRCQD
RLPEHKHYREKIIICMDNQHRDSLQSLLSCTIAEFNISLNYTPRKNIFENGKRKIAIE
MLNRAEYHGFFGSAQGITYKEEKISCVPQALDEFHGMSHLCAVFLKEDGRTYNL
ERAIHPHKRGMEVYKYTIIRDFMLNKDLAVGQKEALKIRELEYQTIGPKTVKNPT
TNLTNKKEEVIPIGKYELCEKIVSKQIMN""

| gene            | complement(17721..18749) |
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ORIGIN
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LOCUS       IHOPMAOI_2              7392 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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ORIGIN

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LOCUS       IHOPMAOI_3              1938 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION  
VERSION    
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT    Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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**ORIGIN**

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LOCUS       IHOPMAOI_4               830 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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LOCUS       BGIOAKBI_1              3741 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM   Campylobacter species Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
  source          1..3741
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/mol_type="genomic DNA"
/strain="strain"
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ELDKIDELRQKF"

gene complement(914..1339)
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   CDS complement(914..1339)
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      /transl_table=11
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ISNYDQFTILFIMIFIFILMFYKTNNFALLLLVIIIIFIIYMKYHEFIYNKIFLLIF
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gene complement(1609..2076)
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   CDS complement(1609..2076)
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      /protein_id="Prokka:BGIOAKBI_00005"
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FHYIYISGYKDYKNNLLLEFDRNAMEDEFIYIIYSCIMFNLYIYNAIPLVLSAVIFLA
FYSSLSFLFVGCCGIGVFILFISIFKRFMFHLSVFLLFAVLYTCTLIFFFYGLATY"

gene complement(2286..2435)
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   CDS complement(2286..2435)
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      /inference="ab initio prediction:Prodigal:002006"
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      /note="conserved domain protein"
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      /transl_table=11
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      /protein_id="Prokka:BGIOAKBI_00006"
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SYNGN"

gene complement(2445..2750)
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   CDS complement(2445..2750)
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      /inference="ab initio prediction:Prodigal:002006"
      /codon_start=1
      /transl_table=11
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      /protein_id="Prokka:BGIOAKBI_00007"
      /translation="MGVFRKFYIFVWVFCSIGFAISPAVGHNPNRHYEFFVMLGWIIF
PLLILMLYRFSSLCEIKFLYIALLLLYYPIALILYMFYYHNSFYVTLYIFLSLFK"

gene complement(2909..3421)
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   CDS complement(2909..3421)
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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MKILKSLYIIWMIFWGFGAILGYYMGYDATFTKMFFLVL"
KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species

Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

source 1..929

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/strain="strain"

gene complement(73..378)
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CDS complement(73..378)
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/inference="similar to AA sequence:RefSeq:AVS37480.1"
/note="DUF2974 domain-containing protein"
/codon_start=1
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gene complement(397..759)
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CDS complement(397..759)
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/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MCKLNELPNWEEMKYNKILGYYFDKLDIDDRFVHKKYNSIEMWL
YIYQYDDLTKTSPSFPQKIEMDNIALKTNQNTKLHIVDMHISPYWNTRYYVLEGNE
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ORIGIN

1 tttgagctaa atacccacca gagaatgtcc tacaaatatg atacttttat tttcattttt
61 taggacaatg ttttaataaa tcatagcgag aaaagaattg tttagcttga gtggggagaa
121 gtcgccattg agagtgtcaa ttttaatatc tttctttaaa gatgagtcat attgatatgc
181 cttataattt ttataactaa tatctaagac attagcttga gtaatgtgct tattaaagaa
241 aggctcatcc gtagcttcat ctttaatttt aatgaaaaaa tcattcttgt catgtgttac
301 caaatcaaaa taaccataac ttgcctgtgc aagttccgcc atatccctta gtttattaat
361 aagttgttta ttggtcatta tttattcctt atattattat tgataaagat taccacaagc
421 aagctcatcc tctataaact caaaattcat attaccctca ttgccttcta acacatacct
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541 attttttgtt tttagtgcaa tattatccat ctctatcttt tcttgaaaat ttgaaggagt
601 tttgtaagta tcatcgtaat atatatatag ccacatttct atactaccat attttttcat
661 atgtgcagaa tcatcttcatg cacccatattt tttcataaa taccctagaa ttttttata
721 tttctcttcc ttagagagaa gttcttttct cttacacata ttttataaaactttgatgagctaa atacccacca gagaatgtcc tacaaatatg atacttttat tttcattttt

LOCUS FHGGBLIP_1 13234 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.

FEATURES Location/Qualifiers
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    /protein_id="Prokka:FHGGBLIP_00001"
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    FDVSLKNYPSFRENFNDISIQFLNIGLKEHDIAKYLKNNLNNNLSRLKRTKTHIE
    RVLQVNFKLKDKLSIIENLPHQLISDSQKNLGKINQHLNFGFLKDFISYQNKIA
    IYIYDQIYQAVKDRGMNGTQHDDKLSIMFILTNEFCVQLYLKINYSSEMFKVFLGDEN
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    IIELENIALSKHQPQLEDNIPAESLINISIPNYTPNLPSLCMQEKFKEQNSKENNL
    IIPKGTILKSKPIDVCFECFTVQVDVLPISINEFIVSFKNQDYNLQLTQNNAKET
    KICDLGLKINLYLGNWTSSSHLYLTKHQLKISLQDTEEEFLNITNEIYKGL
    NPDQILSYYNLDGFEASFLRLETFYUFFHPKFKFNLRINGDLINLNCQKTINEFKSFJP
    FPANCIRFKELLSSMLTPINIFAKSAEPLINNKHDKSYRIFVDRSOPKAYEIQTLQ
    VKAHNSEGKGRLLKNYSIFERFEFLKDNQDFYSNVTNKNSKGEVFSEISFFSSYLDI
    ETISIDLLCSSNGDLPSLKIGQDINTCNKLKGVDTKNEIPESETTRCSCVDGNLLKWLVS
    LSFSYQITLSKQAFFGVLEYSFLDNQSNWKIYKLLQEAIDIQSKSTYLIDNIGHTK"
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FGKKALI"

gene complement(4193..4585)
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CDS complement(4193..4585)
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inference="similar to AA sequence:RefSeq:CKG87312.1"
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/protein_id="Prokka:FHGGBLIP_00003"
/translation="MSLLDKLIHNLEONYYYIPFQNDVFKNIKVLLNAKINDCYAVKNLGMNPWADINLNSCLVESMAKIRKLIDNYEKVICSVSTYDNLSPWQLSFI
VKCFOQDDRFKEFIEIIFKNRNYCEVK"

gene complement(4588..6042)
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CDS complement(4588..6042)
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SPDLMFNLKMASIAAMSHSPFITSFGPKFFGLDDYSELAISQDQLQGEGPQYTRWRT
FRENEDSKTYGILLYVRFLARSLPYPDEENPKSFNYKENHTEHNLWANSSYFTFCRT
LETSAFYKDIVGNIIGPKSSGTVDFLQIYLNEYFGTIQLSKPTEVLIDRREYELAEAGIFILTLRRDSNNAAAFFSANSPLPPIIFQNTPEGEKAEATNLRTQLQPYFLIRSLAH
YLKVLQREEIGSWKERSDIENLNEWIRQYISDQENPSEPVRSPFRAAQVVKVDIP
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gene complement(6044..6259)
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CDS complement(6044..6259)
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/transl_table=11
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/translation="MSDGSHAPKERINITYKAKTNQNDVELPLKLMVANLKGKNE
TPLEREIQNKINFQVQRKMDITTSFSVKNLGAEELDVKLINASMKDFSPDS
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gene complement(6598..7845)
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CDS complement(6598..7845)
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gene 7969..8415
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gene 8425..9822
/CDS 8425..9822
/locus_tag="FHGGBLIP_00008"
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/protein_id="Prokka:FHGGBLIP_00008"
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gene 9819..10592
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/inference="similar to AA sequence:RefSeq:AJK71138.1"
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gene 10818..11390
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gene 11394..11495
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gene 11492..11920
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gene 11913..12146
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gene 12227..12865
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CDS

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/locus_tag="FHGGBLIP_00014"

12227..12865

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KKQVFQAMTNNSRIRKNQKIFYYNKELQNFPSKNEIKLSREIKLGIVGKE
EIEAWYIDDKNNIKYQEFKRYLYNNYSIFLEGDEGAGFHFYEYEILDGDVR"

gene

12906..13034

CDS

/locus_tag="FHGGBLIP_00015"

12906..13034

/inference="ab initio prediction:Prodigal:002006"

codon_start=1

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ORIGIN

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61 cttgagtatt atgaggggt cttagcttag ctttaaacat cggagttaaag attaatattt

121 tttaaaaaag attagaagtg atgcaattacatta attttacttt tattaagttt

181 atagttcatt agtattgtaa aatatcaaatct atcttaaag atttcagcat

241 ttgacaataa ataaatgct cagcctctct tggactttttt gctcactttt

301 cactcactaaaa taaatcctt ctaatattaa cattttaatt ttttaaaattt

361 taagttgcata atactcttttt ttctgctagtt tcagccttttt ttatattatt

421 cttaaagataa agcactgtct ttaatcactt cttctttcttta aatattttat

481 aaataaggctttcttaaattcttta attcatattttaa tttaatcatttt tatttta

541 gaattgggtcctcctattt ctaataatttt tttctcactaa gatgcaacttt cttatattt

601 taatatttct tttctatttt tcttcttcttta tatttttaattt taaaatattttt

661 cttttaatgtc attttttaa attttttaatttttt tatttttacttttt tatttttcatat

721 taagaggttgtc cttaataatttttt cattttttttt tttttttttttt ttttttttttt

781 atctacttct tttttatctt ctattaatatc ttttttttttttt tttttttttttt

841 tattttgagat atcctttcattttctttttt ttttttttttttt ttttttttttttt

901 tcatcacttt cttcactttt cttcactttt ttttttttttttt ttttttttttttt

961 tcaagactca ttgactgtta aaagaaaaaa aatgcttttt tattttattt tatttttttt

1021 aagtcttattt cttattttttt tattttttttttt tatttttttttttt tattttttttttt

1081 ttagttctttt tattttttttttt tatttttttttttt tatttttttttttt tattttttttttt

1141 tatttttttttttt tatttttttttttt tatttttttttttt tatttttttttttt tattttttttttt

1201 aagttgctttg ggtttctttt tattttttttttt tatttttttttttt tattttttttttt

1261 cttcacttctt cttctttaattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
LOCUS       FHGGBLIP_2              4242 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT    Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES   Location/Qualifiers
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               /mol_type="genomic DNA"
               /strain="strain"
           gene            complement(95..1375)
               /gene="trxB_1"
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               /inference="ab initio prediction:Prodigal:002006"
               /inference="similar to AA sequence:RefSeq:CKG86610.1"
               /codon_start=1
               /transl_table=1
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GDRILRNSPQDKYPQLPNDPFNLYTEGEKSTLEFEKWSQYLKDPIKGSIAPWTEKE
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DLINQYQFAYDGGOSTWALYDIEGKLGKDPRDVDPSTPESKEFDEEDYRFGRNM
FASDIRDSSRSEEJRLFDLTILHAKALATPPQGYNAPYFTPRLWEIYKRGYLD
KKLDPRIPAIYRYNPFEPLRAKILKFAENGID"

location

gene complement(1394..4150)
/locus_tag="FHGGBLIP_00017"
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AAW35464.1"
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/codon_start=1
/transl_table=11
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/translation="MYLKNNAILKLNQEDIKQIFYFSYIESPNFNNSKLAEEFFAQKNQ
NAQIDNNTKMSNYLISIPNKYNAGLSESLTEIANYIDQYKRTIKNNIDTSK
TYDSRMYSEYSIEMPQDNEFYPLQVSKISKEAYENSSAKAYDMEYQIYKNTNF
VATPQKLPFANATKKAISENEMIEIVIKTENLHRCEINILAYIDNYNKINDK
WLPYFYIKKFKQNEKDEEISEKKEKKAQHQLTKLFEKSDKSFGNYLSLSDKSS
FNGYSLMECLFISFLVQAKLIPLPNINLDKKYGGNFSYVYKLYEETYVLWTVTPVY
VNGEMNTPNTAYEVWQSSLKILDDKYSVESDSSITIDDFSNELSKDLWTNLDKIK
ILKQMYHDEQCKIFKE4IFEMYQVDKQISLQKVEQMYKLEYNKA
KEKQTSEIFTYAMLKILLSSAPFISFTAOQMLWDFNLYKMYIYQACIKINEGKKEF
KFEQLQGIFTPLKYHIKHSNIIARQLEKTHTQIMAQEQKSNLQKNTSNL
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RDHFIYTPAINSKFSFDLKHYGDLCVGFDTHIFYSEQPNLEENKLLKR
LLSYLIEIERSLKIIEKNDENILOREDYYTFNNQNLSLEILKSEIYKNTLEKYY
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LGMYG"

ORIGIN

1 gccatacaaa acaatattaca agaagataag atcttttttg agaatcttac ccataaaaaa
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181 ttctgaggct aggaggtta cttataaac cttttttttc aaccaattttc
241 gttataaaata atagaggaca ttgagagc atcgaggct ccgcggaggtagtgataggg
301 ctgataagct cttataaact cttttttttc tctagagcagct tgtctgatcagcag
361 tatcagagcg aaaaattttc cttctcalled ctttatttttt ccattctacatc
421 ctttttttgt cttcagagcta cttctattcttat ctttatttttt attttttttt
481 atctttctatttttctatcg aagttctttattttatatc gatctatttc atagcagaa
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LOCUS       FHGGBLIP_3              3467 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..3467
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene            179..595
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CDS             179..595
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inference="ab initio prediction:Prodigal:002006"
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FNLATYKHNSHFIEANNNLNFNLIEFSSNISPLEYAVGYLQKEEIIYNGALEYS
LGTLQKTLNTTTQFHNKFYFKLKERPFESAQYFKQR"
gene            complement(1152..1400)
/locus_tag="FHGGBLIP_00019"
CDS             complement(1152..1400)
/locus_tag="FHGGBLIP_00019"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:AVL47240.1"
codon_start=1
/transl_table=11
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/protein_id="Prokka:FHGGBLIP_00019"
/translation="MEYLLDYQDEMGINKTTFLNFLNLENNLKNKLSKRTKI
TYLRLVSFFISDNDDNFLFSFDKMKLKLKQKKS"
gene            1751..2140
/locus_tag="FHGGBLIP_00020"
CDS             1751..2140
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/translation="MDEVQDINACVIDMLNQKQAQKFQSDTFQSIYFKFRAGISLE"
ILASMPKSHTLCLTQSFRCQPQNSLYKILNAPRNFKGTKSSNENVKNEAKAVCRTNAKLFDIAVENLDKLFCCERDK"  
gene 2124..2327  
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/translation="MREINSYSFDELLDINLLFKKHEYIKNQFIAKFADLKEFLEYINETKEVDLQKIFVLLLNCIAIL"  
/gene 2309..2623  
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/gene 2848..2997  
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/translation="MSSIAKDSHVEMRDFLPKYNKTSRKECAELGISLQTLRDLTKDKK"  
/ORIGIN
LOCUS       FHGGBLIP_4              2982 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

ACCESSION

VERSION

KEYWORDS    .

SOURCE      Campylobacter species

ORGANISM  Campylobacter species

Unclassified.

COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES             Location/Qualifiers
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    /mol_type="genomic DNA"
    /strain="strain"
gene            complement(415..1014)
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CDS             complement(415..1014)
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    /codon_start=1
    /transl_table=11
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    /translation="MANLSELRESLYVIPLKFIHELNYHFIKKEFLPPELQLVVINLPLTFLIKLVDRILTVLVHQLKLSGIVKQIVLEK\n      IYIVYEQSIIVATLKKISRNVEHELRIKVLVSILAVK" gene            complement(1020..1694)
    /locus_tag="FHGGBLIP_00026"
CDS             complement(1020..1694)
    /locus_tag="FHGGBLIP_00026"
    /inference="ab initio prediction:Prodigal:002006"
    /inference="similar to AA sequence:RefSeq:CKG88211.1"
    /codon_start=1
    /transl_table=11
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    /translation="MANLSELRESLYVIPLKFIHELNYHFIKKEFLPPELQLVVINLPLTFLIKLVDRILTVLVHQLKLSGIVKQIVLEK\n      IYIVYEQSIIVATLKKISRNVEHELRIKVLVSILAVK" gene            complement(1735..2508)
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CDS             complement(1735..2508)
    /locus_tag="FHGGBLIP_00027"
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ORIGIN
1 catcattatt atctaaaact aaaaaacttt cacataaaaa caaagctctg aaataagcaa
61 tttctgaatt gatattaata ttatcaatat cttgtaaatt taaagtcttt aatgagtatt
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361 aattagaggt attagaaagtt atactttttt tagttttttt tagtactagg
421 caaattttga ttttgttggaa tagctaggttt agggtgttttt gtggaggaag gtacccaaaa
481 ttgttattt tggaaaaatt tcttacttttt ccttttttgct ctttttcttgca
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LOCUS       FHGGBLIP_5              2702 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..2702
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
ORIGIN
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 61 ttttttatct actctgtttg tttttgagtt tttaaatagt aatactttgta
121 ttctaagttt gtgtttgctta aagcattctaa tttgatattt aaaaattttt ctataataga
181 ataataagc aaacagaatg ctatcattttt aaaaaagcag tgaagtttgg ctatgctttg
241 gctttcatct ttaggagaaa aataataact gggtatatct tgttttataa gattatcttg
301 atctacactc caaagttaca aaggaattt aaaaaagcag tgaagtttgg ctatgctttg
361 ggggtttaggg aatagattag ctgggttagct tttgatattt aaaaattttt ctataataga
421 actagccact cttttcataaa gctcatcaca atcaatcaaa tccttacaat tagcaaaaat
481 aaaaacttct tcttttgata aattaacaaa tatagtcgaa cttgaagaat taaattttac
541 ttttgtttta atgggtttgtt ttttataaag aataataact gttcaataat ttcttttta
601 caaattaatc atttgctttt ttctagcttg aaaaaaatct aaatcatttc ttaaactaag
661 acatttaagc cattggagaa tataataataa agttatatctt tttgatattt aaaaattttt ctataataga
721 tttttgatta ttttttatct ctataataaa aagcattctaa ttttattagc tttgtttttc
781 atctacactc tttttattagc tttttgagtt ttttattagc tttgtttttc
841 ttttattaaat atttggttagct ttttttttttttttta ttttttttttttttta
901 gacattttta tattacactc atataataaa ttttttttta ttttttttttttttta
961 tctttcttctg tttatagcatt ttttttttttttttta
1021 actaatataa ttttgtttctg cattgagatcttttttagtta ttttttttttttttta

LOCUS       FHGGBLIP_6              2651 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain. strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES    Location/Qualifiers
            source            1..2651
            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
            gene            complement(294..668)
            /locus_tag="FHGGBLIP_00029"
            /inference="ab initio prediction:Prodigal:002006"
            /inference="similar to AA sequence:RefSeq:CKG86895.1"
            /codon_start=1
            /transl_table=11
            /product="methyltransferase small"
            /protein_id="Prokka:FHGGBLIP_00029"
gene complement(687..1049) /locus_tag="FHGGBLIP_00030"
CDS complement(687..1049) /locus_tag="FHGGBLIP_00030" /inference="ab initio prediction:Prodigal:002006"
/codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:FHGGBLIP_00030" /translation="MTNMEQINNLKDYTEFVQASYFNFVYTEGQKALGFKISKTRFFK
DKSELEKLDYFKALHDENYGVLIDDSSFYAKLNRDLENYKLEIFLKDMRLNFISPNTL
QVALALLCLMKRQKRMLRGNKY"

gene complement(1441..1641) /locus_tag="FHGGBLIP_00031"
CDS complement(1441..1641) /locus_tag="FHGGBLIP_00031" /inference="ab initio prediction:Prodigal:002006"
/codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:FHGGBLIP_00031" /translation="MCKLNELPNEEKNKILGYYFDKDLGIDDFRHLKKSRIEMWL
CIYYDDTYKTPSNFQEKIEMIANLKTKNMQMSLHKIVDISHYFYWNTRYILENGEM
NMNFKEFIEDELACGNLYQ"

gene complement(1687..2055) /locus_tag="FHGGBLIP_00032"
CDS complement(1687..2055) /locus_tag="FHGGBLIP_00032" /inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ASI87259.1"
/codon_start=1 /transl_table=11 /product="Hypothetical protein" /protein_id="Prokka:FHGGBLIP_00032" /translation="MIKAYFENNKSFEGTLKHYNSIPMTWEIESTRKKLDENHIDKDVSNLSKLKYD
IHNFEKEIKERRVGNKLK"
LOCUS       FHGGBLIP_8              2165 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION  
VERSION    
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
           https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..2165
           /organism="Campylobacter species"
           /mol_type="genomic DNA"
           /strain="strain"
    gene            117..566
           /locus_tag="FHGGBLIP_00035"
           /inference="ab initio prediction:Prodigal:002006"
           /codon_start=1
           /transl_table=11
           /product="hypothetical protein"
           /protein_id="Prokka:FHGGBLIP_00035"
           /translation="MVGGGWFVPYSYHEFKEMCKLNELPNDEHKYNKILSYFGGL
           NLDLTDWENIKNLLTLQGYLEYNSQNDRYMYRENYKSDPRIRKVFLLFNFDSIKLS
           NLYKIDFENVWDKRDYIHGTKVSYDTVIEENFRTCGYFSGYLGKIK"
    gene            566..931
           /locus_tag="FHGGBLIP_00036"
           /inference="ab initio prediction:Prodigal:002006"
           /inference="similar to AA sequence:RefSeq:AVS37480.1"
           /note="DUF2974 domain-containing protein"
           /codon_start=1
           /transl_table=11
           /product="hypothetical protein"
           /protein_id="Prokka:FHGGBLIP_00036"
LOCUS       FHGGBLIP_10             1455 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES    
  source          1..1455
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
  gene           144..695
    /gene="trxB_4"
    /locus_tag="FHGGBLIP_00040"
  CDS            144..695
    /gene="trxB_4"
    /locus_tag="FHGGBLIP_00040"
    /inference="ab initio prediction:Prodigal:002006"
    /inference="similar to AA sequence:RefSeq:CKG87041.1"
    /codon_start=1
    /transl_table=1
/product="thioredoxin reductase"
/protein_id="Prokka:FHGGBLIP_00040"
/translation="MIYDLHDHHYESLLDEFGMLPFLDEIIGADWILDNRYKFALDEGRIIAYDDIEKGLKDPVRDVSTPESRKEFDHYMDGYKNGMVRTRFDIRNERDERSAKLTMDTPLLAKLAALTPQGPQYPNAPRYSPERLEIIYKRRHLDLIDRPAPIYRNYNPRERAKILKFGEENSIKD"

ORIGIN
1 taggatttaa agcaagacaa caacaagcctt tatttttaca agctcaattt ggagataaaa
61 atgccttttaa gatgtagactt ttgttgttctaa ttctttttctt caagggcaac
121 attggaaacat gcttagagcatt tcagagatttt tcagagttttt ccatggacag
241 ttgatattaa tcagatattaa ctagagaaag ctagatattttt tggactttttat
301 atgtagatatt gaaaaagagtt cagatatttttt gtaactttttt tagtatttttt
361 gcagggacact atggacttctt gatataataa aagataatag agatgtttcttgaac
421 atgtagatatt tagaagcagac agagctccta gctccttttt actcactctt gatcactctt
481 tatactcttg ccaactgagc ctgctcttct cctgcttttt cctgcttttt cctgcttttt
541 atctagcct tgaagagctt gaaatctttg ttatattttt agatgtttctt gatcactctt
601 atccagaaag cctgcttttt tatttttttttt cctgcttttttt cctgcttttttt cctgcttttttt
661 tcaaatgttga cagaatttga atatattttttt ccaatttttttt ccaatttttttt ccaatttttttt
721 ctactatatt gattttattt tgaagataaa gtaatttttttt tgaagataaa gtaatttttttt
781 tgaactattc aatttttttttt acacttttttt tgaagataaa gtaatttttttt tgaagataaa gtaatttttttt
841 atatattatt gatatttttttt ttatatttttttt ttatatttttttt ttatatttttttt ttatatttttttt
901 aagctttttt gtaagagaca gacactttttt ctcacttttttt ctcacttttttt ctcacttttttt
961 tataactttc agatattttg agatattttg agatattttg agatattttg agatattttg
1021 ggcaagattt aatatttttt aatatttttt aatatttttt aatatttttt aatatttttt
1081 ttaatattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:FHGGBLIP_00041"
/translation="MNPQELISQIKDYANIADASYAMLIDENDEKFLRYIKYKN"
gene
303..947
/locus_tag="FHGGBLIP_00042"
CDS
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/locus_tag="FHGGBLIP_00042"
/inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:FHGGBLIP_00042"
/translation="MKIAMIILSLFVLFSLACAFKEKKEITIASNYGGIYIFDK
KIREIELEKKEEFKSYLSEIKVNEHTFVNFSLKFFPQILSNGCNYRRSDY
RYKCAHFGFKDPFEAYEDQFKAYMGEENYKLRPYLGMTYVYCEGKYYPVVFAT
MDYKVKNYLFGLGDEGRGFSNISRSKAGGSSHYFTNGKFIKSDKEYTGQSY"

//
LOCUS FHGGBLIP_12 1284 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..1284
/organism="Campylobacter species"
mol_type="genomic DNA"
strain="strain"
gene
complement(584..1273)
gene="trxB_5"
locus_tag="FHGGBLIP_00043"
CDS
complement(584..1273)
gene="trxB_5"
locus_tag="FHGGBLIP_00043"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CKG86610.1"
codon_start=1
transl_table=11
product="thioredoxin reductase"
gene_id="Prokka:FHGGBLIP_00043"
translation="MTGFKAKTOAVNFLLIQLHEQGFTSLYDAYSAYRGLTDGIHKNP LKAQMLKDFAKNPPYDELMPLFDELIGVWDNVNNYDIAVDGAKGNIWALGDDV LGKGLKDPRIDSTPESRFEDNYLDGYKNGMTEYHSHTDEPKANLWLETMLL EAIKIKALTPQOPYNYPFPRLEFVYKHNHDLKLDPRIPAIPYRNFPRDKRKRAI LKFGGEENIK"

ORIGIN

1 catcacttaa atgagctaa cctctattgg cttctacttc tttgtaaagt tctttatagt
61 cttttattgat taaatttccct ttttcatcta cattacaata agcatcataa ggtatatcta
121 taacagtact tctaagttca cttctttataa ttaaatattt atatctttct cttttggttt
181 ttaaagactt ataatagcttt ttttttgcct tagtgcaagt cttcttataa ttaaatattt
241 gatcttttaa atatagcttt tgccattctt taattaacag caaaaggttag ttttgcctt
301 tataaagtt agatcctatt atatatgggtt tatagttggg gaggagagct tttctttaa
361 tcggatcctt ccgcttgatag gtttctttag aagttctttg gtttctttag aatattgatatc
cggatctttt atatatgggtt tatagctttt tgaagtgggg gtagagctttt gtttctttag
421 ccttataaa atttattcct tcttatttt gatctttgag ttttgcctt
taatattcct ttttttttg gtttctttag aatattgatatc
cggatctttt atatatgggtt tatagctttt tgaagtgggg gtagagctttt gtttctttag
481 aaatatttctt ttaaatattt atatatgggtt tatagctttt tgaagtgggg gtagagctttt
cggatctttt atatatgggtt tatagctttt tgaagtgggg gtagagctttt gtttctttag
541 ttttcttata atatagcttt cctcttttca cttcttttca cttcttttca cttcttttca
601 ttttcttctt ttttcttctt aaggggttag ttttcttctt aaggggttag ttttcttctt
661 ttatgagctt cccctttttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
721 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
781 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
841 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
901 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
961 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
1021 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
1081 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
1141 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
1201 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt
1261 ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt ttcgaggtttt

//
LOCUS       FHGGBLIP_13             1228 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES   Location/Qualifiers
source          1..1228
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene           66..869
/locus_tag="FHGGBLIP_00044"

CDS            66..869
/locus_tag="FHGGBLIP_00044"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86263.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:FHGGBLIP_00044"
/translation="MQKTFQIDLEKRKALENFKNLALLGLGGTMLLNLKEQPLDFNQ
LTYINTYDKNLKLDSFYIPSTLLSLQLQNSKEAFYINVLINSDTYKKNPLQQA
ITQKQEQENVVALKNDNINTSFTNLALKALEEKNFYNFIDLNKSLELLSFYNQ
IISNNHLRNYFYFKNQFFIKKDIKNKLFHSSIHSIIISNYLNLNGNFTLSKIELI
KILESLLYNLSTLMQTMQIQSKNEYGGSKFDKGIFLSNMIMNVRLK"

ORIGIN
1 aagatactag cttgtgctaa agaacaaggt atcAAagtt aAaccaacaa aagAAagaaa
61 aaacatgca aaaaaacattt caaattgctaa atcAAagtt aAagAAagttta
121 aaaaatctag ttatatgatt ttaggctggaa caaattgctaa atcAAagtt aAagAAagttt
181 tagattttaa tcaagattta aataatgctaa tattagttat aAAaatgca
241 ttgattcttt ttatatccct tctacacttt tattctttact tcaattaaat cAAataatgca
301 aagagcttatt atatatccttc tttattttct tattctttact tcaattaaat cAAataatgca
361 tataatatgc tatcactcaaa aaacaaagac aaaaaatgt cgtttatgct ttaaaaggtc
421 atgaaaatct taatacttct tttactaatc ttaatgctaa atcAAatgca
481 aagaaaaattc ttatatcttc tatagcttaa aagAAagttta aAagAAagttttttataa
541 atcAAataaat aataatgctaa tttttttatt tttttttatt tttttttatt tttttttatt
601 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
661 ttaaattttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
721 taatatactgg ttttattttt tattttttttt tttttttttt tttttttttt tttttttttt
781 tataatagtt atattaagg tttttttttt tttttttttt tttttttttt tttttttttt
841 atatatattg tatttgtcct aataatgctaa tttttttttt tttttttttt tttttttttt
901 tataatgcaatt tatattattt aatattattt tttttttttt tttttttttt tttttttttt
961 caagagagaa attattattt tttttttttt tttttttttt tttttttttt tttttttttt
1021 tattttattttt atttatttttt tttttttttt tttttttttt tttttttttt tttttttttt
1081 tataattatttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1141 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
1201 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt

//
LOCUS       FHGGBLIP_14             1209 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION     
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM    Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES    Location/Qualifiers
source      1..1209
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene
complement(366..908)
/gene="trxB_7"
/locus_tag="FHGGBLIP_00046"

CDS
complement(366..908)
/gene="trxB_7"
/locus_tag="FHGGBLIP_00046"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CKG86610.1"
codon_start=1
/transl_table=11
/product="thioredoxin reductase"
/protein_id="Prokka:FHGGBLIP_00046"
/translation="MLKDFAKNYPYDNSLLDKDNLPHPFVFLKDTLTVYEEVFNDTILILCAALTPQQGYNAPYYYSYPERLEFIYKHKLDLREDPRIPAIYRNYFPRELRALIKGFGEENGIKD"

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LOCUS FHGGBLIP_16 861 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES
source 1..861
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene complement(97..609)
//
LOCUS       FHGGBLIP_17              804 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM    Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
            https://github.com/tseemann/prokka.
FEATURES    Location/Qualifiers
            source 1.804
/*organism="Campylobacter species"*/
/mol_type="genomic DNA"
/strain="strain"

gene
complement(86..793)
/gene="trxB_8"
/locus_tag="FHGGBLIP_00049"

CDS
complement(86..793)
/gene="trxB_8"
/locus_tag="FHGGBLIP_00049"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87041.1"
/codon_start=1
/transl_table=11
/product="thioredoxin reductase"
/translation="MTGFKARQAVNFLLIQILHEOQFTSYDYAYRGLTDGIIKNPLKAOQLDKFAKNNPDEFGMLPFDLEILGDWDNDANKTATNENNVIDSOGYIIRALEDRVKKGKIKDSPRDSTPESREDFNLYLDGYKMGTEHYTLIESDTPKSIANLWLETMLLEAIKALTPQPGYNAPRYPSPERLEFIYNYKHKLDSLKPLHRPSPAPISIPENSPELEKAILAYAENH"
ORIGIN

1 taggtatttaa agcaagacaa caacaagctt tatttttaca agctcaattt ggagataaaa
61 atgcctttaa gagtttaggt ttagcagtat tgtgttctaa ttcttttctt acagggcaac
121 attggaataa gcttagagca aaaatgattt acgatttaca cgatcatcat tatgagattt
181 tgggtagatg ctaccttttt tagatgagat tataggagca gattggacga
241 ttagttttaa taatatagat tttgcttagt atgaaaaggg tagaatcattt tgggctttat
301 attaatagat tgaaggttttc atggatgattt gttcctggac
361 gtagaatct gcttagagca taaatatgat tttgcctatg atgaagaagg tagaatcattt tgggctttat
421 tattaagtgcc caaactgcca gcctcactcc ctcaccaagc cctttccttt cccttctttt cccttttctt
481 ttagtagatac tgggtagatg ctaccttttt tagatgagat ttaatatgat tttgcctatg atgaagaagg tagaatcattt tgggctttat
541 attttacacc tgaaggttttc atggatgattt gttcctggac
601 atccagaggt cctgtgattc tatagatata atggcgcatc acgtgagat gcttagagca
661 tacaattggc tgaaggttttc atggatgattt gttcctggac
721 cttttcctt gctttccttc taatatagat tttgcctatg atgaagaagg tagaatcattt tgggctttat
781 ttgatatgcc

//

LOCUS FHGGBLIP_19 760 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
  source 1..760
     /organism="Campylobacter species"
     /mol_type="genomic DNA"
     /strain=
  gene complement(420..599)
     /locus_tag="FHGGBLIP_00051"
  CDS complement(420..599)
     /locus_tag="FHGGBLIP_00051"
     /inference="ab initio prediction:Prodigal:002006"
     /inference="similar to AA sequence:RefSeq:AAW35464.1"
     /note="conserved hypothetical protein"
     /codon_start=1
     /transl_table=11
     /product="hypothetical protein"
ORIGIN

1 caaaaaaagt ttcctaaagga aaaaaccaaat catttttgat ataatactca atcacaagt 51
tttcttttgt gatataaatt cttttaatat ttgccattct atagatcttt tgtgcaagtg 101
catatatatgc taaaagaaat gtaaaaaaaa ctataaacca tttataatct atttctttgc 151
taggattaaa taatctagga aataaataaa gaaaaagaca taaaagcaca atatatgtta 201
tccaaaaaag caaaaacgaa ggtatatgct tttttccttc ccaaatgatt tcatcttggg 251

//
LOCUS       FHGGBLIP_20              738 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..738
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
    gene complement(353..706)
        /gene="tssI1"
        /locus_tag="FHGGBLIP_00052"
    CDS complement(353..706)
        /gene="tssI1"
        /locus_tag="FHGGBLIP_00052"
        /inference="ab initio prediction:Prodigal:002006"
        /inference="similar to AA sequence:RefSeq:AOH52008.1"
        /codon_start=1
        /transl_table=11
        /product="type VI secretion system, secreted protein"
        /protein_id="Prokka:FHGGBLIP_00052"
        /translation="MKGENKLLIEKSLTQTIEKEFFLNVHQNLSAHIQDNITSLSKNSM
QTKIEEEQYSLEDSNDFDQDCEVKAGNQLHQVGDQIVTRKDCVIKAGGVEVVI
DSNGLVVRGGEVKA"

ORIGIN

1 caaaaaaagt ttcctaaagga aaaaaccaaat catttttgat ataatactca atcacaagt 51
tttcttttgt gatataaatt cttttaatat ttgccattct atagatcttt tgtgcaagtg 101
catatatatgc taaaagaaat gtaaaaaaaa ctataaacca tttataatct atttctttgc 151
taggattaaa taatctagga aataaataaa gaaaaagaca taaaagcaca atatatgtta 201
tccaaaaaag caaaaacgaa ggtatatgct tttttccttc ccaaatgatt tcatcttggg
LOCUS       FHGGBLIP_21            699 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
          source          1..699
                          /organism="Campylobacter species"
                          /mol_type="genomic DNA"
                          /strain="strain"
          gene            complement(288..467)
                          /locus_tag="FHGGBLIP_00053"
          CDS             complement(288..467)
                          /locus_tag="FHGGBLIP_00053"
                          /inference="ab initio prediction:Prodigal:002006"
                          /inference="similar to AA sequence:RefSeq:AAW35464.1"
                          /note="conserved hypothetical protein"
                          /codon_start=1
                          /transl_table=11
                          /product="hypothetical protein"
                          /protein_id="Prokka:FHGGBLIP_00053"
                          /translation="MYMGINGNEDKTSNTSRSKEDMASKIDANADITSETKTPPNCIG RLATTIIIEDGLYMG"
ORIGIN
  1 gatctttttaa atatatgctt tgccattctt taataatcaag caaagtttagt ttttgccctg
  61 tataaaggtt agatctcga tatattggttt gtaggggag tttcataata
 121 tgcaagttggc ttcacacaaa gccttggaat attcttcggt ataatgcgtt tttggtttag
 181 ctatttctgt cttaccttt ttatatcacttt atccataata aaccaattttag
 241 gtgtgctcag ttatctcggt tttggtttag ggatattctc atcataacag gggagttt
 301 gtgtgctcag ttatctcggt tttggtttag ggatattctc atcataacag gggagttt
 361 gtaggtttgct accctttctt cttcatttttt ttatctcatttt ttttattttta tttctcttata
 421 cattctcttt gacatctata gttcatttttt cttcatttttt ttttattttta ttttctcttata
 481 tttttgcttta tgttgttgtg tgtgttgtgtg tgtgttgtgtg tgtgttgtgtg tgtgttgtgtg
gtttcttatt gctatttttt ttcttttttt ttcttttttt ttcttttttt ttcttttttt
 541 cttttttt ctttcatat gacaatataa agttcatttt ttttttttttt ttttttttttt ttttttttttt
 601 atagtttctt tataaatcag gcgtcgttatt cttcatttttt ttttattttt ttttttttttt
 661 ttttttttttt ttcttttttt ttttttttttt ttttttttttt ttttttttttt ttttttttttt

//

>>BfR-CA-15855_min_cov_30 putative plasmid location
LOCUS       JOBBOHMI_1             28513 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION  
VERSION  
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES             Location/Qualifiers
  source          1..28513
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene complement(198..1001)
/locus_tag="JOBBOHMI_00001"
CDS complement(198..1001)
/locus_tag="JOBBOHMI_00001"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00001"
/translation="MKHFIFGVNQKSKKLALISSLIIIGNNANAFAGGIPYDVSANQV
VKDYAMQLQQYEQMYQSMQLQQMQVQMQKQLRLELTEDWDNLGTAVLYQTRNVMKV
NGISYDIGNVSRKFDETYKDFEGYSNDLENATNESEKNKYSRYQKQIAETNQNTFNG
TLQOLELRYQDLEDSEALATKLKQNSQNSGLAQAVATNDLLAYQIDEIRKLRSV
MQQNLTYLASQNNQRMQQAKIDKFIEDTGYIEKTWGKSNPDALKWK"

gene complement(998..1603)
/locus_tag="JOBBOHMI_00002"
CDS complement(998..1603)
/locus_tag="JOBBOHMI_00002"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00002"
/translation="MLDLLKGVDMSNTISINQEVIFENKDEQVFCTSLDVAKVF
QKHKHEILGEKPHNNEKNCFEPNRLSFKTRKIEGFRGKREKYPYQYLTGDFSF
IAMGLTGRKADKFKIAFIFANMERNIKNQYTPKLNKYNKYKIPNTYPKINIKA
MTEQNRNCEFELAYEITETYKDNKSHIEQKINFKVKGLI"

gene complement(1588..2259)
/locus_tag="JOBBOHMI_00003"
CDS complement(1588..2259)
/locus_tag="JOBBOHMI_00003"
/inference="similar to AA sequence:RefSeq:ASI88311.1"
/codon_start=1
/transl_table=11
/product="IncQ plasmid conjugative transfer protein TraQ"
/protein_id="Prokka:JOBBOHMI_00003"
/translation="MKNFIFGVKKTALTALSATLLISSNADDDLYTGDTKLACEAILC
LSSGTRSECSSSLARYFSIKFKPWTINARRAFLNLCPIQNDANIEDVLNLNVLDD"
VLPVSDPORCQPVNLNVTQVETKRSYTFGIMSYRINPNMPNFCHALINHAYTDYKTP
VYKCTGEFYNSLEWKLSAKQLQITQQAYESLSDDQRYMISRTCDGRNCYDYYQKIPIFTK
EGT"Y

gene complement(2256..4721)
   /locus_tag="JOBBOHMI_00004"
CDS complement(2256..4721)
   /locus_tag="JOBBOHMI_00004"
   /inference="ab initio prediction:Prodigal:002006"
   /inference="similar to AA sequence:RefSeq:ASI88309.1"
   /codon_start=1
   /transl_table=11
   /product="IncP-type conjugative transfer protein TrbE"
   /protein_id="Prokka:JOBBOHMI_00004"
   /translation="MLALKEFRISKRISKAKAKSKIFLDCCFLGRRHFSRGMHRIDNQCI

CDS complement(4725..5012)
   /locus_tag="JOBBOHMI_00005"
   /inference="ab initio prediction:Prodigal:002006"
   /inference="similar to AA sequence:RefSeq:ASI88308.1"
   /codon_start=1
   /transl_table=11
   /product="IncP-type conjugative transfer protein TrbD"
   /protein_id="Prokka:JOBBOHMI_00005"
   /translation="MEELQRIDIYSALNKPNLIFGADRELILMVGVISIFALFSG

CDS complement(5012..5308)
   /locus_tag="JOBBOHMI_00006"
   /inference="ab initio prediction:Prodigal:002006"
   /inference="similar to AA sequence:RefSeq:ASI88307.1"
   /codon_start=1
   /transl_table=11
   /product="Conjugative transfer protein TrbC"
   /protein_id="Prokka:JOBBOHMI_00006"
   /translation="MKKFLILFLFLAGLGLYALASTTGGAGLPWEGRLEQIKASLSGPVA

CDS complement(5318..6256)
   /locus_tag="JOBBOHMI_00007"
CDS complement(5318..6256)
/locus_tag="JOBBOHMI_00007"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:ASI88306.1"
codon_start=1
/transl_table=11
/product="Conjugative transfer protein TrbB"
/protein_id="Prokka:JOBBOHMI_00007"
/translation="MSNLEFQARINEKIKREFGDILTHLEDKETIELMLNSDGKLWLE
 KLQGDICLGEFSEARAKSIAITSTLLDDTNADNPIECELPLDGSRFEALLPPIV
 AKPTFTIRKKAVIFITLDGYDSNIIITPQNEKVLINAIERQNILNVLVGGTSGKTF
 SNAIIDGKITPIHRIVIIEDTAELQCASENVIRATRDKIVMDLRLLKATMRLRPDR
 IVGERTGEKADLLKKWNTGPHGGIATIHANSANGGGLTRMEQLISEATNAKMSKLIE
 AVNLIVFISKSKERGKVKEIIVKVGYENDKYITQAI"

CDS complement(6797..7537)
/locus_tag="JOBBOHMI_00008"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00008"
/translation="MLFNYEIINCQPKNTMkitsRKYKVRICIFKNTKDEASKYYQQA
 WDLaKQVNLKANDTSTQRDKERLIDLALGGILAEGWFYYIKRNFQFIVNFTEFKSS
 IgQIDLNNKTEVRSSFRPNGINFAICNNAKYNKKNCKYDNLYKPMENDKDFAAC
 VLFETTNQVMOIQDEIIYFYLIGGSTRKMDLNTISYDNLTAEDDLLQKTNYKIRL
 YNADILIEGFKEYMTEELGYPKILNDOQT"

CDS complement(7527..8444)
/locus_tag="JOBBOHMI_00009"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00009"
/translation="MNKNSSSKLNNAKNIKNEDEFYQTQYEDINKELNFYKNAFKDRIVY
 CNCDPDQKSNKFTKFKKLNDRLKLKLSTSFNSNGKGIIFIEKNNPKYQGLENNG
 DFRESDETIKLLKESNNIVTNPFPSSREIFIDMLNQDMQLIGNANAIYSKNCNFYM
 MKNKLLWLQNCVRWFINTKGEVLEGARFSFWFNSNNOQKNRKKISLNRKYNNQDYITYD
 NNYNAIEISKSDIPSVDYTGIMGVPITFLDKYNPQQFEIIGADYQVNSGELIYIKRNDW
 NGKTDRAVINGKRLYSRIFIKHRGVNNAI"

CDS complement(8467..8880)
/locus_tag="JOBBOHMI_00010"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:ABS43377.1"
/translation="MNKNSSSKLNNAKNIKNEDEFYQTQYEDINKELNFYKNAFKDRIVY
 CNCDPDQKSNKFTKFKKLNDRLKLKLSTSFNSNGKGIIFIEKNNPKYQGLENNG
 DFRESDETIKLLKESNNIVTNPFPSSREIFIDMLNQDMQLIGNANAIYSKNCNFYM
 MKNKLLWLQNCVRWFINTKGEVLEGARFSFWFNSNNOQKNRKKISLNRKYNNQDYITYD
 NNYNAIEISKSDIPSVDYTGIMGVPITFLDKYNPQQFEIIGADYQVNSGELIYIKRNDW
 NGKTDRAVINGKRLYSRIFIKHRGVNNAI"

CDS complement(8467..8880)
/locus_tag="JOBBOHMI_00010"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:ABS43377.1"
/translation="MNKNSSSKLNNAKNIKNEDEFYQTQYEDINKELNFYKNAFKDRIVY
 CNCDPDQKSNKFTKFKKLNDRLKLKLSTSFNSNGKGIIFIEKNNPKYQGLENNG
 DFRESDETIKLLKESNNIVTNPFPSSREIFIDMLNQDMQLIGNANAIYSKNCNFYM
 MKNKLLWLQNCVRWFINTKGEVLEGARFSFWFNSNNOQKNRKKISLNRKYNNQDYITYD
 NNYNAIEISKSDIPSVDYTGIMGVPITFLDKYNPQQFEIIGADYQVNSGELIYIKRNDW
 NGKTDRAVINGKRLYSRIFIKHRGVNNAI"
/translation="MKKVYLDNTIFLDYFNTERTVHNEAKQLMYVLYLTNNIQIVFSED
MISTIAYLIKLENFLNFTHLKDISLEKNFNITSFGSVINMACDYYDKYRGDFEDYL
QYFCAEKEGCSAITYMDDKNNPNLKIPIKRYGEIDI"
gene complement(8877..9791)
/locus_tag="JOBBOHMI_00011"
CDS complement(8877..9791)
/locus_tag="JOBBOHMI_00011"
/inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CKG86570.1"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00011"
/translation="MSNEIEIKDNEINKNKRQVVYRVDNLSTDYITGEVVERNQII
VKKVQTKEFIKLETFENIDYINLESQKTLFFTLSSVYKYNRFVKSKMQNIVLVD
KVLSRAGMYRALNGLIEKKVIFKINREFVSKYAVGSDDCYLFNPNLVGRSGWNLKNN
LRHITITREDDFENLENRELEEEYLFDEIRNQKQYQVEINQEOHEDETTKVKNTE
IVIEEKNNSINNQYSFDKEPENSINKVLISNDTQPFLDENQKEEEEARLFIEKYAGI
LTGAYDSTKASAKEMKRELLDKDLEEGRI"
gene 10523..10723
/locus_tag="JOBBOHMI_00012"
CDS 10523..10723
/locus_tag="JOBBOHMI_00012"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00012"
/translation="MNKDKKYLNFSEYYEVRDFLELYPEKDREINILITIGDKNS
KNLSFELYDFKFKLGFVKKL""
gene complement(10732..11061)
/locus_tag="JOBBOHMI_00013"
CDS complement(10732..11061)
/locus_tag="JOBBOHMI_00013"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00013"
/translation="MQRGEAKIEFYSNINYLKKEFENGCVVSFLFQDYLKAIKEPNKMT
YKQFKNYCNDFEKKNKIKEKTMQDQNLQQLVNLKNEPIKLIKINTPKKVDFACKDFGKD
IKEDDL""
gene complement(11075..11524)
/locus_tag="JOBBOHMI_00014"
CDS complement(11075..11524)
/locus_tag="JOBBOHMI_00014"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00014"
/translation="MDIKIATFEDIEFIKCYCFLGFKEKHYNRFIEKLEDIIKNN
VSGGIIFIIKDGNTNEKAGFAFCGKSSGNYIEMIYILEKFRNKLATNFIFKYEYKL
PNKIIARCLUDNYSQAQIKIFKHLYQELSKEKTNQYEFMIKESI"
gene 11734..12117
  /locus_tag="JOBBOHMI_00015"
  /product="hypothetical protein"
  /protein_id="Prokka:JOBBOHMI_00015"
  /translation="MRKDKRIAIRLEDEYKHMQKAQNHWGLTISRYLRLDSMNYPIT
               CIVDQKVHAVNHVGLGDIGRGLGFLKHWLVRNEDNKVNFNKRITYNDIDEIVDQILDL
               QILLKEQAQR1IQNDNQKDSKQKA"
CDS 11734..12117
  /locus_tag="JOBBOHMI_00015"
  /inference="ab initio prediction:Prodigal:002006"
  /codon_start=1
  /transl_table=11
  /product="hypothetical protein"
  /protein_id="Prokka:JOBBOHMI_00015"
  /translation="MRKDKRIAIRLEDEYKHMQKAQNHWGLTISRYLRLDSMNYPIT
               CIVDQKVHAVNHVGLGDIGRGLGFLKHWLVRNEDNKVNFNKRITYNDIDEIVDQILDL
               QILLKEQAQR1IQNDNQKDSKQKA"

gene 12080..14236
  /locus_tag="JOBBOHMI_00016"
  /inference="ab initio prediction:Prodigal:002006"
  /inference="similar to AA sequence:RefSeq:ASI88299.1"
  /codon_start=1
  /transl_table=11
  /product="IncP-type DNA relaxase TraI"
  /protein_id="Prokka:JOBBOHMI_00016"
  /translation="MIIKKIPSKQKNSFKNLSNLYLDKDNNAKVLVDYMLDKNE
               DIKQFLAEYDLEFRRRKGVIAKSEKFACKASSIHRLSKQALEKRFKEILDLQEK
               ENRTKNIKEEHEIKEQYQRNPKETSSTLWKEYLRIENEAKEALDKERMLMLKRRENFK
               TSIPSMKFNKNTFAHVKQRMIFNQKQKELYQKYKVRYSRYDLFISLSGNEEATRAL
               RRTTKTNENENTLSSTQEPKIFENVYITKEGYAVYKSGFNKAIKDGMKLVSILIN
               NKDKDEFLNSSLILAIIDRFHGNHNLITGDDKFKRNILEVANDYNLSVFSQDRMQKIQE
               ENNKKREMKTRKVLKNNIEELIKLTEDQDKIDENKEKELKALKFSLKKSNIKSTPSI
               FKGELKGBKFSYKEIDSMDTESVCIEIDGFIIVNSANKEGLVAMNEIEKQTLDDEEIK
               RFEFEDHELFLNTKIDIAKGFYTNRRKDADYEYRKFMQESKIKVANAIASMIDKDN
               IDIMEKYYAKKEKDLKQYQLKKEVVFNASNDIDLNNF"
CDS 12080..14236
  /locus_tag="JOBBOHMI_00016"
  /inference="ab initio prediction:Prodigal:002006"
  /codon_start=1
  /transl_table=11
  /product="IncP-type DNA relaxase TraI"
  /protein_id="Prokka:JOBBOHMI_00016"
  /translation="MIIKKIPSKQKNSFKNLSNLYLDKDNNAKVLVDYMLDKNE
               DIKQFLAEYDLEFRRRKGVIAKSEKFACKASSIHRLSKQALEKRFKEILDLQEK
               ENRTKNIKEEHEIKEQYQRNPKETSSTLWKEYLRIENEAKEALDKERMLMLKRRENFK
               TSIPSMKFNKNTFAHVKQRMIFNQKQKELYQKYKVRYSRYDLFISLSGNEEATRAL
               RRTTKTNENENTLSSTQEPKIFENVYITKEGYAVYKSGFNKAIKDGMKLVSILIN
               NKDKDEFLNSSLILAIIDRFHGNHNLITGDDKFKRNILEVANDYNLSVFSQDRMQKIQE
               ENNKKREMKTRKVLKNNIEELIKLTEDQDKIDENKEKELKALKFSLKKSNIKSTPSI
               FKGELKGBKFSYKEIDSMDTESVCIEIDGFIIVNSANKEGLVAMNEIEKQTLDDEEIK
               RFEFEDHELFLNTKIDIAKGFYTNRRKDADYEYRKFMQESKIKVANAIASMIDKDN
               IDIMEKYYAKKEKDLKQYQLKKEVVFNASNDIDLNNF"

gene complement(14233..14697)
  /locus_tag="JOBBOHMI_00017"
  /inference="ab initio prediction:Prodigal:002006"
  /codon_start=1
  /transl_table=11
  /product="hypothetical protein"
  /protein_id="Prokka:JOBBOHMI_00017"
  /translation="MQYLIDNADYINIIKLIQGLASIGVIGLIIACQLQRNSSKNN
               RINILKTEDEAKSIANEKFVVDYEHLDEKQDEKNNLKNKRREEYKTLNLICLYLKECFTK
               KHFLNEYKNLLKLKYKDNMVLKYNKINIKDVEVEKINLKP"
CDS complement(14233..14697)
  /locus_tag="JOBBOHMI_00017"
  /inference="ab initio prediction:Prodigal:002006"
  /codon_start=1
  /transl_table=11
  /product="hypothetical protein"
  /protein_id="Prokka:JOBBOHMI_00017"
  /translation="MQYLIDNADYINIIKLIQGLASIGVIGLIIACQLQRNSSKNN
               RINILKTEDEAKSIANEKFVVDYEHLDEKQDEKNNLKNKRREEYKTLNLICLYLKECFTK
               KHFLNEYKNLLKLKYKDNMVLKYNKINIKDVEVEKINLKP"

gene complement(14701..14895)
  /locus_tag="JOBBOHMI_00018"
  /inference="ab initio prediction:Prodigal:002006"
  /codon_start=1
  /transl_table=11
  /product="hypothetical protein"
  /protein_id="Prokka:JOBBOHMI_00018"
  /translation="MQYLIDNADYINIIKLIQGLASIGVIGLIIACQLQRNSSKNN
               RINILKTEDEAKSIANEKFVVDYEHLDEKQDEKNNLKNKRREEYKTLNLICLYLKECFTK
               KHFLNEYKNLLKLKYKDNMVLKYNKINIKDVEVEKINLKP"
/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00018"
/translation="MNKNQYEVNENLKNESYDDQRVFAALDLSYKMQTAYNQNQTNS
NQNQNQTNQNSNQNSQSDKK"

gene
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CDS
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gene
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CDS
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VFDQMRQSNSLEFLSNVSKTSGLDEIKRMKNAFDSCDITGRDEKSKERKAILSS
NIIIIIPSPSYQVNVNLHMLIEYNEVIEINPNLLALVLVNRVSPNPFLAKELENLKE
YINEAkekEGLDRVIMLESVYERQAYRKAEGKMSKEDCDKNDKLNDNFQYEL
LKIANEKLGV"

gene
complement(15952..16347)
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CDS
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/translation="MRKTIAYAFASFAFLSLISLIFYFGGFHFNYTRSMPLGLYKEI
NSSTFKNNDIVLLKIPQKEILKIIAIIAVGCIVEVNTQGFVINESLILPNKSFDFS
EGNLLEFKPFKRKLKENELVVMENIKSYDSRYFGVNIQLQNEVKVKKMISF"
gene complement(16885..17538)
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CDS complement(16885..17538)
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/protein_id="Prokka:JOBBOHMI_00025"
/transl_table=11
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/protein_id="Prokka:JOBBOHMI_00026"
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QKDLRRLFNNLINVQ1FRFLTDDSFLFKNGENVKRYHMLVLADELMFGBKLGVLE
LALAYMAGYGMIFQGDIQPIQYLISYIGEKETIISNCHIRIFAPKXKTAKLASEMGG
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/protein_id="Prokka:JOBBOHMI_00027"
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LDSSKAIHWHGKRAFYANANDTITLPLKENFLSSEGAYTTLAHELHWGHELNR
RLDKNPFGSKKYAKEMIARAIASFLNGKIGLDDPQHLSYIDSQILEDKPYE
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IEQGPIMDGLKHLRVSGIDGKREKSGDYGFLNPVQKNYKTFGKNSANSLE
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VLPNFLQNEAQKQLGSDFNLDKSRGIELLIEKQILKEAQKLMVEKAATKLDK
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/codon_start=1
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/product="hypothetical protein"
/protein_id="Prokka:JOBBOHMI_00028"
/translation="MNKDFFFFETPFSYYEVDPRTAELGAFKNALESEDDAEGTED
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/locus_tag="JOBBOHMI_00029"
/CDS (22762..23124)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ASI88284.1"
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/product="Single-stranded DNA-binding protein"
/protein_id="Prokka:JOBBOHMI_00029"
/translation="MNINIGGRLTAELRHNCQGSIICTFLANNNRKYKEIEN
STYIEVSLFGSFANAMHPPULKKIGISDVVGELTQDTWEHEGKIIYSHRK
AKEIDFRTPKKEKQTIPNIEGENYE"
gene complement(23117..23218)
/locus_tag="JOBBOHMI_00030"
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/inference="ab initio prediction:Prodigal:002006"
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/product="hypothetical protein"
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/translation="MENENLEENKPTQFDNEPSLFDNLEDEEQDND"

gene complement(23221..23766)
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/CDS complement(23221..23766)
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ASI88282.1"
/codon_start=1
/transl_table=11
/product="T-DNA transferring Peptidoglycan hydrolase VirB1"
/protein_id="Prokka:JOBBOHMI_00031"
/translation="MIDIALIEQCKNPVETQIIQKIIQVESNNQQAINEKVGSI
LKNKEAENLANFIFKGYSGVIGQMFSNILSSSTFSVHYSVDLDTCNKIKAGSD
IFLYAYEMTNNKLAKEDRINQALISNYTGGDLKGFNSGYVAKYDSTAKIDLEEKAR
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gene complement(23759..25000)
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/inference="similar to AA sequence:RefSeq:ASI88281.1"
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/translation="MLEVNMSPKFLPNKKNRLSKVPILLIIIAAIALLFSIFYVALS
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QAINFPNNPNNEDINLGAINPQNLGLESQNDVQGFQFLSQKDKNGYKXQKPK
LTEIKAQWNPAILTVNSDLPQILAQQVTQVYDSATGKXLLLIPQGTVYNGAYS
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gene complement(25004..25447)
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/inference="ab initio prediction:Prodigal:002006"
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/translation="MKILFALALAFFITSCAKNMDYFNSSFAVEETKINYNIADD
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| 19891     | tccacctttta tataaaat aagtgcacag ccttttattttt gcataataac cctcttttctt |
| 19971     | aacctttatt aacaatcatc ccgcagcttta gttttgatgtta agtcagctaa |
| 20051     | ggcttatttt tttttttttt gcataataac cctcttttctt |
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| 20291     | ggtttttttt ctttctttttt ctttctcactt cttccccgctttt gcgtttcttttt gcctcttttt |
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| /mol_type="genomic DNA" |        |
| /strain="strain"  |        |
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| CDS       | complement(64..303) |
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| CDS       | 803..1234           |
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| gene      | 2561..2905          |
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| CDS       | 2561..2905          |
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| gene      | 3070..3420          |
| /locus_tag="LBFOAKKB_00004" |        |
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| gene      | complement(3675..4316) |
| /locus_tag="LBFOAKKB_00005" |        |
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gene 4702..5037

CDS 4702..5037
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gene 6041..7183

CDS 6041..7183
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FSLRNLENFYLKDDEIEQIEIFINLNNIVEMYSYKNNFEENKEFKEYYFLEH
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DKITQIIKEGKIIFIELDSSLSTALILIFNNLINTEENHNGQLIVSSNVLLFDV
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gene 7173..7775

CDS 7173..7775
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GDFEDWRLFHVDSRSN5KTIFYKKGYSDSKNFSSTNDLYSQILNKGGHIAEKY"
FCNIKVFFNEQCEIDKNSLNLTQSNLYYFRKLLEQYNAG

**gene complement**
- **locus_tag** = "LBFOAKKB_00009"
- **CDS complement**
  - **locus_tag** = "LBFOAKKB_00009"
  - **inference** = "ab initio prediction: Prodigal: 002006"
  - **codon_start** = 1
  - **transl_table** = 11
  - **product** = "hypothetical protein"
  - **protein_id** = "Prokka: LBFOAKKB_00009"
  - **translation** = "MIINEDKKIEDLIKEAFAEKIWLPEFQRPFA"

**gene**
- **locus_tag** = "LBFOAKKB_00010"
- **CDS**
  - **locus_tag** = "LBFOAKKB_00010"
  - **inference** = "ab initio prediction: Prodigal: 002006"
  - **inference** = "similar to AA sequence: RefSeq: AVS36970.1"
  - **note** = "DUF4065 domain-containing protein"
  - **codon_start** = 1
  - **transl_table** = 11
  - **product** = "hypothetical protein"
  - **protein_id** = "Prokka: LBFOAKKB_00010"
  - **translation** = "MEQNNAYCGKIANEFIRLNCNKNNILTMHIQKLVYFAHAMS"...

**gene**
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- **CDS**
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  - **inference** = "ab initio prediction: Prodigal: 002006"
  - **codon_start** = 1
  - **transl_table** = 11
  - **product** = "hypothetical protein"
  - **protein_id** = "Prokka: LBFOAKKB_00011"
  - **translation** = "MDFLEKNKKEIREQENQENQENQENQESKESKEITALCSLYYA"...

**gene**
- **locus_tag** = "LBFOAKKB_00012"
- **CDS complement**
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  - **inference** = "ab initio prediction: Prodigal: 002006"
  - **codon_start** = 1
  - **transl_table** = 11
  - **product** = "hypothetical protein"
  - **protein_id** = "Prokka: LBFOAKKB_00012"
  - **translation** = "MFGRNLKKIRKASGLTQLLELAKINNTTQRTISLWETGNFEPPLN"...

**gene**
- **locus_tag** = "LBFOAKKB_00013"
- **CDS complement**
  - **locus_tag** = "LBFOAKKB_00013"
  - **inference** = "ab initio prediction: Prodigal: 002006"
  - **codon_start** = 1
  - **transl_table** = 11
  - **product** = "hypothetical protein"
  - **protein_id** = "Prokka: LBFOAKKB_00013"
  - **translation** = "TILLLCDIFKVTNDLLLEGCFYDDNEYLAHIWIRLTKELNCRTYTKRFNIHLLRRLET"...

**gene**
- **locus_tag** = "LBFOAKKB_00014"
- **CDS**
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  - **inference** = "ab initio prediction: Prodigal: 002006"
  - **codon_start** = 1
  - **transl_table** = 11
  - **product** = "hypothetical protein"
  - **protein_id** = "Prokka: LBFOAKKB_00014"
  - **translation** = "TILLLCDIFKVTNDLLLEGCFYDDNEYLAHIWIRLTKELNCRTYTKRFNIHLLRRLET"...
CDS             10964..11242
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15550..16818
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complement(16822..16898)
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note="tRNA-Asp(gtc)"
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/inference="COORDINATES:profile:Aragorn:001002"

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/inference="COORDINATES:profile:Aragorn:001002"
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1561 aataattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
LOCUS       PIMPEBOA_1             17665 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
            https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..17665
     /organism="Campylobacter species"
     /mol_type="genomic DNA"
     /strain="strain"
complement(370..1278)
     /locus_tag="PIMPEBOA_00001"
CDS             complement(370..1278)
     /locus_tag="PIMPEBOA_00001"
     /inference="ab initio prediction:Prodigal:002006"
     /inference="similar to AA sequence:RefSeq:AJK71146.1"
     /codon_start=1
     /transl_table=11
     /product="type VI secretion protein"
/protein_id="Prokka:PIMPEBOA_00001"
/translation="MNDLASYSFFKLKLEKDYGRKNIFLRTNKLHPIKNDIEKII
FSEHEEQSVELINFNGSVSLPFSMLDKLTSRSNEDGEQGWTLFFDFFHNYLWIF
FDVVSFLKNYPFRSENFKDSDIQIFNLFILGIEHDIAXKLYLFPALLLLSRRPKHIE
RVQLVQKVFLKDLSILEINPLHILSDQKNKLGIKVNHLGNFHLGKFISYQASONIA
IYIKDISYQAVKFPMNGTKHDDKLNSIMFLTNEFCDVVLKYKINYSSEMKFVLGDE
TAKLWAKILGANQKQTVYLVKLEC"

gene complement(1275..2996)
/locus_tag="PIMPEBOA_00002"
CDS complement(1275..2996)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71145.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:PIMPEBOA_00002"
/translation="MKDNYQKELEYKREHFIKNYPKLTPFLAHDSKDPDIER
IIENLAILSIQEKEDNEDNIIAEISLNIISPWNTPLCLMCEFKEQQSNESNKL
IIPPKGTLKSKPIKDCVCVFCTYDVLVYPISINEFVSSHKNYDFYTNLTVQVAET
KCDGLQGENLRYQCGTMLLNYMMHSLKELKIQSLRTDEEFFFLNTYNEIKGL
NPDESSTLYNIDGFAFSSLREYFMPHKNFLRSLGKLNLNCQGTKINIEFKFSKP
FPANCIFREKELLSLMGTPSIMIFASAEPLINHKDSYRIFVDRSQPKAYEVIITLQ
VKAHNSEGRRKLNKNYSFHEREFLDNQKDFYSVNTKNSKGEVEFSEISSCFSLC
EDTISIDLLCSGSGLPSKLINKDIGINTCNLKVDKTEIPSTECSDVGNLLWKLVSV
LSFSYQTILSSKAFPGVLESYSFLDQSNWKLYKIIQAEADQSYSTLKEDINTK
GTVAIFSSDKFYTVLGEYVLGLISKALASIFASINFSCELKCLSKDEILHYPS
FGKKALI"

gene complement(2993..3385)
/locus_tag="PIMPEBOA_00003"
CDS complement(2993..3385)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71143.1"
/codon_start=1
/transl_table=11
/product="type VI secretion system lysozyme-like protein"
/protein_id="Prokka:PIMPEBOA_00003"
/translation="MSLLDKLIHNLDEQNIHIPFYQNDFDVKNNKVLNAKINDCY
AVRNLMGPNMADINLNSLCSMAKEIRKLDIYKRICVVSITYDNSLPSWQLSFI
VKCFFQDDRKFENIEIFKNNEWCEVK"

gene complement(3388..4842)
/locus_tag="PIMPEBOA_00004"
CDS complement(3388..4842)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71143.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:PIMPEBOA_00004"
/translation="MANTKVIDPIIEQIMEKSYSKTDESYSIARKGVAEISEIKV
SDNEEKEKNFALDEMIAHIDHLLSKQMDLAVHNEEFQKLESTWRGRLFLVRFDFNE
NIKIDLDFITKEEALFENNPDITQSYSIVKNYSEYQGFGEPVGAIGDYQVLGSA"
gene complement(4844..5329)
/locus_tag="PIMPEBOA_00005"
CDS complement(4844..5329)
/locus_tag="PIMPEBOA_00005"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71142.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:PIMPEBOA_00005"
/transl="MSDGSHAPKERINITYKAKTNGQEDVELPLKLMVANLKGKNETPLEEREILQINKINFDQVMRKLDTITTSFSVKNLTLGAEELVCLNIAASMKDFSPDSLAKQIPELNKLQLREALMALKGPMPGNIQPDFRKAVLEALKNEKTEKELLEIKQEEQG"

gene complement(5399..6646)
/locus_tag="PIMPEBOA_00006"
CDS complement(5399..6646)
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71141.1"
/codon_start=1
/transl_table=11
/product="nucleobase:cation symporter"
/protein_id="Prokka:PIMPEBOA_00006"
/transl="MSFCNQLKNNLDELQEFHLEDEMSKYTKLHENVISWDKVQYQSQFILLHHSLDFKVCNYFLSCLFNKLNEICEFKLLLFQHLKLMENNTYISAQKRKIQIFIQNFQIEYNTKVLVLSSEIIDQFIALFSEFENLSCSNFAKEIAQVAPQLPKSPVAPQVSNVIRSDNINLNCVHKFQLFELLESDKEDNNLNYAFQAMWNGKIKCLPENCNNEKTIRKPDADIIIRLLSDEKENDIEHIKCFHELILNPFWIEVGLVQLCDFLEKKEKKNKQDLILMTDSFISKDAIELLRQFNGDFICEEYYVFKPKENKSKFSSSKKTDKETHLQDFEQMLMNNDKENFNNINNISLDMVKEFKESGKMKNKSNKINLNIYVELMKETLLKDYLAEYENAKKIK"

gene 6769..7215
/locus_tag="PIMPEBOA_00007"
CDS 6769..7215
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71140.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:PIMPEBOA_00007"
/transl="MFRKSSLFLLLPFLFCSSVVSVKINNISNLNNRYDVPVTAVVQKLKDIKFEEASDIDLATERDGVLKDLDLSIKTQAPIKDNIAAVKVEDGEVPVTVGVLVLFANNTKVTKINAKTEDANGFGKNKYLKFEISKEIKKIK"

gene 7225..8622
/locus_tag="PIMPEBOA_00008"
CDS 7225..8622
/locus_tag="PIMPEBOA_00008"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71139.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:PIMPEBOA_00008"
/translation="MANKLKVAWFDGLNIGQTHFEQGERFFNRNIDLTINYSNLGYIIDLFSQEMMLQGKIALSISGIAQDGSMNAPEQDPLLPEPIEINYESLIDSVVLIPIGVTDIAEADLSRNTPSNKICLRLNSIALRNYYDDSKSNAMDIEDEYELENLTFTQEKKDILLASRLKLGLGNSTPDELPEELPIAKIKNIDINKKIELSEDSPSTFICTCLNSKISSTIRSFLEEIIIFSINQHKVLNSVFKIGDQTNKTFLDFSTFSLNLKLKKWYLIHFSLKSKDKHPEFLYKFLFQGELSAFSEESFLDFDFPIYKHDNLNYTFLMMNRRLLLLFSKITSPKYFIAKTSINGNFYDFIDNSGILEDAEIYFAIRADYTTEYLLNNFKIQSKIHTQSKINIVATQLEGNDVQPNIPPSSIPYLNGYVYXKDREDHFLDFKKNSESIMLYTNKIKPDIWMAWFQ"
gene 8619..9392
/CDS 8619..9392
/locus_tag="PIMPEBOA_00009"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71139.1"
/codon_start=1
/transl_table=11
/product="glutamyl-tRNA amidotransferase"
/protein_id="Prokka:PIMPEBOA_00009"
/translation="MKEINEKALKSSLDSLNFGLKNNKKIDYSELULLLSYRLSISKMDTSNINQRLETINKLDITAKLMSCKEDEIKIYFFCQLVFIDESLMKNLFINFWAHTLLTVRLFDETQLGGNFTFDIASSFWINPNKFDFLFEIIYATICYLQGKYNIAKDRDKEHIHFCNNIATSLRPYKTEELAFKNAYKIGLEENIWQKFIRLYFKKLIIIVPVLILGVLSDLAFNLETNNKLVDNNISVLIKLNTHIE"
gene 9615..10175
/CDS 9615..10175
/locus_tag="PIMPEBOA_00010"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86955.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00010"
/translation="MTYILLLIIISTISYLKLIFKIIKFKTSKSVKFLVFLGSIGLIIFYTYPSYYLEPSYQFRNMCKLNLNPNEEYKNKILGYFDKGLDIDDDFRHVKKYGSIEMWLYIYDDTYPKTSNQFEKIELMDIALKTNNQMSLHCVDMHISYPWNTTRYVLEUGNMMNFEFIEDELACGNLYQ"
gene 10194..10520
/CDS 10194..10520
/locus_tag="PIMPEBOA_00011"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86955.1"
/codon_start=1
/transl_table=11
/product="methyltransferase small"
/protein_id="Prokka:PIMPEBOA_00011"
| gene            | 10719..10820 |
|-----------------|-------------|
| /locus_tag      | PIMPEBOA_00012 |
| CDS             | 10719..10820 |
| /locus_tag      | PIMPEBOA_00012 |
| /inference      | ab initio prediction:Prodigal:002006 |
| /codon_start    | 1 |
| /transl_table   | 11 |
| /product        | hypothetical protein |
| /protein_id     | Prokka:PIMPEBOA_00012 |
| /translation    | MTNKQLINKLRDMAEALAQASYGVDFDLVTHDKNDFFIKIKDEATESTAFFNKHTQANVLDISYKNYKAYYDSSLKIKGTLKGDFSPLQAKRFFSRYDLLKHCPPK |

| gene            | 11244..11756 |
|-----------------|-------------|
| /locus_tag      | PIMPEBOA_00013 |
| CDS             | 11244..11756 |
| /locus_tag      | PIMPEBOA_00013 |
| /inference      | ab initio prediction:Prodigal:002006 |
| /codon_start    | 1 |
| /transl_table   | 11 |
| /product        | hypothetical protein |
| /protein_id     | Prokka:PIMPEBOA_00013 |
| /translation    | MGILKKVYIVFGGYYFGEFLLVCLVLMLILVI |

| gene            | 11799..11948 |
|-----------------|-------------|
| /locus_tag      | PIMPEBOA_00014 |
| CDS             | 11799..11948 |
| /locus_tag      | PIMPEBOA_00014 |
| /inference      | ab initio prediction:Prodigal:002006 |
| /inference      | similar to AA sequence:RefSeq:AAW35443.1 |
| /note           | conserved domain protein |
| /codon_start    | 1 |
| /transl_table   | 11 |
| /product        | hypothetical protein |
| /protein_id     | Prokka:PIMPEBOA_00014 |
| /translation    | MKILKSLYIWMIWGFGAIGGYMGERATUTERSFFLVLVLYLFPLPLLHYLILEFTKNNKIFISICFYLLLLVITAYYFTLISGGCTGNFLTFFIMITLMYIICSAILWKFKNLRLYFYIIICITYLYIVHLHIFACYEIEWTDILLDKDVRIVIYI KEINLLTTEQ |

| gene            | 12158..12628 |
|-----------------|-------------|
| /locus_tag      | PIMPEBOA_00015 |
| CDS             | 12158..12628 |
| /locus_tag      | PIMPEBOA_00015 |
| /inference      | ab initio prediction:Prodigal:002006 |
| /codon_start    | 1 |
| /transl_table   | 11 |
| /product        | hypothetical protein |
| /protein_id     | Prokka:PIMPEBOA_00015 |
| /translation    | MKTQINNLRDYTELAWASYFYFDLGYLQENETIVILNELVSL SYNGN |

| gene            | 12639..12791 |
|-----------------|-------------|
| /locus_tag      | PIMPEBOA_00016 |
| CDS             | 12639..12791 |
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00020"
/translation="MKYYATIYIDPLDFKDATHAFLGLPKAVLMS"

gene 14208..14687
/locus_tag="PIMPEBOA_00021"
CDS 14208..14687
/locus_tag="PIMPEBOA_00021"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00021"
/translation="MQIPIYSKLAKLESKGDINSTSGQIACGLGGYAALICAVFV
VYKLKNLEEFELIVFFIPILLIFIAIFWFIFLSFYKNNIFFHFLCYSTEYIFNIPN
FYLNVLMNLLLLITIWLFFVKLHKFRFLFLMMYCFEFAIFIGIPYGLGETISK"

gene 14684..14899
/locus_tag="PIMPEBOA_00022"
CDS 14684..14899
/locus_tag="PIMPEBOA_00022"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86410.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00022"
/translation="MKEIIKYYVTYIDELLNMLKHVDFSLFLFKAFFSQISKQIDF
THAFLGTLKDSSDELDKIIDEELQKF"

gene 14946..15221
/locus_tag="PIMPEBOA_00023"
CDS 14946..15221
/locus_tag="PIMPEBOA_00023"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00023"
/translation="MQIPIYSKLAKLESGIGIDNITSGIQIAWCLGSLGIALICAVFV
VYKLKNLEEFELIVFFIPILLIFIAIFWFIFLSFYKNNIFFHFLCYSTEYIFNIPN
FYLNVLMNLLLLITIWLFFVKLHKFRFLFLMMYCFEFAIFIGIPYGLGETISK"

gene 15468..15647
/locus_tag="PIMPEBOA_00024"
CDS 15468..15647
/locus_tag="PIMPEBOA_00024"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86410.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00024"
/translation="MVECFLDFKNQCYWQREDFTHAFLGTLKSPDELKDKEELQRF
EYLNKKEFKLXKISK"

gene 15689..16147
/locus_tag="PIMPEBOA_00025"
CDS 15689..16147
/locus_tag="PIMPEBOA_00025"
| ORIGIN |
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| 1   | gttgtaggg  ttgcttcatg  atagtaaag  cagagggctt  ttgggttaaaag  tattaaaaga  aaataaatct |
| 61  | ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 121 | ttgatgaggg  ctttagtgat  tttaaagggt  aggggatttg  agtgatgatt  taatatatca |
| 181 | agactctat  aagaaattaag  ggacattgat  gatccttttg  ggtttgttga  tggattaatag |
| 241 | ccataagctt  attgtgattta  ttttagcata  aggtgggtaa  aataaagttt  attttagggg |
| 301 | gtaagaaag  agatgtgggt  ttttaaagaa  aatatatattg  aaataaatct |
| 361 | tttgtaggg  tttaggtcat  gttcctata  tactgtgta  ttttttacct  gtcattgccc |
| 421 | taaatatttt  gccaacaca  gtttgggcat  atggttttac  atctacagt  ctctagcagc |
| 481 | ttaaattttt  gcccaaccaa  gtttggcagt  attttcatct  cctagcacaa  acttcatttc |
| 541 | tgaagaatag  ttgattttaa  gatataaatc  aacacaaaat  tcattatcct ctaagataaa  aaataaatct |
| 601 | atataggaata  tctttttat  aaatgcttat  tttggtttga  taagagataa  atttacatct |
| 661 | ccataagctt  atgtgattta  ttttagcata  aggtgggtaa  aataaagttt  attttagggg |
| 721 | cagagggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 781 | aaataaatct  cttgagttttt  ttttttacct  gtcattgccc |
| 841 | tttgtaggg  tttaggtcat  gttcctata  tactgtgta  ttttttacct  gtcattgccc |
| 901 | tttgtaggg  tttaggtcat  gttcctata  tactgtgta  ttttttacct  gtcattgccc |
| 961 | cagagggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 1021| accttggctt  accttggctt  accttggctt  accttggctt  accttggctt |
| 1081| tttgtaggg  tttaggtcat  gttcctata  tactgtgta  ttttttacct  gtcattgccc |
| 1141| ttttggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 1201| accttggctt  accttggctt  accttggctt  accttggctt  accttggctt |
| 1261| tttgtaggg  tttaggtcat  gttcctata  tactgtgta  ttttttacct  gtcattgccc |
| 1321| ttttggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 1381| ttttggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 1441| ttttggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 1501| ttttggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
| 1561| ttttggctt  ttgcttcaaac  ttttaaaaaa  gccttcacat  tctatagaaa  aagactttct  aagactttct |
4861 ctgagtggat ttctaaaagt aacttttttc tagttttttc attttttaac gctttctaaa
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DEFINITION Campylobacter species strain strain.

ACCESSION .

VERSION .

KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species

Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

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DEFINITION  Campylobacter species strain strain.

ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.

COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES             Location/Qualifiers
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| 3061 | ataagatgaa aaatctaata atactttatc atctataatt aacacatcag ataaaatctc |
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| 3181 | agcaaaatca taataaatc tttttccttt atctcttgga tattcagagt aagaattata |
| 3241 | agcttcaaat aatgtattta caatcaaaac ataaggattt ttttttaatta aagaaatggg |
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| 3421 | cgtatctaaa gtaaccttga tctttgctt gatttcttga tcaaaatata tagatctttt |
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| 3601 | atcatttttaa agtttatctg cttcattttt tagatctttt atgtatatat gttttgatgg |
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| 3721 | tttaaaagtt tttgtatgtg caatcttttaa atattattaata agtatttata atgtatatat |
| 3781 | cagagaattt tcagcttctt tatatccatc aaaatcactg catataaaaa taattttatt |
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SOURCE  Campylobacter species

ORGANISM  Campylobacter species

Unclassified.

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES

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LOCUS       PIMPEBOA_7              2139 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION  .
VERSION    .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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DEFINITION  Campylobacter species strain strain.

ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES
Location/Qualifiers
source          1..1875
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene           7..630
/locus_tag="PIMPEBOA_00047"
/CDS            7..630
/locus_tag="PIMPEBOA_00047"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00047"
//translation="MSIKGYPIFAIPKKNNQKIQFALAKIQASPLAKIEYDRIRWWEEIGG
KLKAQRRRREKKSKAKMILYLENENKDKVSDQEVHLYKHKAGHKIPKPRSSDY
ILEDGEIILNIKREMILNGGYSISIKTKDLTRYDGLPKFYKETSKKIIDT
PHKIEYTHINPOQTDSDKYRSQGAVEPISHKDLDIVENYLKROQNEI"

gene           620..1006
/locus_tag="PIMPEBOA_00048"
/CDS            620..1006
/locus_tag="PIMPEBOA_00048"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00048"
//translation="MKFENLKHSLFKREFYLKDVKDLRNDVFYVYISITMNKNTLEIF
FKSEKKDQDLQQIFDYKKLHPKSYCKKFNQLEANFDLIRNNWDDITGYIEKKEEM
LISFYFNDYLITEILEKYNFIDFD"

gene           1021..1578
/locus_tag="PIMPEBOA_00049"
CDS
1021..1578
/locus_tag="PIMPEBOA_00049"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87579.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00049"
/translation="MTREQAELIIKEEKLIDTDWYPSYKHSGEFHLTMWFDSDNNKYE
TFYVGERGSVELYSFDEKAEIDKLMQMNYYQKDKDYEKLKVEALRIIKEEN 
LEVIWYDEALKPRAGIKHDQKDYISFITNAKAEIIYEYRSEFDGDYRETJKEM 
NDENIALYALINRARIKIMQRISFT"

ORIGIN
  1 ataggagtga gtataaaagg ctatcctata ttgcttacat ctaaaagaga taagacataa
  61 tttgcttttag cttaatatc agctcttgtc ctgtctaaag tgtagatag taaggagaag
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 181 gagaagagaa atattcccg tttgatttaa gctcatctata cttgaagac caaaaagatg
 241 caagagaatt ctctcttataa atacagatct acttacatctc cttgaaatagt ataaagatg
 301 agtctaggtt aatggtagta agtattttag aaatcttataaa cttgatatag ttaaaaatgtaa
 361 cagaccctaat attctatttaa aaattgataa gctgatatata tataaaatcttctatatg
 421 attgatcataa gctaagttta gctcatctctt attgatatag cttgaaatag tttatgctttc
 481 gatactctct ctaaaatgag tatctctttaaa ctgtctacatc cttgaaatag aaatatgtca
 541 agtaaatcag tcctcttttttag ctctttcttaa cttgaaatag tttatgctttc
 601 attttaaatg ataagtttaa gctcatctctt attgatatag cttgaaatag tttatgctttc
 661 cagaccctaat attctatttaa aaattgataa gctgatatata tataaaatcttctatatg
 721 atgataaatc agtattttag aaatcttataaa cttgatatag ttaaaaatgtaa
 781 gagaagagaa atattcccg tttgatttaa gctcatctata cttgaagac caaaaagatg
 841 ttgcttttag cttaatatc agctcttgtc ctgtctaaag tgtagatag taaggagaag
 901 cagaccctaat attctatttaa aaattgataa gctgatatata tataaaatcttctatatg
 961 attgatcataa gctaagttta gctcatctctt attgatatag cttgaaatag tttatgctttc
1021 atgataaatc agtattttag aaatcttataaa cttgatatag ttaaaaatgtaa
1081 cagaccctaat attctatttaa aaattgataa gctgatatata tataaaatcttctatatg
1141 attttatcatt atcttgtctt gttgttgttga tttggtattc atgaatatatg ttggtttgtg
1201 attttttttttttt taattcttttaaaa cttgaaatag tttatgctttc
"
COMMENT
Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES

source
1..1821

/organism="Campylobacter species"
/mol_type="genomic DNA"

strain="strain"

gene
67..321

/locus_tag="PIMPEBOA_00050"

CDS
67..321

/locus_tag="PIMPEBOA_00050"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86821.1"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00050"
/translation="MLDPLEIEKLSPEQYVRWNYFKLTATFMTFLVITFIILPCLLQAYLFKCYSTGKRKKSLSNFIFGVCNAPILASVYVVYENL"

gene
440..931

/locus_tag="PIMPEBOA_00051"

CDS
440..931

/locus_tag="PIMPEBOA_00051"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86719.1"
/codon_start=1
/transl_table=11

/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00051"
/translation="MGEDITLSIFWGLFGILACSVIEFLIALSVLIVFSILNYWIKNIKEFVKSYFLIFSIIIFMMMAIVIVFYLYTDLETGRLVLLGPPEEEKLSPEQYKARNYFDFLGGITFIFLVTITFLIPCLLQAYLFKCYSTGKRKKSLSNFIFGVCNAPILAMVYVMY"

ORIGIN

1 ttttttacag ctattattat catatttttat cttagctatg atcttgaatt ttataaatcg
61 cttgtattgc ttgatcctct agaaattgaa aaattatcac cgcaagaata tagaagcgt
121 aattttttta aattttttta ctttgcaact atgttttttt tagtatattc attttatata
181 cttctctgttt tatgcaagct ttattttattt aaaaatgtaa gacagagaaa aaaaagcga
241 aaaaaattttt gttttatatg gtttttgtgt aattttttca tattttatgc caggtgtat
301 gttgttatag aatattctata aagactatca aaaaattcact ctttttattt tggatattta
361 acctattagtt acagagttta tcaactaagct tattaattat gaaaaagctt atttttatgt
421 ttatatctat gtttttaataa tgggtattgc aatgggttatattctatattt gatttttattg
481 agatatattat cttgctgtga gggtgctattat tattttttta atagagattt cggagctctt
541 tgtttttttc attttttta atgggtgat atatatataa cggagtattt ccattttattt aaaaattttc
601 tttttttttt cttttttttt cttttttttt gttttttttt atatattttt atattttttttt aaaaattttc
661 tggatcatta ccttttctag gacttctgttt actttcaattt cccagaatc cccagatctaatc
tttttttttt cttttttttt cttttttttt ggggttatattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
LOCUS       PIMPEBOA_10             1275 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES   Location/Qualifiers
            source          1..1275
            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
            gene           112..609
            /locus_tag="PIMPEBOA_00052"
            CDS            112..609
            /locus_tag="PIMPEBOA_00052"
            /inference="ab initio prediction:Prodigal:002006"
            /inference="similar to AA sequence:RefSeq:CKG86821.1"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:PIMPEBOA_00052"
            /translation="MGDSITLSIFWGLFGFILAFTNIKFYLTTLSVLIVFSILNYWIKIN
IKEFVKSYFLVYFTIIFTAIVIIFYLTYGIELSKDLALLSSAKELESPQEVRYNKF
KLFTRAMMFVLFITFIIPLCQLQAYLFKCYSAGEKRKKLSWFIGFCNIIILIASAYL
MYIFI"
            gene           728..1231
            /locus_tag="PIMPEBOA_00053"
            CDS            728..1231
            /locus_tag="PIMPEBOA_00053"
            /inference="ab initio prediction:Prodigal:002006"
            /inference="similar to AA sequence:RefSeq:CKG86821.1"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:PIMPEBOA_00053"
            /translation="MGEDITFSIFWGLFGFILAFTNIKFYLTTLSVLIVFSILNYWIKI
NIEFVKSYFSYFIIFFTAIVIIFYLTYGIELSKDLALLSSAKELESPQEVRYKF
NMYIFI"
LOCUS       PIMPEBOA_12             1123 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES    Location/Qualifiers
            source          1..1123
            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
            gene            complement(113..265)
            /locus_tag="PIMPEBOA_00054"
            CDS             complement(113..265)
            /locus_tag="PIMPEBOA_00054"
            /inference="ab initio prediction:Prodigal:002006"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:PIMPEBOA_00054"
            /translation="MNENIYGSLEFSKETQSTPSDKRLGVFGDVAPYLGITESFTKAFKG"
            gene            complement(258..890)
            /locus_tag="PIMPEBOA_00055"
            CDS             complement(258..890)
            /locus_tag="PIMPEBOA_00055"
            /inference="ab initio prediction:Prodigal:002006"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:PIMPEBOA_00055"
            /translation="MSEINNYGSLFYYSKETQSTPSDKRLGVFGDVAPYLGITESFTKAFKG"
ORIGIN
  1 aacaaaacca acacagaaaa aagagctaa taatataaag agagcaaaaa aacaaactaa
  61 aaggaataaat ttttctctta cttttctcaa ataataggag atatatcatt ccttacccct
 121 taaagtccat tataatatgt cttctctgtta tgcctaaagc ataaggagca ataatcctcaa
 181 atactcctaa atctcttttt tcactaggag tctttttggt tttttagaa taaaactcta
| Line | Sequence |
|------|----------|
| 241  | aacttccata aatatttc ttttcctttc tggagttcatt tgcattcttta |
| 301  | aggaagtag tatcaatcgt gctaaaaagg cttatagttt aatagtattt tcaaatattct |
| 361  | tcatcacttta atataacgatt atgtaggtta ttataatggtc attaattttt |
| 421  | tcacaacac ctttggtagt atacagccgca gggactataa aacaggttttc aaggtattct |
| 481  | ttgagctttcata cttcagaaaa gtatatatcc atatcttcctt tggatgagccaa |
| 541  | ctactagcata aataaaaaa aatgtcttcaag gaaaaacacca aataacattttaa aataaatac |
| 601  | tcaacacaaaa gtttttctttc tgtgacataaa attctttttaattttagcctttgatagct |
| 661  | tctctgtgca gctaaaaagga aacataaaat aacaccaaaaa ccataaaaa |
| 721  | ttcttagttat gctgaagggat ccataagagccc aataaatcaca aagcacacaata |
| 781  | tatgtagataa aataaagccaa aaagcaaggtt atttcttttt tttttctttc aataaatcaca |
| 841  | tctgtagttt cttgtcctttc tttatgtatttt tttatcttcctt tttatcttcctt |
| 901  | tactctcgttttt ttatcctttccc aaccttttaacc aacaagcctattagctttcatactccttt |
| 961  | acctccacctgctt ttacttctcc accttttaacc aacaagcctattagctttcatactccttt |
| 1021 | tcttgagtggtt cttgttctttc gattttctgtg tttatgtatttt tttatcttcctt |
| 1081 | tatgtaggatggagtt cttgtaggtc cttgttctttc tttatgtatttt tttatcttcctt |

**LOCUS** PIMEBOA_13
**DEFINITION** Campylobacter species strain strain.
**ACCESSION**
**VERSION**
**KEYWORDS**
**SOURCE** Campylobacter species
**ORGANISM** Campylobacter species Unclassified.
**COMMENT** Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

**FEATURES**
- **source**
  - 1..1121
  - /organism="Campylobacter species"
  - /mol_type="genomic DNA"
  - /strain="strain"
- **gene**
  - 161..541
  - /locus_tag="PIMEBOA_00056"
- **CDS**
  - 161..541
  - /locus_tag="PIMEBOA_00056"
  - /inference="ab initio prediction:Prodigal:002006"
  - /inference="similar to AA sequence:RefSeq:CKG87598.1"
  - /protein_id="Prokka:PIMEBOA_00056"
  - /translation="MQMDKYYKAKKGRISLNKVKGLDDKIHEDMDIYYPDKNLKPKY IIIEAEGFTSKLDRKTKQMSEWLIKNLKQLKDNVEKQAIEIKKLLNSVEKDHFHVDEEGKETIDYLKDKANKIKPKG"
541 gaaatggta agggatacta gtaaagatga agcgtatttt actaaagaga taatagaaag
601 tgaagaagat atccaaagat ccgaaaaaat accttttagag cttctctttt gacaaagaga
661 aaccttgcct ttttgtatag aagatagaaat atttcatcttt gcatatggatatatctctcg
721 tgggtatagat atagacataag ttttaaaagaa ttttagagcattatactagt aaaaagaaaa
781 aatcggttta gaaagaaatgtaaagatag ctggtttttgatt ggaagtgccatt ggaactcttg
841 tggtagatga taatagatactgaaagttggtttgttggat gttgatagagatagatg theaagagta
901 gagaaaaaga agagatatgct tcaatagaga tttggtttttta cattttatatgtactaatagg
961 taagatattta aatttagaac gcagaatttgctg caagcagctta gattataagatg
1021 ttttagctact agagatatgctg agttttttatgctg cttctttagtttttagttt
1081 gagaagatatgactagagag ctttttttagtttttagttttagttt tagtttttagttttagttt
PIMPEBOA_15

DEFINITION  Campylobacter species strain strain.

ACCESSION  .

VERSION  .

KEYWORDS  .

SOURCE  Campylobacter species

ORGANISM  Campylobacter species Unclassified.

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES  Location/Qualifiers

source  1..909

/gene=/locus_tag="PIMPEBOA_00058"

CDS  29..160

/locus_tag="PIMPEBOA_00058"

/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

/locus_tag="PIMPEBOA_00058"
/inference="ab initio prediction:Prodigal:002006"
/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:PIMPEBOA_00058"

/translation="MKKHTRLRDPLDTWDLEGAAIVKLMNLDKEEFKSYKYFPYDLY"

PIMPEBOA_16

DEFINITION  Campylobacter species strain strain.

ACCESSION  .

VERSION  .

KEYWORDS  .

SOURCE  Campylobacter species

ORGANISM  Campylobacter species

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES  Location/Qualifiers

source  1..909

/gene=/locus_tag="PIMPEBOA_00058"

CDS  29..160

/locus_tag="PIMPEBOA_00058"

/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

/locus_tag="PIMPEBOA_00058"
/inference="ab initio prediction:Prodigal:002006"
/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:PIMPEBOA_00058"

/translation="MKKHTRLRDPLDTWDLEGAAIVKLMNLDKEEFKSYKYFPYDLY"
DEFINITION Campylobacter species strain strain.

ACCESSION

VERSION

KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES

Location/Qualifiers

source 1..895

/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene complement(320..889)
/gene="trxB_3"
/locus_tag="PIMPEBOA_00059"

CDS complement(320..889)
/gene="trxB_3"
/locus_tag="PIMPEBOA_00059"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86288.1"
/codon_start=1
/transl_table=11
/product="thioredoxin reductase"
/protein_id="Prokka:PIMPEBOA_00059"
/translation="MHKNPLREQQIKTLAKTLKPDEFGMLPFIDEIMGVDWVIDLKNKY DIASDQFGSMYKALRSVDEVGKIDPRIDSTYESRRERFDRHRGGYKNGMLQGYGTDT PNDWSEERRAQLFNDTILHAKAALTPPGYPNAPYYFTPENLEWYKRKLDLKDLP RIPAIVYRNPFLRLRAKILKGEENGIE"

ORIGIN

1 tggatttttg ccctggtgta aattcaggat ctagatacct aggttggataa ttaatataag
61 gagaggttct taaatctta tcggcttcaa acaaagcttt agaatattct tgggtgtatt
121 tgcctacttc acgcccatct tctcttttat caaatataat ttgatttgta ttttatcaaa
181 cttctaatat aagtccatta gaagtataga tctcgtaaat atctttatta tcactcatct
241 tttatccttt cttaatttat cccatatata aaccatcttc catgattata gttagtgctca
301 atctgctctg taaattactt tattttttaa tgccattttc ttcgccaaat ttgagtatct
361 tagctctag tttctctggg aaattatatc tataaatagc aaggttcctt ggtacaaaga
421 gtttatcaag cttatatcct ttatatatac attctaggtt tttcggaatt aaataataag
481 tgtcattagg atagccttga aagaggtgta ggggtcgag tttgcatga agtattaaga
541 tatcattaaa aagtttgtgc cttctctcct tcaatcatt aggtgtatcg gttccatacg
601 cttgacagat gcctttctcttat cttcacttct cttctcctat cttcacttct tctgctcact
661 aagtgaatcat tatatccttt ggtatcttta ctctctctct aaccacatca ctctactagg
721 ctcttctact ctctccactt ttataattca cttatcatact cttatcatact tcctttaaattc
781 aatcctctccataatcct tttataaaag gaagcataact aatttrepcaac ctttttaaag
841 ttctagttta ggtttaatt tgtgtgttgc tttatgggtt cctacta

LOCUS PIMPEBOA_17 877 bp DNA linear 12-APR-2021

DEFINITION Campylobacter species strain strain.

ACCESSION

VERSION

KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species
COMMENT
Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES

source
1..877
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene
2..571
/gene="trxB_4"
/locus_tag="PIMPEBOA_00060"

CDS
2..571
/gene="trxB_4"
/locus_tag="PIMPEBOA_00060"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86288.1"
/codon_start=1
/transl_table=11
/product="thioredoxin reductase"
/protein_id="Prokka:PIMPEBOA_00060"
/translation="MHKNPLREQIYRALKPDYEGMLPYEIEIMGVWQVDNLVY
QNFDAMGKGYRALSRDVVEKIDKPMDVSTYERSREFDRYMDGQGYNQMTINYHVDI
NNTNYTSEASEKLFMDSLVLEAKLAAALTPPGYYPNYFSTPERLEWDYKNQYLDKLLDP
RIPAIYRNPFLRAKILKFGEENGIE"
gene
 145..639
  /locus_tag="PIMPEBOA_00061"
CDS
 145..639
  /locus_tag="PIMPEBOA_00061"
  /inference="ab initio prediction:Prodigal:002006"
  /inference="similar to AA sequence:RefSeq:CKG87598.1"
  /codon_start=1
  /transl_table=11
  /product="methyltransferase small"
  /protein_id="Prokka:PIMPEBOA_00061"
  /translation="MKKKIQELKSINKYYAKMDLYYLKQGYKRISLN
KGLDDKHGIDGITYAIAAAHHNAPNLKCIYDIEKEELDKNATKNIERNGKY YEER"

ORIGIN

1 ggaaggtaaaa gaagtaagaa aaataaaaaat gatagagcaa agcaaatca aagcatta
61 aataatacacg ccaaaacaaca acaaaactca tttttacaag aagttaaaca acaaaagaa
121 gaggctgaaa aagttttgac agatatgaa aaaaagatac aagatttaaat aagatttata
181 aacattacga caaaaaacaa aggttaaatc ggcaagacg aatattgatt gtattatta
241 aaaaaagcct ataaagagaa tagtttaggt aaagttcaag tagtttaggt aaatttcat
301 catgtgaattg atgaagtaaat tatttaatat tatttaatat aattttatct
361 gctagttcg gaaaaagttc tttttttttt ttttttttttt ttttttttttt
421 ttggataacag aagagagctt aaataagattc ggttggattc attaaacca tagtttata
481 atagggattcat atctttaagaa aaataaactt cagagcaatt cactattttat
541 aaaaaaggcct aaagaattgta aaattttttgt aataaaaaag taatatattt
601 gaaaggattt gaaaagattttg aagagacgaa gagagatgaa gcgtattttta caaacacat
661 aatagattgt gaaaaaaaat caaagagaa tgaaaaagaa tcttttagaa tttctttagt
721 agatgcaaaag aagagagttt tttttttttt ttttttttttt ttttttttttt
781 ggataaatatttctctttcct ttaaatattt ctcttttcttt ttaaatattt ctcttttcttt

//
LOCUS      PIMPEBOA_19       736 bp   DNA   linear  12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
           Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
    source          1..736
        /organism="Campylobacter species"
        /mol_type="genomic DNA"
        /strain="strain"
    gene
      52..183
        /locus_tag="PIMPEBOA_00062"
    CDS
      52..183
        /locus_tag="PIMPEBOA_00062"
        /inference="ab initio prediction:Prodigal:002006"
        /codon_start=1
        /transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00062"
/transluation="MPYLLSLSDEEFEKIIFHVSGFSEIDTTLKEAMELRKEKKDE"

ORIGIN

1  ccaacaaaaa attgttttga aagaattaat gccattataa aacctctagt aatgcccttat
61  ttatattaagt taagttgagaa aagaatcttt tcattgttaag cggttttgac
121  gaaattgata ctaccttcct taagaagaca atggaactca gaaaagagaa aaaaatgtgaa
181  tgaataatatt tataaaaaaa tacaagagat taaaacttgt ttaaaggata aataagaccc
241  aacaaaaaac taacacagaa aacacacca acagacaccc aagatgaaaat attgggaag
301  gaaaaaagcata caccttcctg tttgttgttt atgggataac atatattgtg tttttgtt
361  ttatgctttta tttgtcctctc aagagcttgg aacatactaa gaaatgtttaa ttgttggttg
g
421  ttatattatatg gatgtatagt cacctgacat agatgcttat aagggcgtta
481  atatttaaaag aatattatatca aacaaagaa aacttattgtg taatattatat attaaatcg
541  atattttgtt tcccttagga aacaaaaatg tgtattatgctc ctacgtgctca ttgtgtctta
601  ctccaggaga tatactggta tacaatttcg gatgatttat gttttatgtt
661  ttatgttta tttcgtgcctg aggagttgat cttgttttttg gttttatgtt
721  ttatgttta tttcgtgcctg aggagttgat cttgttttttg gttttatgtt

LOCUS      PIMPEBOA_20    708 bp   DNA    linear    12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
       Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES              Location/Qualifiers
   source          1..708
       /organism="Campylobacter species"
       /mol_type="genomic DNA"
       /strain="strain"
   gene          28..558
       /locus_tag="PIMPEBOA_00063"
   CDS          28..558
       /locus_tag="PIMPEBOA_00063"
       /inference="ab initio prediction:Prodigal:002006"
       /codon_start=1
       /transl_table=11
       /product="hypothetical protein"
       /protein_id="Prokka:PIMPEBOA_00063"
       /translation="MLLCFALYLFPRLFNPSKEIDYKWFIVFFTLVIYALAQKIYMANIKRIYVTKEKLVEYKYKNDLVPLGTFFVYRRSLPSISNPQDIVYTFGDKVKEYELPGLFSGDDPTKDCFERINAIKPHVMPYLLSLSDEEFEKIIHVSGYEIGNTTLKEAMELRKEKKDE"
   gene          551..703
       /locus_tag="PIMPEBOA_00064"
   CDS          551..703
       /locus_tag="PIMPEBOA_00064"
       /inference="ab initio prediction:Prodigal:002006"
       /codon_start=1
       /transl_table=11
       /product="hypothetical protein"
ORIGIN

1 tttttgcttt tttggataac atatattgtg cttttatgtt ttgcgcttta tttgtttcct
61 agattatatta atctcagcaa agaaatagat tataaatggt ttatatgttt tttacatatt
121 ctttttagtta tatagtacgt tcgacaaag actctataaa tggcacaat taaagaaatt
181 tattgtcaca aagaaaaaact tgtgtgtagg tatttatata aaaaagatttt ggtttttcct
241 tttaggaactt ttsgtgata ttctcgtagt tgtgctcttc catccatatc aatatcaggagga
301 gatatactgta tataacacttt cggagatataa gtcacaagaa acttgaacc tgtttttcac
361 agtggtggcc agtgctcaac aaaaagttgt ttcgaaagaa ttaagctct tatataagctc
421 tctgtaattgc ctatatttatt aagcttaagaat gatggaagat tttgaaaaat cattccacat
481 gtaagcgggt ataacgttaa tgtgctcttc tttcttaaag aagaagttgc acaccagaaaaaa
541 gagaaaaag atgatgtgaa atatattgag aatgtagag ttatctattct aagaaactcactc
601 aagacactctt agtataaaaaa gggattttag aagatgggata gatgtgctct cttatctcctt
661 aggcttacca gaaggtttttctactaaagc gtttaggggg aaagcaaat

//
LOCUS PIMPEBOA_21 586 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..586
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN

1 aatcaatcac ccaatctact ccataatctt cctctataaa aggaagcata ccaaatccat
61 caggtttttta agttctgatct aagggatttta tttgtggctt tctttaaggg gtttaggca
121 cttcctactaa acacctctct actgtcataaat ctgctataacc ataataagca ccaataaat
181 tagtttttcttg tagtataactg cttctctccttg ttaatgttta atataagaagatatgtcttga
241 taatcttgct attaaacaaattttgtagcag tagatattta tagatatttatataacaccctc
301 gtatccctgc gcccataaacc cattttattt ctatgatctt atttagtttatttatgtataattt
361 tatcgttcctg tgtgctgtag tattctccttc actattttattgctgtaggacactcatttctctcattc
421 caagttcctac agttcctaat ggtatatata taacacactc tttctataacc ctttttattatataatcct
481 ctataaatttt atctctctctt cttttagtttct ttagttgatct ataataagcct tttctctttttcctt
541 tagttcaagg agctatgcct ctttttaatggt gacttttttaa aatatatagttttttttaa tataatctgctt

//
LOCUS PIMPEBOA_22 554 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..554
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN

1  tgtgcattttc ttgcccaaat ttgagtatct tagctctaaag ttcccttggg aaattatatc
  61  tataaatagc agggattctt ggatcaagga gtttatcaag cttatatacc
 121  atttctagttt ttcaggggta aaataataag gtgcattagg ataaccttgtt ggaggaggt
 181  gggctgcgag tttggcagtt aatatcatag aatctatttt taattgcgca tcattccaat
 241  catttgggaat atcataacca taggcattaa tcatgccatt gtaataaacc tccatataat
 301  atatcaacat ccttttgttt tcataaagac aatcatatct cctttggtct tttatatcgg
 361  cctcaactac atcacttctt aaggctttat atatatcccc aatattcact tccagaatattt
 421  gagtttcttt ataatcact acacaccata cttccataat cttctctataa aagagagaca
 481  tccaacaactc atcagttttt aagttccttag ctaaggtttt aatttgccttt tctcttaaag
 541  gatttttagt cact

LOCUS       PIMPEBOA_23              518 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..518
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN

1  cccttgggaa attatatcta taaatagcag ggattctttt gatgcaaggt ttatcaagct
  61  tagttctttt taatcattcat ttctcttttt caggggttaaa ataataggt gcattaggat
 121  agcttttggt aggagttagg gtgcagatgt tggcatttta tctctctat tcatatatctt
 181  tgggtgtcact ttctctcttt cgtccatgg taataacca tccatagcc tccatatggt
 241  cggatataaa ttcttctctctt tggcagatcc aatccctctctgtcctcacac gtagaatctt
 301  tatcttttgc atctttttatc tgcctctctct cctctccata gttctctgct ttatcatacc
 361  ttcacaacatc atgcgagacaa atcatttactg ttctctacta ttcatcaca cttactcccca
 421  tatcttctac tataaaagga aagcaataacc cttattcaggg ttttaagagtc ttagctaaag
 481  ttatatttgg tttttctctc aagagagtc

LOCUS       PIMPEBOA_24              518 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source 1..518
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN
1 taagttccct tgggaaatta tatctataaa tagcagggat tcttggatca aggagtttat
61 caagcttatg tcttttataa taccattcta gtttttcagg ggttaaaataa taaggtgcat
121 taggatagcc ttgaggagga gtgagggctg cgagtttggc atgaagtatt aaagtatcat
181 taaaaagttg tgccctttct tcactccaat cattgggtgt atcggtttca taaccttgcc
241 tcataccctt tcctatatca actctataac gatcaaattc cttctctgct tcataagtag
301 aatctatatc tcttggatct tttatcttgc cctcaactac atcacttctt aaggctttat
361 atatatcccc aaattcatca ttagctaatc tatatttatt taaatcaatc acccaatcta
421 ctccccataat cttactctaa aaaggaagca taccaaatct ctacagggtt aaagtcatat
481 ctaaggtttt aatggtttgt tctcttttaa gattttttta

LOCUS PIMPEBOA_25 507 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..507
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene 67..207
/locus_tag="PIMPEBOA_00065"

CDS 67..207
/locus_tag="PIMPEBOA_00065"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86746.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:PIMPEBOA_00065"
/translation="MWYMKIFKDYKFTPYGLDFRLYSKDFIAKLDFKDKAYNVLYNT GV"

ORIGIN
1 aacgcaaaaa attaatctggg ttattatggt tttatgtttaa tggctctata ttaattgcca
61 tgttattatgt tgttatgtttaa gtttatatat aatctcttataa aatggtgttgg
121 gaattatatc ataatgtatt tggaaaccttg aaggaataa aatagtatttataa aatcctacct
181 aatctatcctt attctactttc tcatattttc tttactttttc cttactctct tatttttttt
241 gtttatattc gatttatctt ttcttttatctc atataaatc aatattcttt tttactctac
301 gttttatttc ttttcttct ttttaattaat ctctaatgag tatttttttga tatttttttt
361 aatcctacttt ttttatctctct aattattttt tttactctact tttactttttt catttttttt
421 cctacccactt gtattttataa ctcttttactttctctctct cttcatcctt cttcatcctt
gtattttttt gatgttttttt gatgttttttt gatgttttttt gwtttttttt

//
LOCUS       ECFEEEMN_1             17665 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..17665
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene complement(370..1278)
/locus_tag="ECFEEEMN_00001"
complement(370..1278)
/locus_tag="ECFEEEMN_00001"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71146.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00001"
/translation="MNDLASYSFFKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"

CDS complement(370..1278)
/locus_tag="ECFEEEMN_00001"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71146.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00001"
/translation="MNDLASYSFFKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"

gene complement(1275..2996)
/locus_tag="ECFEEEMN_00002"
complement(1275..2996)
/locus_tag="ECFEEEMN_00002"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71145.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00002"
/translation="MKDNIFYYQKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"

CDS complement(1275..2996)
/locus_tag="ECFEEEMN_00002"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71145.1"
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00002"
/translation="MKDNIFYYQKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"DFVQVSYQIVKMDKLYQKMDYLGKMPYKLMDQPLTVK"
FGKKALI

**gene**
complement(2993..3385)
/locus_tag="ECFEEEMN_00003"
CDS
complement(2993..3385)
/locus_tag="ECFEEEMN_00003"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87312.1" 
/codon_start=1
/transl_table=11
/product="type VI secretion system lysozyme-like protein"
/protein_id="Prokka:ECFEEEMN_00003"
/translation="MSLLDKLIHNLDEQNIHIPFYQNDVFKNNKVLLNAKINDCYAVRNLGMPNMAINLNSELCVSMAKEIRKIDNYKICVVSITYDNLSPLWSQFSLIKFKFKEFNFIEIKNNYRCEVK"

**gene**
complement(3388..4842)
/locus_tag="ECFEEEMN_00004"
CDS
complement(3388..4842)
/locus_tag="ECFEEEMN_00004"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71143.1" 
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00004"
/translation="MANTKVIDPTIQEEMSKYKSDTDESIAKRQVAEFISEIVKSDNAEENIKFALDEMIAHIDHLSKQMDVLHNEEFQKLESTWRGLRFLVETDFNE
NIKIDLFDITKEALEDENPPPIDTSIVYVKNYSEYQGFGEVGAIDYQQLGSA
SPDMTELKNSMACSASHPSFGLTSGFKGFGLDDYESLAINIQDLEGLGQPYTRWRT
FRENESKTYGTVRFLASPRPDPEENPIKSFNYKENVHSHNHHLLWANSSYTFCR
LTTESFAYKWRGPGNIGPKSGPTVCLPTLTYVENFGITIQSISKPEVLITDRREYELAEAGFIITLRLRSNAAEFFSANPLPKIFQONTPEGKEAETNYRLGTQLPYIFLISRLAH
YLKVLQREIEIGSWKSDIENLNEWIRQYISDQENPPVEVSRRPFRAAQVQKVDIP
GEPGWYKGLSVPKPHFKYMGNFELSLVGKLDKE"

**gene**
complement(4844..5329)
/locus_tag="ECFEEEMN_00005"
CDS
complement(4844..5329)
/locus_tag="ECFEEEMN_00005"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71142.1" 
/codon_start=1
/transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00005"
/translation="MSDGSHAPKERINITYKAKTNGQEDVELPLKLMWANLKGKNE
TPLEEREILQINKFDAVFQMRKLDITTSVSKNTLGTGAEELDVKLKNASMKDFSPPDS
LAQIPELKNKLLQLREMLAKIIKPGMGNIPDFRKAVKLEALKKENTKEKLLEIKQEEQGN"

**gene**
complement(5399..6646)
/locus_tag="ECFEEEMN_00006"
CDS
complement(5399..6646)
/locus_tag="ECFEEEMN_00006"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71141.1" 
/codon_start=1
/transl_table=11
/transl_table=11
/product="nucleobase:cation symporter"
/protein_id="Prokka:ECFEEEMN_00006"
/transl
"MSFCNQLKNNLDELQEFHLLEDEMSKYKTLNHENISWDKVVYQYS QFILLHSHDLDFKVCNYFLLSCFNLNEECFKEKLLLLFFQLHLKKMDENNTYISAQKRKI QIFIQNFQFYNKTVKLVSISEIIDQFIALFSEFNLLSNSCFKKEIAQVAPQLPKSPV AQAVSNVSHSNLSDNLYREYKNFQYKLEFELLEDNLENNLYALFTQAMWGKIKCLPE CNNEKIKIRKPADIIILLSDKENDEIHKCFMHELINPFWIEGVQFCDFEKK KKNKQLDILMTLSDFKDAIERRQNGDFICKEVYVFYKPKPEKNKSSFKSSK TDKEHTLQDFEQQMLMNIDKENFNNSNINMNLMLDMVKIFESGKMKNKSKILNYLVE LMEKTLKDYLAEEYENAKNKIK"

/gene 6769..7215 /
/locus_tag="ECFEEEMN_00007"
/CDS 6769..7215 /
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71140.1"
/codon_start=1 /transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00007"
/transl
"MFRKKSLFFILLPLFFACCSVSVKINNIENSNLNNRYDDVPVT AIVYQLKDIKFEAASIDLAREDGGVGLKDLSIKTQAPIKNIAKAVKDEGEPYV VGVLVFLANNKTVKTQAKTEDANGFGKKNKLFKEISKEIKRIK"

/gene 7225..8622 /
/locus_tag="ECFEEEMN_00008"
/CDS 7225..8622 /
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71139.1"
/codon_start=1 /transl_table=11
/product="type VI secretion protein"
/protein_id="Prokka:ECFEEEMN_00008"
/transl
"MANKLKVAWFDGLNIGQTIEQERRQFERFFRNIDLKTKINIIYSNLYG IIIDLFSEQMLQGKIALSKISIAQDSIFNEPAEQDLLPEPIEMYNELDSV∀LVK IPIVTDIDIALSRNTPFSKCYLNRASONLARNNDDKSNAMKIDYEYELENLFQT EKDLILLAALRKLGLGNSTPDELPIAIKNNIDKIELEDSDFTCNKIS TIRSFLEEIIIFSINOHKVLSNLFKIQDQTKNTDFSTFSLLNLLKWYLIFSHLKK DKIHPEFYKELFQGELAHSNNESSFDFIPIHKDYNLYLFNLMNRLLSKITE SPKFIKTSINGNGFYDFIFDNSGILEDAEIYFAIRADVFTEYLLNNFKIQSIKIHQ SKIKINQAQLGELVQVNPISISIPYLNGYVYKIDKRDHLFDFKNESIIISMYLT NNKNDPIMIMAVFQ"

/gene 8619..9392 /
/locus_tag="ECFEEEMN_00009"
/CDS 8619..9392 /
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AJK71138.1"
/codon_start=1 /transl_table=11
/product="glutamyl-tRNA amidotransferase"
/protein_id="Prokka:ECFEEEMN_00009"
/transl
"MKEINEKKALSLLLLDSNFDGLKNNKIIDYSLELLLLSYRLSKI"
SSMDTSNINQLRETILNKLITAKLSMCKEYDEKEIIKFKYCLVFIDESLKNLFE
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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 1.14.6 from
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7741  aaaaaaattt  tttatattata  tttttttttt  gatgtttttt  gctctttttta  gagaattttt
7801  gcctgaaagga  aataaagattt  tttttttttt  gatgtttttt  gctctttttta  gagaattttt
LOCUS   ECFEEEMN_3   4060 bp   DNA    linear   12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS
SOURCE  Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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gene
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CDS
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gene
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CDS
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ORIGIN

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121  ataaatttttcatactcttttcttaaactttttaa ctatattttct atatggctt gataaagctt
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3481 tggctcattt ttatccttta aacaagtttt aatctcttgt atataaaata aaatattttc
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3601 cgctaaaacc gcttacatgg aaaatgattt tttcaaattc ttcatcactt aagcttaata
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LOCUS       ECFEEEMN_4              4049 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM    Campylobacter species Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..4049
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gene            complement(403..3918)
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inference="ab initio prediction:Prodigal:002006"
codon_start=1
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LOCUS       ECFEEEMN_5              3161 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES   Location/Qualifiers
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            /strain="strain"
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KNPAILRKEYYKERRK"
gene 550..1116
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CDS 550..1116
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gene 1199..1750
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CDS 1199..1750
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gene 1821..2171
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CDS 1821..2171
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gene 2171..2803
/locus_tag="ECFEEEMN_00050"
CDS 2171..2803
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/inference="ab initio prediction:Prodigal:002006"
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/transl_table=11
/product="hypothetical protein"
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181  ctaaatggag atattgatag tagtgagaag atagaaatat taagatattc
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locus ECFEEEMN_6 2527 bp DNA linear 12-APR-2021

DEFINITION Campylobacter species strain strain.

ACCESSION .

VERSION .

KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

source 1..2527

/organism="Campylobacter species"
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gene complement(192..1442)
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CDS complement(192..1442)
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gene complement(1439..1900)
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CDS complement(1439..1900)
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gene complement(1946..2374)
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CDS complement(1946..2374)
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ORIGIN

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361 caaatacatct ctttatagtct atataacata tcttttataat ctttataaat cacaataataa
421 atatattatat tttttttttt ttgagaagag taatgatgat ctttctttttct ttttctttttc
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601 tctataattt cttttaataa attttaataa ttttttttta gggatatc taaataataa
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DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 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 1.14.6 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 1.14.6 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 Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
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/inference="similar to AA sequence:RefSeq:CKG86821.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:ECFEEEMN_00063"
/transl=MLDPLEIEKLSPLQERYVRNYFKFLTFATMFFLVITFILPCLLQAYLFKCYSTGEKRKKLSWFIGFVCNAPILIASVYVYVYENL"
gene            440..931
/locus_tag="ECFEEEMN_00064"
CDS             440..931
/locus_tag="ECFEEEMN_00064"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86719.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:ECFEEEMN_00064"
/transl=MGEDITLSIFWGLIGFILACSVIEFYLIALSVLIVFSILNYWIKINIKEFKVSYLSIFIFMAIVIVFYLYTDLETSRGLVLLGPPIEKLSPLQEQYKARNYFDLFLGIGITFILVITFILPCLLQAYLFKCYSTGEKRKKLSWFIGFVCNIPILMGVYVMY"
ORIGIN

1 tttttagc ctattattat catattttat cctagctatg atcttgaatt ttataaatcg
61 cttgtattgc ttgatcctct attgtgag atgatcata aatattacg cctagctatttc
121 aatattata aatattata atattata atatatatat atatatatat atatatatat
181 tttctctttt tttctctttt tttctctttt tttctctttt tttctctttt tttctctttt
241 aatattata aatattata aatattata aatattata aatattata aatattata
301 ggttgggttt gttgtatag tttacttttt cttttacttt tttacttttt tttacttttt
361 cttgtggtgt ggttgggttt gttgtatag tttacttttt cttttacttt tttacttttt
421 ttataaatct atatattaca atataactata atataactata atataactata atataactata
481 atatattata atataactata atataactata atataactata atataactata atataactata
541 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
601 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
661 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
721 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
781 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
841 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
901 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
961 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1021 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1081 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1141 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1201 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1261 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1321 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1381 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1441 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1501 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1561 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1621 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1681 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1741 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct
1801 aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct aagagacgct

//
LOCUS       ECFEEMN_12             1275 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
  source          1..1275
              /organism="Campylobacter species"
              /mol_type="genomic DNA"
              /strain="strain"
  gene           112..609
              /locus_tag="ECFEEEMN_00065"
  CDS            112..609
              /locus_tag="ECFEEEMN_00065"
              /inference="ab initio prediction:Prodigal:002006"
              /inference="similar to AA sequence:RefSeq:CKG86821.1"
gene
728..1231
/locus_tag="ECFEEEMN_00066"
/CDS
728..1231
/locus_tag="ECFEEEMN_00066"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86821.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:ECFEEEMN_00066"
/translation="MGDSITLSIFVGLSLSIAVTKFYLYIALSVLIVFSILDNYWIKIN
IKEFVKSYFLVYFITTAIVIYFLTYGIETSKDLALLSSLEAEKELSPQYVRNYFY
KFLTFATMFFLVITFIIILPCLLQAYLFKCYSEGERKRKLSWFIGFVCIINIIILASAYLY
MYIF"
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES             Location/Qualifiers
source          1..1183
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene            complement(159..572)
/locus_tag="ECFEEEMN_00068"
CDS             complement(159..572)
/locus_tag="ECFEEEMN_00068"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AOH52023.1"
/codon_start=1
/transl_table=11
/product="immunity protein 70"
/protein_id="Prokka:ECFEEEMN_00068"
/translation="MVGFSIDNLWYEIGSGDFLHAFFSNVAYHLEKGNWGSRPFILMN EVYQGKLNFSKLALNELENIQKEFKNSFQQPQQ1WQIENSLTPWPWGNISSDITDLS NYFVTSGNDGFLFMLQVLFADNEKANLTFKS"
gene            complement(587..1183)
CDS             complement(587..1183)
/locus_tag="ECFEEEMN_00069"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:ECFEEEMN_00069"
/translation="MSIKYPILFAIPKKNQQ]].CQKASPLAKIYDRAWEGIES KEERAMLLYENNKDSKIKQISINIPKPHWREEDDISLQLYDYEKQKSFLNGN EVPYGTKHSVRLKYNSSIEIXKNYLKDSTSSANNLIVITYKQYQQRLQHPKTEQ IFIGDQSNGNISKEIQEKIKIRNCDILQIFKTK"

ORIGIN

1 tcttttttta gccatgaaa gctttgtggg ttttaagt gttttctagt tggtttacct 61
tggcataaag aagcggcttt cttaagagac aatctaaat taaagaaag gttcttaggg 121
tgctttttttct taagaaatct ccaagagta taattattt taaaatcctt atatgtaagg 181
ttagcttttt catgctcagc tagtttcaac acctctatgaa aatcctctat ttgtaaatct 241
tccatgcttg cttaaaataa atttgatatt cctctagttc atttaacctt attatcctct 301
ttgagttgccc taagagataa gtttttttata cctctatttc acctcttatgaa aatcctctat 361
ttaaatcttt cttaagtctt ccctattctt ccttttattct cccttttttatt cttaaatcct 421
ttgagttgcccc cttaaatcctt aatcctctctt cctcttattct cctttttattct 481
tttagttctt ctaaacttat cctctattct cctctttattct cttctttattct 541
tttaaatctt cctctattct ctcttattct ttaaatcctt cctctttattct 601
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tttttttttatt cctctattct ctctttattct cttctttattct 721
tggcataaag aagcggcttt cttaagagac aatctaaat taaagaaag gttcttaggg 781
ttgagttgccc taagagataa gtttttttata cctctatttc acctcttatgaa aatcctctat 841
tttagttctt ctaaacttat cctctattct cctctttattct cttctttattct 901
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tttttttttatt cctctattct ctctttattct cttctttattct 1081
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Comment: Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

Features:
- Source: 1..1183
- Organism: Campylobacter species
- Mol Type: Genomic DNA
- Strain: strain

Gene:
- CDS: Complement(159..572)
  - Locus Tag: ECFEEEMN_00068
  - Translation: MVGFSIDNLWYEIGSGDFLHAFFSNVAYHLEKGNWGSRPFILMN EVYQGKLNFSKLALNELENIQKEFKNSFQQPQQ1WQIENSLTPWPWGNISSDITDLS NYFVTSGNDGFLFMLQVLFADNEKANLTFKS

Gene:
- CDS: Complement(587..1183)
  - Locus Tag: ECFEEEMN_00069
  - Translation: MSIKYPILFAIPKKNQQ]].CQKASPLAKIYDRAWEGIES KEERAMLLYENNKDSKIKQISINIPKPHWREEDDISLQLYDYEKQKSFLNGN EVPYGTKHSVRLKYNSSIEIXKNYLKDSTSSANNLIVITYKQYQQRLQHPKTEQ IFIGDQSNGNISKEIQEKIKIRNCDILQIFKTK

Origin:
- DNA Sequence:
  1 tcttttttta gccatgaaa gctttgtggg ttttaagt gttttctagt tggtttacct
  61 tggcataaag aagcggcttt cttaagagac aatctaaat taaagaaag gttcttaggg
  121 tgctttttttct taagaaatct ccaagagta taattattt taaaatcctt atatgtaagg
  181 ttagcttttt catgctcagc tagtttcaac acctctatgaa aatcctctat ttgtaaatct
  241 tccatgcttg cttaaaataa atttgatatt cctctagttc atttaacctt attatcctct
  301 ttgagttgccc taagagataa gtttttttata cctctatttc acctcttatgaa aatcctctat
  361 ttaaatcttt cttaagtctt ccctattctt ccttttattct cccttttttatt cttaaatcctt
  421 ttgagttgcccc cttaaatcctt aatcctctctt cctcttattct cttctttattct
  481 tttagttctt ctaaacttat cctctattct cctctttattct cttctttattct
  541 tttttttttatt cctctattct ctcttattct ttaaatcctt cctctttattct
  601 tttaaatctt cctctattct ctctttattct cttctttattct
  661 tttaaatctt cctctattct ctctttattct cttctttattct
  721 ttgagttgccc taagagataa gtttttttata cctctatttc acctcttatgaa aatcctctat
  781 tttttttttatt cctctattct ctcttattct ttaaatcctt cctctttattct
  841 tttagttctt ctaaacttat cctctattct cctctttattct cttctttattct
  901 tttagttctt ctaaacttat cctctattct cctctttattct cttctttattct
  961 tttagttctt ctaaacttat cctctattct cctctttattct
 1021 tttagttctt ctaaacttat cctctattct cctctttattct
1081 tttagttctt ctaaacttat cctctattct cctctttattct
LOCUS       ECFEEEMN_15             1123 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

SOURCE Campylobacter species

ORGANISM  Campylobacter species
Unclassified.

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES             Location/Qualifiers
    source          1..1123
        /organism="Campylobacter species"
        /mol_type="genomic DNA"
        /strain="strain"
    gene            234..866
        /locus_tag="ECFEEEMN_00070"
    CDS             234..866
        /locus_tag="ECFEEEMN_00070"
        /inference="ab initio prediction:Prodigal:002006"
        /codon_start=1
        /transl_table=11
        /product="hypothetical protein"
        /protein_id="Prokka:ECFEEEMN_00070"
        /translation="MSEINNTEIKEQTQDEIIWEGKEIPSSFLLWITYIVLCCFM
LYLLPRPFDTNKFWFVFIMLLIIFAREIYKMANIKRYTVKELVEYYIKNDLVFLGLTFYVYRSLPGFLTPGDVIYTFGKVKEYLEPGLSAGDDPTKGCEKIN
AIIKPHTMPYLLSDEEEFEKISHVSGFSEIDTTFLKEAMELREKKEKDE"
    gene            859..1011
        /locus_tag="ECFEEEMN_00071"
    CDS             859..1011
        /locus_tag="ECFEEEMN_00071"
        /inference="ab initio prediction:Prodigal:002006"
        /codon_start=1
        /transl_table=11
        /product="hypothetical protein"
        /protein_id="Prokka:ECFEEEMN_00071"
        /translation="MNENIYGSLEFYSKETQSTPSDKRLGVFGDVAPYALGITESFT
TKAFKG"

ORIGIN
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61 aacagatttg tgaagtaata ccacacagat aatcctcca tcaagtaggt gatactcaa
121 tttgtaccaaa gaaagagtgt ttgtacatta aacagacctg attagaggtt attagagc
181 gtaatgactt tgtgttaaa gttggagaag taaaagcaga gtaaaggata aaaatgagtg
241 aaataaacc taaacacagaa atccagcata aacactctca aagactcaat aagtcggaaag
301 gaaaagagag aatccttcg ttttctttg tttttgatat atatattgtt ctcttctttgg
361 ttgttctttt aaccttacctg aggacatttc aataactaa gaattttataa tggggttgtt
421 tttttatat tttttttttttt ggcatatatata tattttgagc agatctattt aataagcag
481 atatattatg agtatattgc acaaaagaa aacatctgttt tgaagcttat gattttataa aatattttc
541 atagtttgccc tctctttggaa cttttttttt tttttttttt ggggctttttgggctttttgc
561 ctggcagag aatacttgc tttttttttt gataagcag ctitatttttt ttgctttttttt
611 tttttttttt tccttttccttttttttttttgaatatttttt aagagcattt caatagtgc
721 taaaccccta tgaatgtcct tatttttaaa gcttaagtga tgaagaattt gaaaaaatca
781 tttcacatgt aagcggtttt agcgaaattg atactacttt ccttaaagag gcaatggaac
841 tcgaaagaaga aaaaagat gatgaaat atttatgaa gtttagagtt tatttctaaa
901 gaaactccaa gcacctctag tgataaaaga gatattgagg tatattggaga ttttgtctct
961 tatgttttag gcattacaga aagtttact actaaggct ttaaaagttg agcaatggaat
1021 aatctctatt tattttggaag aagaaagtag ccattttttt gtttttttttcg ttattttttttt gtt

//
LOCUS ECFEEEMN_16 1091 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
  source 1..1091
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
  gene complement(551..931)
    /locus_tag="ECFEEEMN_00072"
  CDS complement(551..931)
    /locus_tag="ECFEEEMN_00072"
    /inference="ab initio prediction:Prodigal:002006"
    /inference="similar to AA sequence:RefSeq:CKG87598.1"
    /codon_start=1
    /transl_table=11
    /product="methyltransferase small"
    /protein_id="Prokka:ECFEEEMN_00072"
    /translation="MQMDKYYKAKGYKRISLNKQLKLQKDDIKIKAKGGKQKAEIKKLKLNSEQVRKDLF HVDEGGKETYLDKDKANGKPKG"
ORIGIN
  1 ctagaggatc tcttaatcct gtatgttttt tctatatgag atgtaaaacc tcaataatcct
  61 tagtagctac aataattttta aaaaagcttg gttctttttcg aatacatttg cgttctaat
  121 ttaaatttct acctattag cctataaaaaa gtaaaaaacc attcctttcg agaattatcct
  181 tttttttttt ccccttctct tctattaatt ctactaatcag ctactaatcag ctactaatcag
t  241 ctactaatcag ctactaatcag ctactaatcag ctactaatcag ctactaatcag
  301 ctataaatcag ctactaatcag ctactaatcag ctactaatcag ctactaatcag
t  361 ctataaatcag ctactaatcag ctactaatcag ctactaatcag ctactaatcag
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t  841 ctataaatcag ctactaatcag ctactaatcag ctactaatcag ctactaatcag
t  901 ctataaatcag ctactaatcag ctactaatcag ctactaatcag ctactaatcag
t  961 ctataaatcag ctactaatcag ctactaatcag ctactaatcag ctactaatcag
1021 ttaaattctt ctttatctaa attcattagt tttcaaatg ctgacacctc aagatcccaa
1081 gatcttagag g

//
LOCUS       ECFEEEMN_17              980 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
  source          1..980
          /organism="Campylobacter species"
          /mol_type="genomic DNA"
          /strain="strain"
  gene            complement(12..641)
          /locus_tag="ECFEEEMN_00073"
  CDS             complement(12..641)
          /locus_tag="ECFEEEMN_00073"
          /inference="ab initio prediction:Prodigal:002006"
          /codon_start=1
          /transl_table=11
          /product="hypothetical protein"
          /protein_id="Prokka:ECFEEEMN_00073"
          /translation="MSFELIFLFFCSSWEVVLASAIISKVFALSVPSSLSLAC*G
  F*RLSSIICFSTLS*FLCKNSSSLPSRLSFSFVLGGFRNNSIXIFFFNFSVSSVITSFKLS
  SSLSKILVISASSAFQPQALPIACILSSSVFNFSFPRKAKKSSGLCKAKLGFILAM
  LL*KVKSIIFFSPFPFLKSVTTPKLSSGKSCNFSFLSKDINLGIKT"
ORIGIN
  1 aaaaaaggaa tttatgtttt aataccaaga ttaatatctt tagataaaaa cgaaaaatta
  61 cactttgatc ctgtgacctt agaagataag ggcctttgag ttactgtatt tagataaaa
gaaaaaga
  121 aaaaaaggag aaaaaaatat agatattaacc tttaaaaag aagatcactta aaaaaaac
  181 cctaatattag ctttgcaag aatcttgagat ttttctaaag ctttgcaatgg aagatcata
  241 ttacagaga atgataaaaa aacaaagcc aagttcatttta aaaaaacaaa gaaaaaaaag
  301 gcagatgaaag tgcctaaat cttgtctaaat gatgataaa gttctaaaaa gttctata
  361 gatgagagaa aatattatg aataaaaggaa aatcagaaaa aaatacagaa aataaagaga
  421 aaactaagc acctaggcag acttgagatttt ttcaaaaaag aatcagaaaa aatcagaaaa
  481 cataagatgt ttaattgataa tctctaaaac ccttcaacaag cctcattgaa tgaatg
  541 ggtactgata atgcagaaacc atggctgtaga atgcaagaaacc tcaccaac
  601 aagaagagc aaaaaaaaat aatcagaa tcaaaaagaca cgggtatgta aacctgcctt
  661 ggtactcctta tctcttttac taaagacta atagctgtttt actcatttag aagaaaaaca
  721 gatgacatttt tattaataact aatgggtattt cattataaag cattataattttttctatt
  781 aatagtagttt cacttattttt aagaggtgtaa ataatcagaa atgggtatatc tgggtatt
  841 ataatagttttt cctatattttt ataggtattttt aatatctagaa atgatcaagagagagag
  901 cactataaca aatgtttaaa aatctaaaacc aatctaaaacc tatttaaaaag atagctgtttt
  961 aaacacaaag gatcaagag

//
LOCUS       ECFEEEMN_18              965 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species

Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

source 1..965

/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene complement(637..849)

/locus_tag="ECFEEEMN_00074"

CDS complement(637..849)

/locus_tag="ECFEEEMN_00074"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:ECFEEEMN_00074"
/translation="MTSEQIRKKFNYYWDKKECKKDKNYEIKSKLLNDAIKKAKESEGNRNLY*CQFSYQRISKGLYTGKL"

ORIGIN

1 tctatatatttt tttctccccct tttttcttttt ctaaaatcag taaccacaaa gcccttatct
61 tctataaggca caggatcaaa ggtgaatattt tcgctttttat ctaaaatcag taaccacaaa gcccttatct
121 attaaatat attcctcttc ttgaaagcat ttatcaaaaa aatctgctcc aactttggct
181 attgcctattt ttaattttat gccatcaccg aatctgctcc aactttggct
241 tattgtcttt tactgtata acacatcagta aagatatcat agttttttata atcacttgta
301 tttctttgata aaggttttac ttgctttttct tcataggctt catttagctt attaatata
361 ttctcatcaa ataaacacatt gcctttttcttccattgtt catttagctt attaatata
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//LOCUS       ECFEEEMN_21              869 bp    DNA     linear       12-APR-2021
//DEFINITION  Campylobacter species strain strain.
//VERSION     .
//KEYWORDS    .
//SOURCE      Campylobacter species
//ORGANISM    Campylobacter species
//COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
//FEATURES
//    source    1..869
//        /organism="Campylobacter species"
//        /mol_type="genomic DNA"
//        /strain="strain"
//    gene     68..565
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DPRDIDSTYESRREFDRYRVGYRKGMRQGYETDTPNDWSEERAQLFNDTLILHAKLAA
LTPPOYNAPYYFTEKLEWYYKRHKLDKLLDPRIPAIYRYNPFRELRAKILKFGEE
NGIKE"

ORIGIN

1 taaaaatcct ttaagagaac aacaaattaa aaccttagct aagactttaa aacctgatga
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//
LOCUS ECFEEEMN_23 835 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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ORIGIN
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601 tttaaatgga gcttttaccc aagagagctt aataaatttc aatattgac gatgtgattggtctgaagtttagcgattagtaaaatcaagtagtcatatggtcagatagcagaccaacttactaatcaaggttctgtaccttcagtacgatagcagtatagcatttctggtgcttacatggtcttacattttgaagatgagccattttttcatatcattatctggtctttacagatgagctatttttcctatttttcttttcttttctttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
KEYWORDS

SOURCE Campylobacter species

ORGANISM Campylobacter species

Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

source 1..614

/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN

1 atctagaatg ttattataaa agacataagc tttgataaact ccttgatcca agaatccctg
61 ctatttatag atataatttc ccaagggaac ttagagctaa gatactcaaa tttggcgaag
121 aatagatggat aagagaaag attaggttta gcagagcctg gaaagtcttttt gttttctttt
181 atatcttttt atatatggga taaattaaga aaggataaa aagagataa ataatagatat
241 ttacgagatc tatacttcta atgctagttt atataagattt gataaaata caataacaat
301 tatatttgat aaagaaaaag atggggttagg agtgagcacaa attatccttag taccacacag
361 agctcttttt gaagcagccc aatcctttaac aacccttccc tctaagagct ataacaagttag
421 gtatcttagt cctgataattt acacagcctt ttccttttagg ttaagagtttag
481 gcgaagctaa taatttataag atcccataaa agagagcatg gctcctggag ctaaagcaga
541 aagagcattt atatacctac taataactaa aaaaagaaga ataatctatttatagtag
601 aagtggtata agaa

LOCUS ECFEEEMN_28 586 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.

ACCESSION

VERSION

KEYWORDS

SOURCE Campylobacter species

ORGANISM Campylobacter species

Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

source 1..586

/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN

1 aatcaatcac ccaatctact cccataatct atacatataaa aggaagcata ccaatttctt
61 caggttttta agttctttgct aaggtttttt ttgggttttc ccaaggttaa gttttatagc
121 cttcgcttta accactcttc actgcaatct cctgataacc ataataagact ccccaatttac
181 taggtttttc tagtatactac ctttctccgc ttaattttat ataaagaattg cttgcttgga
241 taattttttc atataaaaaa ttttggagct tatagttttt tagatatatta ataatcaca
301 gtatcttttc gcccatatcc catttattaac gaaataacat gttatttttag tttggtttttt
361 tatctactttc gtttgttata acatttttac atctgtggtc atacccctgct tttccatctt
421 cagctctttttc agttctttta taataaatgc tacattttaac cttcatttata
481 ctaataattt atatacttttt ttgttttttt ttagttgatt atataaatct cttttcttctt
541 tagttacagc agcttttttt ccttttagtt gcattttttta atatat

LOCUS ECFEEEMN_29 537 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.

ACCESSION
Organism: Campylobacter species

Version: Campylobacter species

Accession: Strain

Features:

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1 cccttgggaa attatatccta taatactcagc ggatttctgg ggattttgggtaatctatacatc
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SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..518
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

ORIGIN
1 taagttccct tgggaaatta tatctataaa tagcagggat tcttggatca aggagtttat 61 caagcttatg tcttttataa taccattcta tttttcagg ggttaataa taagggtcat 121 taggataacc ttgtgaggtg agtgaggttgg cgagttgggc agttaatc atagaaatca 181 ttttaatttg cgcacatcct caacatcttg gaatcatcata acctaggca ttaatcatgc 241 cattagaata acatatcata taatcttcaaa accctccatt acttttcatga atagaaatca 301 tatcctcttg atctttttacct tttcctctaa ctatcactc tcttaaggt ctatatatat 361 ccccaatttc atctcxgagaa atttgatatt cgttataatc aatcaccceaa atcactcccc 421 taaccttcac ttttggagaa acgataacag atcttchagg ttttaatcgc ttagctcatttacgg 481 ttttaattttg ttgttctcttt aaaggatttt tatgcact

//
LOCUS ECFEEEMN_32 514 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..514
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene complement(231..380)
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CDS complement(231..380)
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/codon_start=1
/transl_table=11
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/protein_id="Prokka:ECFEEEMN_00081"
/translation="MALILSKQSFVGSSPSLNKPGSRYSLTPKVVITISPGFDMDG SDEL"

ORIGIN
1 cttttatgtt ttgactctata tttttttcttt aggtattta atccttgtca aaagaatagat 61 tataaatgtt ttattgtttt tttttacattt tttattttta tattgcact tggcaaagaa 121 atcttttaaa tggcaaatat taaaagaatt tatgtcataa aagaaaaact tttggttgtg 181 tttttatcataa aatgtattttt gttttttcttt ttaaggaacttttttattatctgcgctagt 241 tcgggtctatc catctcatgc aatacaggg atatatgcgct tatatacctctt cggagataa 301 gtctaatagata ctctttattt tgggttcattc agttgatgct agtagcaac aaagatttga
361 ttgaaagaa ttaatgccat tataaagcct catgtaatgc cttatttatt aagcttaagt
421 gatgaagaat ttgaaaaaat catttcacat gtaagcggtt ataacgaaat tggtaccact
481 ttccttaaag aagcaatgga actcagaaaa gaga

LOCUS       ECFEEEMN_33              507 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION     
KEYWORDS    
SOURCE      Campylobacter species
ORGANISM    Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES    Location/Qualifiers
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            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
            gene            complement(301..441)
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            CDS             complement(301..441)
            /locus_tag="ECFEEEMN_00082"
            /inference="ab initio prediction:Prodigal:002006"
            /inference="similar to AA sequence:RefSeq:CKG86746.1"
            /codon_start=1
            /transl_table=11
            /product="hypothetical protein"
            /protein_id="Prokka:ECFEEEMN_00082"
            /translation="MWYMKIFKDYQKFTPYGLDFRLYSKDFIAKLDFKAYNVLYNT
             GV"
ORIGIN
1 cgccttttat tcttggtgtg acaattctttt agctttctag aatgtcagca atgcaagatc
61 tttgaaagaa ttaatgccat tataaagcct catgtaatgc cttatttatt aagcttaagt
121 ataatatatata tgggttttct tggatttttct tatttttttct tatttttttct tatttttttct
181 atttttttt ttgtttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
https://github.com/tseemann/prokka.

FEATURES

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gene complement(474..1034)
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CDS complement(474..1034)
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gene complement(1261..2034)
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CDS complement(1261..2034)
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gene complement(2031..2612)
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CDS complement(2031..2612)
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CDS 2622..4835
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SOURCE     Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

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gene         733..831
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CDS          733..831
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gene         963..2465
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CDS          963..2465
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gene         2466..2969
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CDS          2466..2969
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gene 2947..3087
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CDS 2947..3087
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DEFINITION    Campylobacter species strain strain.
ACCESSION     .
VERSION       .
KEYWORDS      .
SOURCE        Campylobacter species
ORGANISM      Unclassified.
COMMENT       Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
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gene              449..589
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CDS               449..589
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gene              1362..1466
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CDS               1362..1466
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CDS               1470..2036
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gene 2036..2188
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LYENLQLSILHLWGF"

gene 2725..2856
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SOURCE  Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES  Location/Qualifiers
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  gene  1341..1496
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LOCUS  CIKGKLNE_5   1595 bp   DNA   linear   12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS
SOURCE  Campylobacter species
ORGANISM  Campylobacter species
Unclassified.
COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES  Location/Qualifiers
source  1..1595
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mol_type="genomic DNA"
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gene
242..778
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CDS
242..778
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transl_table=11
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gene
857..1360
/locus_tag="CIKGKLNE_00023"

CDS
857..1360
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ORIGIN
1 caagcttatt tatataaatt cctatacaca gggagaaaaa gcaaaaaatt aatgtgtgttt
61atatggtttg tgtgtatcct tatatttaatt ccaaatcttg gttggttttt taaattattg
121 taatactgcg ccttcctttc cttctctctc tttttttttt tttttttttt
181 tatataagttt cttctctctc tttttttttt tttttttttt
241 aatgtgtgat ttctctttt tttttttttt tttttttttt
301 ccaaatctgc ccttcctttc tttttttttt tttttttttt
361 tataagtttt cttctctttc tttttttttt tttttttttt
421 tttcctcttc cttctctttc tttttttttt tttttttttt
481 ggtgctcttt cttctctttc tttttttttt tttttttttt
541 ttatggtttt cttctctttc tttttttttt tttttttttt
601 cctccttttt ttatactgct cttctctttc tttttttttt
661 aagatatttc cttctctttc tttttttttt tttttttttt
721 ttctttctttt tttttttttt tttttttttt
781 ttctttctttt tttttttttt tttttttttt
841 ttctttctttt tttttttttt tttttttttt
901 ttctttctttt tttttttttt tttttttttt
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1081 ttctttctttt tttttttttt tttttttttt
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1201 ttctttctttt tttttttttt tttttttttt
1261 ttctttctttt tttttttttt tttttttttt
1321 ttctttctttt tttttttttt tttttttttt
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1501 ttctttctttt tttttttttt tttttttttt
1561 ttctttctttt tttttttttt tttttttttt

LOCUS  CIGKLN_6               718 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS  .
/locus_tag="CIKGKLNE_00026"

CDS
253..384
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/codon_start=1
/transl_table=11
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tttataattt atttattattttatttattttattttattttattttattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
LOCUS       HHHABCBJ_1              1844 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   .
VERSION     .
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
          Unclassified.
COMMENT     Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
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              /mol_type="genomic DNA"
              /strain="strain"
        gene            1..468
              /gene="trxB_1"
              /locus_tag="HHHABCBJ_00001"
        CDS             1..468
              /gene="trxB_1"
              /locus_tag="HHHABCBJ_00001"
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              /inference="similar to AA sequence:RefSeq:CKG87041.1"
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              /transl_table=11
              /product="thioredoxin reductase"
              /protein_id="Prokka:HHHABCBJ_00001"
              /translation="MDWVIDLTEYEFADDADGKAIRSLDDDVLKGLKDPRIDSTPE
              SRREFNREMWAYRRGSVAFYNTDPDNWQEAEEAEDSLILIESKLAVLTPQGYPNA
              PYYWPEHLEYVYKHKLKDPLPRPACIYRNYFPRLRAILKFAENGKL""
        gene            550..1827
              /gene="trxB_2"
              /locus_tag="HHHABCBJ_00002"
        CDS             550..1827
              /gene="trxB_2"
              /locus_tag="HHHABCBJ_00002"
              /inference="ab initio prediction:Prodigal:002006"
              /inference="similar to AA sequence:RefSeq:CKG86610.1"
              /codon_start=1
              /transl_table=11
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              /translation="MSDTTYEIYTPHGSILDVNNKTCNEYFDQSSKPTGKYTKEYSKAL"
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KAYKYLKTKRERYKLYLVRSGIRSTVIDIPYDAYANDEKGNLINEDYKELYKEVEA
NRGLALHDGFLYLMPGWEWLAAAGILGDIKGFLIGALQLSMTGFKARTAVNFLLIQGHE
QGFPSLYSDSYAYRLTGDIHKPQLAQLKDFSKNPYPDEFGLMPFDELGMVDWVDID
LTYEYFADDAGKAIROLEDDLDVVVLGKLLKDRPIDSTEPSRFREMVWAYRRGSVAFY
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ORIGIN

1 gtggattgg gtagttgattt aacagaatat gaatttgcag atggatatagct
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g181 tggctactca ttttggcatttt cttatgccaat cttatgccaat
c241 atagacatttt tagatgatagtt gttttaaaga gtaaatattga
c301 aagatccagt ttgattttat gttttaaaga gtaaatattga
c361 gagaagtagt atttggctat gttttaaaga gtaaatattga
421 atagacatttt tagatgatagtt gttttaaaga gtaaatattga
481 ggagattgag caagacactca cattatatga atagatcatttt
g541 gcctactac gtaactgatttt gttttaaaga gtaaatattga
601 aagatccag ttttggcatttt cttatgccaat cttatgccaat
661 gttagcctact cattatatga atagatcatttt
g721 gagattggtt attgatcatttt cttatgccaat cttatgccaat
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841 ggctactac gtaactgatttt gttttaaaga gtaaatattga
901 tatcacttttaga ttttttttttttttttttttttttttttattatatagatagtga
961 gttaattttaga ttttttttttttttttttttttttttttattatatagatagtga
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g1081 atagacatttt tagatgatagtt gttttaaaga gtaaatattga
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1801 atagacatttt tagatgatagtt gttttaaaga gtaaatattga

//
LOCUS HHHABCBJ_2 1739 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS Campylobacter species
SOURCE Campylobacter species
ORGANISM Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..1739
/organism="Campylobacter species"
/mol_type="genomic DNA"
gene
complement(703..1482)

/CDS
complement(703..1482)

/locus_tag="HHHABCBJ_00003"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86610.1"
/codon_start=1
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/product="thioredoxin reductase"
/protein_id="Prokka:HHHABCBJ_00003"
/translation="MHKGWLFMA..."}

/strain="strain"

/orig=1
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LOCUS HHHABCBJ_3  1177 bp  DNA  linear  12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
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    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
  gene 74..571
    /gene="trxB_4"
    /locus_tag="HHHABCBJ_00004"
  CDS 74..571
    /gene="trxB_4"
    /locus_tag="HHHABCBJ_00004"
    /inference="ab initio prediction:Prodigal:002006"
    /inference="similar to AA sequence:RefSeq:CKG86610.1"
    /codon_start=1
    /transl_table=11
    /product="thioredoxin reductase"
    /protein_id="Prokka:HHHABCBJ_00004"
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DPDRDSTPESRFEDAMGYENGMVTRFDVTPNEWSEQAAALDRDTLVLSAKLAA
LTPPOQYPNYFTRLEWYKRGYLDKLLDPFRIPAILKILFAEE
NGIKD"
ORIGIN
  1 gatacataaa aatccctttaa gggctaaaat agtaaaagat ttagctaaaa ctatacagcc
  61 tgatgaattt ggtatgctac cttttatatg tgagattatg ggagtagatt gggtgattga
 121 tttaatataa tatgattttg cctatgatga agaaggtaga atcatttggg ctttatataa
 181 tgatattaaa aaaggtaaat taaaagatcc aagagatgtg gattctactc ctgaaagtag
 241 aaatgaattt gatgatgcta tggatggata cgaaaatgga atggtaacta gatttgatgt
 301 agatactcca aatgaatgga gtgaacaaca acgctctttt atagagagata cctgattgg
 361 aagtgcacaa ccacgcagcc tcactctctc acaaggctat ctaattttgc tctattaatt
 421 tacacctgaa agatttggaat ggatttataa aagaggatat ttagatataa tccaacctttc
 481 aagaatcctt gctatttataa gtaaaaacag tttcagatgt gtttagaggt gcacttttatt
 541 aatgtcatgaa aaaaaccttt ttaaagatgtg taaagagagat aatattttgt gctttggatt
 601 tataaataag tataataggtg tattataggg ttaaaatagaa aagagtggct aatattttga
 661 accttaatatattatgacattttatgtgaaatagcagc aatcataaacc aattttatattttaaat
 721 atacctttta aagaaaatat taacccacaa ggcaatatttt attaatatttt tacccataaagt
 781 ttagttgaac cacagacat taacagaaac tccccctaca agaagatata aatatttattc
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 901 agcataatct taaaagactc cattltaagga acagataagct tcctcagac agcagagaaa
 961 gctttattataaactttttt aaacaaagaaattatatatat ttaaaagactc
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ORGANISM  
Campylobacter species
Unclassified.

COMMENT  
Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES  
Location/Qualifiers
source  
1..1010
/organism="Campylobacter species"
mol_type="genomic DNA"
strain="strain"
gene  
complement(440..937)
gene="trxB_5"
locus_tag="HHHABCBJ_00005"
CDS  
complement(440..937)
gene="trxB_5"
locus_tag="HHHABCBJ_00005"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CKG86610.1"
codon_start=1
transl_table=11
product="thioredoxin reductase"
protein_id="Prokka:HHHABCBJ_00005"
/translation="MLPFIDEMGVDWVIDLNQFYQFAYDGKGDSTALYDIEKGLKDPRDVSTPESREKEFEDETVRYRFGRNMNFBADSDRDSEESTRLFDDTLIHLAKLALTPQQGYPNAPYFTPERLEWIYKRGYLDKLDDPRIPAIYRYNFPRELRKILKFAEE NGIKD"

ORIGIN  
1 ctagatatttt atatctttct cttttggttt ttaaagattt ataataagct ttttctgctt
61 tagtccaagg agctatgctt cctttaatgg gatcttttaa atatatgctt tgccattctt
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181 tatagtttt gtagggagg gttttcataa tataataaga ttccaaacc gctttggaat
241 attctccggt ataattgcct gtgggtttaa tattttcttt aaatagtatt ttattggtat
301 cttttcttcc atctaatgtt aacccattgg gtgtataaat ctcataagtt tcgctcatta
361 tttatccttt ctttatattg assatatttt tattatatat gtagtggtgct
421 gtctacatct gcaattctct taatctttaa tcagcacaatt ttgaattctt
481 tagctctaat tttcccttggg ataatatac tataaatagc agggattctt ggtatgtatct
541 gtttatcataa atatacttt ttatataacc tattcacttt tattatattgta aaatatagcctt
601 gggcattaggg gaggagagga gggtcgccag tttgctgatg agtatattag
661 tatatctatg gttctcttac ttcctccttct cagatatatt gtggactaat"aag
721 tcatttccttg accaactctca taagcgtcag tttctctatc acatcttattcttctcag
781 gaggatttta cccttttattg atttatatttt ttttatttattttttctttaatgatattcttctg
841 cctactattt atcaatctttt ccgtgtgttt gcattatatc atgatagtaatgtaaatcattttttt
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FEATURES
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/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene 36..818
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CDS 36..818
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/product="thioredoxin reductase"
/protein_id="Prokka:HHHABCBJ_00006"
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ORIGIN
1 ataagaagt aagagctaat agaggtatgg ctaatatgca taaaggttgg ctctttatgg
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121 aacattccat gacagagttaa aagacagaa ctcaagcagt aaatttttta ctcatacaac
181 tattctctaatgctttaa tgtatatcag ctaaaatcct taatatttgg ctagaaacaa
241 atggcatata aagagtcttta ctcagcttta aatgactgaa aaatatgctcc tacccctgc
301 ctatagatgat gtaatgactt ggaatactag atggcataca caaaaaccct cttaaagctc
361 attacaagag attggctttgc gtcgagaggta ttggctgcct gattatctta gttagttgga
421 tataagatga ataagtaattc gagagccatt aacatctggt aagatctgag aagagctac
481 acacataata aagagacccat atataatgctaa gatgggtgta ttgctgcctg
541 atacttggct aatgacttcgcc gattatcttta gattctaaaa aatgactgaa gatgggtgta
601 tattctctctatgcttta aatgacattgg ttgctgatgt tttatatattataatgcttta
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781 tattatattcttctctta tattatattcttctta tattatattataatgcttta
841 tattatattcttctctta tattatattcttctta tattatattataatgcttta
901 tattatattcttctctta tattatattcttctta tattatattataatgcttta
961 tattatattcttctctta tattatattcttctta tattatattataatgcttta

//
LOCUS HHHABCBJ_6 892 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..892
/organism="Campylobacter species"
gene
complement(393..890)
/gene="trxB_7"
/locus_tag="HHHABCBJ_00007"
CDS
complement(393..890)
/gene="trxB_7"
/locus_tag="HHHABCBJ_00007"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86288.1"
/codon_start=1
/transl_table=11
/product="thioredoxin reductase"
/protein_id="Prokka:HHHABCBJ_00007"
/translation="MLPFLDEIGVDWIDLNEYQAYOGDGSVKALDEKVRQGKLDPRIDSTPSRSKEFDEEEANYTGFNRMFFSDIRDSRSKESARLFDDDLILHAKLAA
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NGIKD"

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LOCUS HHHABCBJ_7 849 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS 
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES
source 1..849
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene 114..656
/gene="trxB_8"
/locus_tag="HHHABCBJ_00008"
CDS 114..656
/gene="trxB_8"
/locus_tag="HHHABCBJ_00008"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87041.1"
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/transl_table=11
/product="thioredoxin reductase"
/protein_id="Prokka:HHHABCBJ_00008"
/translation="MLKDFAKNPPYDEFGMLPFLDELIGVDWVIDPNRYRFAEDEKGRVNDALKDDVEKILKDPRIDSTSESRLFEYKLDAYRNGMKTRFDGNPWNHWSKEQVERFNDTLILCAKLAALTTPQGYPNAAPYYSPERLEFIYKKHKLKDLKDPRIPAIVYRNFPRERAKILKFGGEENGIKD"

ORIGIN
1 taaatattatt actatacaaa ctaggagatat aacaaatctct tcttaaagctc taaatgctaa 61 atgcatatag agatgttaaac gatggcatac caaaaaactct ctttaaagctg caaatgcta 121 aagatctttgc taatatgtact cctttagatg gaaatggtat gctacctttt ctagatgaac 181 ttataggagt gatttggttg atagatccaa ataggtatcg atttgagaaaag acgagaatag 241 gaagagtttaaa tggagcatac acaaaaactct ctttaaatcttc attggaagctg tccataaag 301 atatatatttg tagtttttgc ccaactctgc agcctctact cctctctcaag 361 attggaatgaa aactagattt gatggagata atccaaactct ctttaaatcttc attggaagctg tccataaag 421 aaagattttta gaaatgctctt attaatgtact caaaaactct ctttaaatcttc attggaagctg tccataaag 481 acaaaaaatttg taatatgtact cctttagatg gaaatggtat gctacctttt ctagatgaac 541 gggaaatgct ctaaatgtact cctttagatg gaaatggtat gctacctttt ctagatgaac 601 gggaaatgct ctaaatgtact cctttagatg gaaatggtat gctacctttt ctagatgaac 661 attggaatgaa aactagattt gatggagata atccaaactct ctttaaatcttc attggaagctg tccataaag 721 taaatttgata ataggttaaac gatggcatac caaaaaactct ctttaaatcttc attggaagctg tccataaag 781 tagatgttaa taaaatatgtact cctttagatg gaaatggtat gctacctttt ctagatgaac 841 aatatcctc

//

>>BfR-CA-15867_min_cov_30 putative plasmid location

LOCUS   NLMJPNJI_1    24409 bp    DNA    linear   12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT    Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES   Location/Qualifiers
            source  1..24409
            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
            gene  159..1055
            /locus_tag="NLMJPNJI_00001"
            CDS 159..1055
            /locus_tag="NLMJPNJI_00001"
            /inference="ab initio prediction:Prodigal:002006"
            /inference="similar to AA sequence:RefSeq:AAW35468.1"
note="conserved domain protein"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00001"
/transl_table=11
/gene
locus_tag="NLMJPNJI_00002"
CDS
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inference="similar to AA sequence:RefSeq:CKG88019.1"
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/transl_table=11
/gene
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CDS
locus_tag="NLMJPNJI_00003"
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codon_start=1
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/protein_id="Prokka:NLMJPNJI_00003"
/transl_table=11
/gene
locus_tag="NLMJPNJI_00004"
CDS
locus_tag="NLMJPNJI_00004"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
/transl_table=11
/locus_tag="NLMJPNJI_00009"
/inference="ab initio prediction:Prodigal:002006"
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/protein_id="Prokka:NLMJPNJI_00009"
/translation="MLYDVKKLNENDYKKECAKLLIAFENPNYKQENAIHITGNVTIG YGLDLKTGNNPKLLELYGYPDSDSKKLGDEETLFYEIEIIKEYRANKAGFTDPKIVKGY LQNKVFNSLTQEQAEQIEILERTFDSYKCYISQ"
gene  6433..7029
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/locus_tag="NLMJPNJI_00010"
CDS  6433..7029
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/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AOH52008.1"
/codon_start=1
/transl_table=11
/product="type VI secretion system, secreted protein"
/protein_id="Prokka:NLMJPNJI_00010"
/translation="MLLASDREKLNANEYFYPYRLGGIGISAFEKLVGLSNTLNVGV DNKRIAKNSHEFVENKDEIAGANONIIKDEIRNVKENKLIEKSLTIKEKFL NVHQLSADHDNSSLKSNMQTKEIIEQYSELESENSTDFQTDSEVKAGNQLHQPVD TQIVTTKDCVIIKAGGVEVIIIDSNGLVVRSQIAEIA"
gene  7046..7684
/locus_tag="NLMJPNJI_00011"
CDS  7046..7684
/gene="tssI1"
/locus_tag="NLMJPNJI_00011"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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gene  7677..9263
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CDS  7677..9263
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/locus_tag="NLMJPNJI_00012"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
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/translation="MNENIYGSLEFYSKEIQSTPSDKRLGVFGDIAWLYGITEGFA TKAKEIELOVFIKYHSRIATMMHSSKIMNFGILNFFLAKAEGKSVRALTONS VGSTIIIIMNETPAGKEIYKGSHAVKLQTLQQTQTSVASNAATKIAKSGVAVSNIAARAGVISL SRIAGQATGAAAVGSSFIPVTVGAVGAVGLXFDNLIFGDDEEELKQEEAKEKY LEIILDEKMTKHNYLTHQYIELRNVLNEDEALKLICEINSAYFTKILLMLSFY YRDKDEQSYKEAQQEKNPTIIRIQIPALNLKNKIEINECFLAKNLEGKLKEVYVNYHR FDRVVTAMSDQGEKIFENVYVGYKESTIDKISFIIDRFENFNDNFYESVLYAPMFN"
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FSCNFYYNNFQOSKLHNLINIQNEKEVYKIFLNEQLNYFNQFQNNYLVSQQVINN
LKIAYIQKLSLQDINNININELYKALYFEDYVLFDKQALFKNKTIKELEFDS
SFYTIFSVHKAKLNDTYLQARKELYSINEFKRGBKFQDLENAYQTYIHSLVINKEINS
KDKTINKNENKEIKNLNQDNSQESNISKADNATKEDFNLSSHSLNHLHFILEN
KDNKRIIFLNNASSMSNLHIYDNNCDVFINKDSSLDDIKKEKEYIFKKEFNTVRV
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EESNLKLEPKEKKEIAYNNNASFKLKEPLNEFSSAKEPFITLYLKEEHNPIA
NATIIKGFQHNEALRIVNLRKRSDEKGKIRFDKEYSFDCYFSVKLDSEKAYFTFP
LQNKRIIFNYYTHVKGILFKKAKDHLVYDFGNYYKYNELXSINMARTSAGADN
EKRSKQIIAHFYQDEKDKSNGKAFAYYDFIDESIQDFGTLEPEGYLYKINIAKTDK
PNFALDYPPEIGTKWRYCVLRNYTDECSKTFKEIIEKESEKNFNKTSDKKKEFSSQI
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NKIIIFVFKVYE"

gene	13335..14090
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VEFLKACQLKSEEKNEIDNYIFFKNNPQAGKIAYIYRFDLANEEFISKVDGNKYL
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gene	14059..14592
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//protein_id="Prokka:NLMJPNJI_00019"
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ELDSRIMAYYFRKEIKL"

gene	14592..15857
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SEKKMRYLLEDKTEDCHISIEAKDLKFIIDSFKNGIFHFPLPSRDNEPTKDIDKYYIIV
FAYDEKAKIPSLEDHIFIDSFRAGVKGKESELFREDHNLKRDIFNSIQRNCIFSFVFA
VEFLKACQLKSEEKNEIDNYIFFKNNPQAGKIAYIYRFDLANEEFISKVDGNKYL
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YWFKFMNMLDKWYNPKFGLGKVFDKDNLKIPYIAAKFNELEEEVKKNPL
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NTIIKNYIDAINKDYGIPKFVFSDEYIDLGEGVGIANTQANNKDKSYIKDPILL
AMLDDYALQNKDEYDLTDDFYTYTLWVLDFLELPSYGLFQDETELLFNPAAAY
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CDS 16413..16619

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/protein_id="Prokka:NLMJPNJI_00023"
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ISDNNDLFLFSDMKKLGLKLKQKKS"

CDS 17775..18647

/gene 17775..18647
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/inference="similar to AA sequence:RefSeq:ABS44566.1"
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LKELEYINETKVEDLKRKIVLFKYAHIQDIKLIKEKSSVKQEQADLILSTGHK
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18644..18856
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\*gene\*
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TKDDK"

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19693..20613
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\*CDS\*
19693..20613
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IAEMLNRASEHYGGFGLRSGGITYKKEKISCVPQALDFEHGMSHLCAVFLKEDGRTYNL
ERAPIHPKFRMMEYVYKTIITIDRFLMIKDALGKVQEQALKIRELEYQTIGKPTKVTKNPT
TNLTKKKEEKVIPGYKELCIEKIVSOKNAK"

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complement(20713..21741)
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CDS
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/gene="flgS"
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inference="similar to AA sequence:RefSeq:CAL34921.1"
codon_start=1
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/product="signal transduction histidine kinase"
/protein_id="Prokka:NLMJPNJI_00028"
//translation="MNENILKSLDSSEKETLQGLQSLIEQTYIVENEKILNENYNS
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AVKIIAHNEKIVATSIDESKRNELASMGVAAHLAHEIRPNPGISILLLASLFSR
SELKNKHILEIQAIARVERIVNLFTKGVHINASFKNLLELTEECESAINSYNY
SSQIDEFEINFLDMGKALSVQLQNLIYNAIDAEIESECEPSKIQASCQDEQNL
YIRYVDNGCEIKDENLVFEAFKTKLKNGNLGLSLSKIEINAHGKELK FEIWPNFYF
VLPLHYN"*/
gene
complement (21738..22559)
CDS
complement (21738..22559)
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inference="similar to AA sequence:RefSeq:CAL34920.1"
note="conserved hypothetical protein Cj0792"
codon_start=1
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/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00029"
//translation="MAKIFDFYSVFEGFESLDSLNFEEDVFHNSIEYLLKYNLIDIKDC
FKLDEASYALSLLASKNRKRFSLRQHKALSTKLKLMLERIALKLESHAEKVR
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YQSFCEFQLSRENELEKQFGVGSQSYWDKNLELDDLYKDKDISIFGEKVKFNKICRN
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/* locus_tag="NLMJPNJI_00030" */
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inference="similar to AA sequence:RefSeq:CAL34919.1"
/* locus_tag="NLMJPNJI_00031" */
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CAL34919.1"
/transl_table=11
/product="putative aminotransferase"
/protein_id="Prokka:NLMJPNJI_00030"
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THSDSSLNFSDKTVQYERQARKIDTSNLSDEFAICGSGSSSAKFKQELLGIYIP
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VLKENGQKHIIASAFLSANVIGLSDYKRIKSVKLVRKFGIVAFAEDSIPFYKNIACKY
YDAlFISSHKLLGIGGSLLAIKKELGNKPSFAAGTVVYVSRTSQYLCNNEAELE
EGGTPGILQLIRASLAFKIKDEIGEIEEIEKKEIELKEYFEKLELTIPHLILYANNIKT
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gene
complement (23935..24011)
/* locus_tag="NLMJPNJI_00031" */
/* tRNA */
complement (23935..24011)
ORIGIN

1 atactgattc taagataat acaaaacttca caaactttcc taatcattta ccaagcaatg
61 cttataaatc ttatcatcat actccttttt taagagtagc aacaagtata gcaagcaatc
121 attcaggctt ttttcatact ccaagagttg gagatgaagt gattgtttct tttttagatg
181 atgatataga taaaccctat gtgagctcta gtttgtataa tgggaccaat ccaagcttag
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421 ataaagattc taaggtagat ggaatttata atgaaaggat taaaaaggtt catactcaaa
481 ccatagatttt ggctaaaat gtcaatgtag gggctgaata tttaatcaat gtaggcttat
541 ctaaagatac catagtagga ttaagcaata cttttaaatgt aggagtagat aataaagtaa
601 gaatagctaa aaaccttcct gatggtvcac gaaaaaaca agatatatgaa ataggtgcac
661 atcaaaatct cattaggatt cattagagaa taggggaat taaragagag
721 tgggttgaggg gcattagttc attaatata aagaaacatt aaaaaatccaa acagaaaaa
781 agacccctct aatatacttta catttaccaat gttgctttca tcaatgctttg
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901 atgaagcatg ggccagccca ctaaagctta ctatcagata gtaggtcact aatcaagaga
961 agaagagttg gttaatattt gaaagccatg cttatgtaga gttattagta aatcagttttg
1021 ttgtggagag cattaggcag attaatgga gactcaaatc ccagattaataaaaagttt
1081 tcacacacaaa acagcagactt aatttattttct ctaatgtttc ctataaact ttaaatcagtt
1141 ttatgaataa gacagggccg aatatgtag aatcagactt aatattttaaa ctagaatgga
1201 aggagaagct catttaaatg ctagtgcaat ttatagtaaa gcaacacaa gctttggaatt
23941 agcggacggg gctcgaaccc gcgacctccg ccgtgacagg gcggcattct aaccagctga
24001 actaccgctg cacccaagaa gtaataattt aatggtggtc actataagac tcgaacttat
24061 gacatccacc ttgtaagggt ggcgctctac caactgagct aagcgacctt aatttttggc
24121 gacccctaga ggatttgaac ctctgtttcc acacagagag agtgtgtcc tgggccacta
24181 gacgaaggg tctaaaccgg ataaaccttg tccccgttgc gattcgaacc aacggcgcgc
24241 tcctttaaaag ggagatgctc taccggctga gctaacgaga cagatggcgc agcggacggg
24301 gctcgaaccc gcgacctccg ccgtgacagg gcggcattct aaccagctga actaccgctg
24361 cacccaagaa gtaataattt aatggtggtc actataagac tcgaacttat

LOCUS NLMJPNJI_2 7512 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
source 1..7512
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene complement(400..1680)
/gene="trxB_1"
/locus_tag="NLMJPNJI_00036"
CDS complement(400..1680)
/gene="trxB_1"
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/transl="MSDTYMIYAPNQGVEVFVKEVTHYFYFAQSVDPVGKVTAKQTRVF
FKAEEIKSNPQYKYDPOPDNYTGAQATLFKDLQISIKGAIAPWTKAE
KAYYKSLKERYKYKLYRSGLRSVVIDPYAEYCVNVEKGNLYKDKELYKVEEA
NPRNMMNHKGLMFAEWELAAGILGDIGFVGALQLSMTGFKARTQAINFULLIQGHE
QGFKSLYDSAYRDNLTDGHIKNPLQAQLKDFSKNPPYDELGMPLFDELIGVDWVID
PNDDYVFYDFAGKRNDALKDDVEKGLKDPIDSTSESRLFELYKLDAYGMMKTR
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KLLDRPIAIPYRNFPRRELRAKLFGEENGKE"

gene complement(1701..5414)
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CDS complement(1701..5414)
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/transl_table=11
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/transl="MNKEFTCQYIYNQNEKLK lyCKQAKNIVLYCNFSRKNVL"
gene complement(5476..6063) /locus_tag="NLMJPNJI_00038" CDS complement(5476..6063) /locus_tag="NLMJPNJI_00038" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:NLMJPNJI_00038" /translation="MKFKVLETINAELEFPQWDVLDDLHINSFILDIFSTHKQWNKDIT EIIYESFLCDELCSYAEFFMNFLYTKYQGVEFQVTKLEHDLFDIYDENQNL TLSAYTKDKNWYFLONYNECFYIDFCIASWDPSSWNKYNINAIITPKGTY FIFOILPKFYKDYKLEVEIDDKGKLVRLWGEINR"

gene complement(6063..6542) /locus_tag="NLMJPNJI_00039" CDS complement(6063..6542) /locus_tag="NLMJPNJI_00039" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:CKG86671.1" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:NLMJPNJI_00039" /translation="MEEWRNKSSRVIKPLFTPLEGIVGDISNSLENVSIIGDALAMLG AVKNPKNAWIKSSKLTDIHELNEIYKLLLKSHRIVLYDINELMVLWGTKLNQYKV EIVETNSKRRIRIREDTRLMLRNYSSNSDKNMTIDTKKINDDKYKIHNLGKP"

gene complement(6621..7508) /locus_tag="NLMJPNJI_00040" CDS complement(6621..7508) /locus_tag="NLMJPNJI_00040" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:CKG86671.1" /codon_start=1 /transl_table=11
5941 attttttttttt cttgtggaaa tatataaaga aatgaattta tatgcaaatc
6001 aagcaagaca tccccatttgga gaatatttc tgcatttata tcttctaaa ctttaaaat
6061 cattaagttct tcattctgtttttt atatatatatatatatatatatattaat
6121 ctctatttatttattttttt attttattttattttattttattttattttttttttttttttttttttt
6181 cttttattttattttattttattttattttattttattttattttattttattttattttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
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CDS 889..1008
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/codon_start=1
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/product="methyltransferase small"
/protein_id="Prokka:NLMJPNJI_00042"
/translation="MNNKEQIKKLKDNAELAMASYYFHADKSYNHNKDYEK"
gene 1366..2307
CDS 1366..2307
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00043"
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CDTKDGFALKVSTSFKFDSDPDEEGLGEQSKNQTELKEPIIRLKHSKSDTYPQKDNLPIYNIIKKEQDOQALKNEFNLIEQKDLDKIEDINFINQFQKDHSKDEFFKELNLSFDTNLKLKYFIIPKNIACKVYSAYKEFKNKDAGYFT"
gene 2398..2514
CDS 2398..2514
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86393.1"
/codon_start=1
/transl_table=11
/product="methyltransferase small"
/protein_id="Prokka:NLMJPNJI_00044"
/translation="MQNLKLQIAQGLDKEIFLDKQELYVCKFV"VNGKV"
gene 2511..5918
CDS 2511..5918
/inference="ab initio prediction:Prodigal:002006"
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LOCUS       NLMJPNJI_4              6436 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain.
ACCESSION
VERSION
KEYWORDS .

SOURCE Campylobacter species

ORGANISM Campylobacter species

Unclassified.

COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES Location/Qualifiers

source 1..6436

/organism="Campylobacter species"
/mol_type="genomic DNA"

strain=\"strain\"

gene complement(305..1516)

/locus_tag="NLMJPNJI_00047"

CDS complement(305..1516)

/locus_tag="NLMJPNJI_00047"

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/transl_table=11

/gene complement(1525..1983)

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CDS complement(1525..1983)

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/inference="ab initio prediction:Prodigal:002006"

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CDS complement(2025..2204)

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/transl_table=11

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/protein_id=Prokka:NLMJPNJI_00047

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inference="ab initio prediction:Prodigal:002006"
codon_start=1
transl_table=11
product="hypothetical protein"
protein_id="Prokka:NLMJPNJI_00050"
translation="MWIVCIINFFNIKNLIPITLNWIISYCYFVLEINIYFILILCITLCVVFYLQRLLYTFLFYFYVYMVLTYTLYLFGGYK"
gene complement(2464..2724)
locus_tag="NLMJPNJI_00051"
CDS complement(2464..2724)
locus_tag="NLMJPNJI_00051"
inference="ab initio prediction:Prodigal:002006"
codon_start=1
transl_table=11
product="hypothetical protein"
protein_id="Prokka:NLMJPNJI_00051"
translation="MQIPIYSKLTKLESKIDNITSGQIAWFCSVIFTYLLFLLIVIINTRIFENLKFFFEGFFKSLAFIFANHFFYLFLCGLFV"
gene complement(2784..3020)
locus_tag="NLMJPNJI_00052"
CDS complement(2784..3020)
locus_tag="NLMJPNJI_00052"
inference="ab initio prediction:Prodigal:002006"
inference="similar to AA sequence:RefSeq:CKG86410.1"
codon_start=1
transl_table=11
product="hypothetical protein"
protein_id="Prokka:NLMJPNJI_00052"
translation="MKEIIKYYVTIYIDELLENEMLKHVDFSLLFKAKFSQISKQIDFTHAFLGLTKDSDKDELKIDEELRREYLKNKNSN"
gene complement(3017..3496)
locus_tag="NLMJPNJI_00053"
CDS complement(3017..3496)
locus_tag="NLMJPNJI_00053"
inference="ab initio prediction:Prodigal:002006"
transl_table=11
product="hypothetical protein"
protein_id="Prokka:NLMJPNJI_00053"
translation="MQIPIYSKLTKLESKIDNITSGQIAWFCSVIFTYLLFLLIVIINTRIFENLKFFFEGFFKSLAFIFANHFFYLFLCGLFV"
gene complement(3713..4138) /locus_tag="NLMJPNJI_00055"
CDS complement(3713..4138) /locus_tag="NLMJPNJI_00055" /inference="ab initio prediction:Prodigal:002006" /inference="similar to AA sequence:RefSeq:CKG86435.1" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:NLMJPNJI_00055" /translation="MKYCATIYIDPLVECFLDCENKNFINAEDFTHAFLGTLKGLSD ELDKIDKELRQKF"

gene complement(4180..4341) /locus_tag="NLMJPNJI_00056"
CDS complement(4180..4341) /locus_tag="NLMJPNJI_00056" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:NLMJPNJI_00056" /translation="MQIPIYSKLAKLESKGIDNITSQIAWFCVSFGIIPIMFMYFY ISNYDQFTILFIMIFILNMFYKTNFFALLLLVILIFIYMKYHEFIMNKILFFIF APIIIIFLRAWRILITFLGYYFLVAMVYFELLGFYF"

gene complement(4978..5082) /locus_tag="NLMJPNJI_00058"
CDS complement(4978..5082) /locus_tag="NLMJPNJI_00058" /inference="ab initio prediction:Prodigal:002006" /codon_start=1 /transl_table=11 /product="hypothetical protein" /protein_id="Prokka:NLMJPNJI_00058" /translation="MLDLMENDENSTLAPLWLYADGVTLKNHKSROQ"

gene complement(5326..5574) /locus_tag="NLMJPNJI_00059"
CDS complement(5326..5574) /locus_tag="NLMJPNJI_00059"
LOCUS       NLMJPNJI_5              2833 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION   
VERSION     
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
            Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES    Location/Qualifiers
            source          1..2833
            /organism="Campylobacter species"
            /mol_type="genomic DNA"
            /strain="strain"
            gene            9..560
            /locus_tag="NLMJPNJI_00062"
            CDS             9..560
            /locus_tag="NLMJPNJI_00062"
            /inference="ab initio prediction:Prodigal:002006"
            /codon_start=1
/transl_table=11
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/protein_id="Prokka:NLMJPNJI_00066"

/gene 560..712
/locus_tag="NLMJPNJI_00063"
/CDS 560..712
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/protein_id="Prokka:NLMJPNJI_00063"
/transl_table=11
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/protein_id="Prokka:NLMJPNJI_00064"
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/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00065"
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00066"

/gene 765..1262
/locus_tag="NLMJPNJI_00064"
/CDS 765..1262
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86719.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00064"
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/protein_id="Prokka:NLMJPNJI_00065"
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00066"

/gene 1249..1380
/locus_tag="NLMJPNJI_00065"
/CDS 1249..1380
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86746.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00065"
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00066"

/gene 1381..1875
/locus_tag="NLMJPNJI_00066"
/CDS 1381..1875
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG86719.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00066"
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00066"
INIKEFKSYFLISFIIFFTAIVIIYFLTYDLETSRGLVLLGPPEVEKLSQPQVEKHAHNYFGFLSGITIIIFLVIIFILPCLLQAYLFKCYSTGKEKRRKLWSFIGFVCNIFLLTASVYAMY"

LOCUS       NLMJPNJI_6              1956 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.

SOURCE  Campylobacter species
ORGANISM  Campylobacter species
Unclassified.

COMMENT  Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.

FEATURES  Location/Qualifiers
source  1..1956
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"

gene  113..334
/locus_tag="NLMJPNJI_00067"

CDS  113..334
/locus_tag="NLMJPNJI_00067"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87598.1"
/codon_start=1
/transl_table=11
/product="methyltransferase small"
/protein_id="Prokka:NLMJPNJI_00067"
/translation="MSDEWITEESRNRLGIVDKKDREKIANNLKKNSNEVRKDLFHVDKKGNIKELDKNATKKBINERIKKGY"

gene  318..965
/locus_tag="NLMJPNJI_00068"

CDS  318..965
/locus_tag="NLMJPNJI_00068"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87616.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00068"
/translation="MVRDTSKDEAYFTKHIIEEDEKKEKIELLELPFGKGREKLFCIDRKCIAMDKYSRGDDINLVKDKLEALMLRLQKRNLGEGDTSYRGVNAIELCVLVDMSACVLELIIEDEERKKDDIFNDRWFLHFMGSKGNLNLKRCNCEKELSEKKEVATKDEFLHQYMKKHKTRLDPLTDLEGAAIVKLMLNDKKEEFKSYKFKPDYLV"

gen  1162..1815
/locus_tag="NLMJPNJI_00069"

CDS  1162..1815
/locus_tag="NLMJPNJI_00069"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CKG87616.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00069"
/translation="MLRDTKREAYFTKHIIEEKEKKEKIELLELPFGKREKLFCIDRKCIAMDKYSRGDDINLVKDKLEALMLRLQKRNLGEGDTSYRGVNAIELCVLVDMSACVLELIIEDEERKKDDIFNDRWFLHFMGSKGNLNLKRCNCEKELSEKKEVATKDEFLHQYMKKHKTRLDPLTDLEGAAIVKLMLNDKKEEFKSYKFKPDYLV"
VRVLDMSACVLELEERKKKDFNDRDWLHFMSKGNLNERKNCHEHEL
EFVATKDELHQMKKHRLRDPLDTELGAIVKLMLNLDKEFKQKYFPYDLYL

ORIGIN

1 taaatattcat catggaattg atggaattta tcacaatcca aataaaaaacc caaataatatat
61 catcgcagaa gctaagtttg gaacaagcaa attgtagaga attggaattta
121 tggtaatgata aacagagatc gtaagggata ttagaagtttc gtaagggata
181 ataaattttta aagttttttt aatgttttttt ttagaagtttc
241 gccttattttc ctggggtttg gtttaataaat gtttaataaat
tagagaattt gagatggagtt ttagaagattc
301 ataaattttta aagttttttt aatgttttttt ttagaagtttc
361 ataaattttta aagttttttt aatgttttttt ttagaagtttc
421 gccttattttc ctggggtttg gtttaataaat gtttaataaat
481 ataaattttta aagttttttt aatgttttttt ttagaagtttc
541 ataaattttta aagttttttt aatgttttttt ttagaagtttc
601 ataaattttta aagttttttt aatgttttttt ttagaagtttc
661 ataaattttta aagttttttt aatgttttttt ttagaagtttc
721 ataaattttta aagttttttt aatgttttttt ttagaagtttc
781 ataaattttta aagttttttt aatgttttttt ttagaagtttc
841 ataaattttta aagttttttt aatgttttttt ttagaagtttc
901 ataaattttta aagttttttt aatgttttttt ttagaagtttc
961 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1021 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1081 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1141 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1201 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1261 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1321 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1381 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1441 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1501 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1561 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1621 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1681 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1741 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1801 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1861 ataaattttta aagttttttt aatgttttttt ttagaagtttc
1921 ataaattttta aagttttttt aatgttttttt ttagaagtttc

//
LOCUS NLMJPNJI_7 1591 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION .
VERSION .
KEYWORDS .
SOURCE Campylobacter species
ORGANISM Campylobacter species
UNCLASSIFIED Unclassified.
COMMENT Annotated using prokka 1.14.6 from
https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
  source 1..1591
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
  gene complement(267..824)
    /locus_tag="NLMJPNJI_00070"
CDS complement(267..824)
/locus_tag="NLMJPNJI_00070"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:CG87579.1"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00070"
//translation="MTREQAELIKEEKLTIDWPSYKHSQEFHLTMWDSEMNKYE AVYGERSVEYSLDESEAIDKMLQMNVEQKGYDGDIEKEYLTEVALRIIKEEN LEVIWYDEALPMAGIKHDKQDRKDYISPFTNAAEIIEWKSHEDFDDYRSETFKEM "

gene complement(838..1413)
/locus_tag="NLMJPNJI_00071"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:AOH52020.1"
/note="putative protein (DUF4237 domain)"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00071"
//translation="MLLYLENENKKGVSDEKLYKHNGIWPKUPKPPSPDYIRKN GRIKYPDDGYIKPPPREITLEKGTGDLYDGNSGSTRCPFEEKGAISYERKSLPY EDNEMQKTYKREVEIDINEMIENIKEMSGNRELKIKDLKKEKNKHFSEKPKGK " PYFDQEGGTQIKLPISIENMLQGFIKPQ"

ORIGIN
1 ttgcatttca gcataattac ctttttgctg attatttttt aatgcttgta tttgctttgc
 61 tctatcattt ttatttttct tacttctttt atctcctatc ccttcccatc ttatcctatc
121 atactcagtc ttagcaagag gactagcttg tattttagct aaagcaaatt gaatcttatt
181 ctttttaggt atagcaaatt ctagccatga aaagccttgt gggtttttaa acccactaag
241 ataaatttgc atataagag taagctggct cattctcttc cttttttttt
301 ctttggctcg cttttttttt attttttttt ccattttttt
361 gttttttttt attttttttt attttttttt ccattttttt
421 gttttttttt attttttttt attttttttt ccattttttt
481 gttttttttt attttttttt attttttttt ccattttttt
541 gttttttttt attttttttt attttttttt ccattttttt
601 gttttttttt attttttttt attttttttt ccattttttt
661 gttttttttt attttttttt attttttttt ccattttttt
721 gttttttttt attttttttt attttttttt ccattttttt
781 gttttttttt attttttttt attttttttt ccattttttt
841 gttttttttt attttttttt attttttttt ccattttttt
901 gttttttttt attttttttt attttttttt ccattttttt
961 gttttttttt attttttttt attttttttt ccattttttt
1021 gttttttttt attttttttt attttttttt ccattttttt
1081 gttttttttt attttttttt attttttttt ccattttttt
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1201 gttttttttt attttttttt attttttttt ccattttttt
1261 gttttttttt attttttttt attttttttt ccattttttt
1321 gttttttttt attttttttt attttttttt ccattttttt
1381 gttttttttt attttttttt attttttttt ccattttttt
1441 gttttttttt attttttttt attttttttt ccattttttt
1501 gttttttttt attttttttt attttttttt ccattttttt
LOCUS       NLMJPNJI_9               519 bp    DNA     linear       12-APR-2021
DEFINITION  Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS    .
SOURCE      Campylobacter species
ORGANISM   Campylobacter species
Unclassified.
COMMENT     Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES             Location/Qualifiers
source          1..519
/organism="Campylobacter species"
/mol_type="genomic DNA"
/strain="strain"
gene            113..277
/locus_tag="NLMJPNJI_00074"
CDS             113..277
/locus_tag="NLMJPNJI_00074"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:NLMJPNJI_00074"
/tranlation="MSDEWLIKNKLKRLKNDVGEVEAEKIANLLKKIAMKSEKIYFML
IKKAM*VLKN"
ORIGIN
  1 taaaattcat catggaattg atggaattta tcacaatcca aataaaaacc caaaatatatat
  61 catccgcaag gctaagtttg gaacaagaattagataga aaactaagc aatagagta
 121 tgaatgggtttta aacccctctat gcttaaaaat gatgtaggag aagtagaagc
 181 taaaattcat catggaattg atggaattta tcacaatcca aataaaaacc caaaatatatat
 241 tggtagtagt gaagaattta gaagaattta gaagaattta gaagaattta gaagaattta
 301 taaaattcat catggaattg atggaattta tcacaatcca aataaaaacc caaaatatatat
 361 taaaattcat catggaattg atggaattta tcacaatcca aataaaaacc caaaatatatat
 421 taaaattcat catggaattg atggaattta tcacaatcca aataaaaacc caaaatatatat
 481 taaaattcat catggaattg atggaattta tcacaatcca aataaaaacc caaaatatatat

//

>>BfR-CA-15875_min_cov_30 putative plasmid location
LOCUS JIMAIP_1 7184 bp DNA linear 12-APR-2021
DEFINITION Campylobacter species strain strain.
ACCESSION
VERSION
KEYWORDS Campylobacter species
SOURCE Campylobacter species
ORGANISM Campylobacter species Unclassified.
COMMENT Annotated using prokka 1.14.6 from https://github.com/tseemann/prokka.
FEATURES Location/Qualifiers
  source 1..7184
    /organism="Campylobacter species"
    /mol_type="genomic DNA"
    /strain="strain"
  gene 348..851
    /locus_tag="JIMAIP_00001"
  CDS 348..851
    /locus_tag="JIMAIP_00001"
    /inference="ab initio prediction:Prodigal:002006"
    /codon_start=1
    /transl_table=11
    /product="hypothetical protein"
    /protein_id="Prokka:JIMAIP_00001"
    /translation="MKILEKDFDLICKIYIQWKELNNNIKKFSSRGVNF PROVIDEIP CYAFNYNWNNNETGATDSGELIEIKAT5NFSDFSPNFKDVLIFVRDLQER DLAYIDLELNEIFQILEVNNKETVLQQQKQRRPRSLIQIEKEKIEPLYVDFI KKIVTKN"
  gene 921..1844
    /locus_tag="JIMAIP_00002"
  CDS 921..1844
    /locus_tag="JIMAIP_00002"
    /inference="ab initio prediction:Prodigal:002006"
    /inference="similar to AA sequence:RefSeq:ASE91810.1"
    /codon_start=1
    /transl_table=11
    /product="DNA (cytosine-5-)methyltransferase"
    /protein_id="Prokka:JIMAIP_00002"
    /translation="MKVASFFAGVGGIDLAFSNHIDIVVYNEIDNATKTYKFNFDVEI DCRDQVNEKELPDFDILLGGFPCAFSVAKRKFEDSRGNLFFDIIREKEKKPK IFLENVKLVLHDCGKTIFILKLESGLVYYVYDFLANMHzNTPQRREIYIVCF KNKQYKDFNPNPFLMNKIDNIVDFNKLKVDKDFFTEKNKHYEMLLQMTKNV IYQWRKRYVREKSNVCPLTANMGTTGGHNVPLVLTKHIGKLTPECFMFQGFNSYK LPDIANSHLYQAGNSVCVQVIQRIADRSN"
  gene complement(2128..2328)
    /locus_tag="JIMAIP_00003"
  CDS complement(2128..2328)
    /locus_tag="JIMAIP_00003"
    /inference="ab initio prediction:Prodigal:002006"
    /codon_start=1
    /transl_table=11
    /product="hypothetical protein"
    /protein_id="Prokka:JIMAIP_00003"
    /translation="MGFKNINTEASINFINNARKDQYQKRDKLISFTQYEYDR"
VKESALQIGMVQNYRKLFI

gene
complement(2329..3009)
/locus_tag="JIMAIPOP_00004"
CDS
complement(2329..3009)
/locus_tag="JIMAIPOP_00004"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ASI88294.1"
/codon_start=1
/transl_table=11
/product="Plasmid partitioning protein ParA"
/protein_id="Prokka:JIMAIPOP_00004"
/translation="MIISICNEKGGSKSTAVLNSSSLTDGSDLFFDSDPQRSTE
VFINIRNSNLQKFHSDONLNSGFKNELNYDAIIDTFGRDSREMRRAMLSS
VIIIPTIASQYDSVLDMLNYEKEKLINNKIIILINVRVSPNPFLIKELNNLIDY
IHEKKEVNLNDVLSEVLYERQAYKRAVIEGKISEFCNDKALKDFKQYQEIQF
QILKNDK"

gene
complement(3542..4945)
/locus_tag="JIMAIPOP_00005"
CDS
complement(3542..4945)
/locus_tag="JIMAIPOP_00005"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
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/protein_id="Prokka:JIMAIPOP_00005"
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VRPDAIYIGELVFDLGGYAEALLEKIVSEAEAYEKNKSPKAPFKASKYEWL
NIIKPTSSMNLKNSHKQFQKEYGQCYQIAHRDEGFHEQGKAILNNHAFSETLD
KETGKNNFRREKPSKVXLEIQTIEAEILMGMEGDKRISGAKRIPRAYAALKEEK
REKKNINLEQKGEQFLNKSEYKKIIENFRKSQINQGLMDFKEKESLKKNFQEAKE
DDLSELNLDEHLEIREKLLKESPILKQENILQKQKIDQEQKNASERNFIN
EPKNDKIKLEDMDNFVKNPNDMSEEYFKLKKLYTENYDNLAEKSFPDYDLVN
FFKAPQNINDLIVQKASIMKDVELQENIQFYLKTLKHEKSHDTQLNKVTNTKIK
TKNYHQNYLKKLGFFER"

gene
complement(4949..5113)
/locus_tag="JIMAIPOP_00006"
CDS
complement(4949..5113)
/locus_tag="JIMAIPOP_00006"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JIMAIPOP_00006"
/translation="MDYEKYSKMKNRQINAYRNAEKKEKLIIDDFQKLDENKNLME
FLKTKIKESL"

gene
complement(5515..5850)
/locus_tag="JIMAIPOP_00007"
CDS
complement(5515..5850)
/locus_tag="JIMAIPOP_00007"
/inference="ab initio prediction:Prodigal:002006"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="Prokka:JIMAIPOP_00007"
gene complement(5847..6884)
/locus_tag="JIMAIPOP_00008"

CDS complement(5847..6884)
/locus_tag="JIMAIPOP_00008"
/inference="ab initio prediction:Prodigal:002006"
/inference="similar to AA sequence:RefSeq:ALW35761.1"
/codon_start=1
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IYANDFKINQKLNSREYLTENINSLYKFFKANFKQIETKTEIVHYKNLVFETMEI
HYVRKNPDGDYGSTLFRRIILKINPDFAVLNYQLTNFTAELEEFIGSRLGRYAKTL
YRLLQFQRTTGTKRFEWEEFCRIMIDPODQYRQSEIDKRIKPAIKELKERNLFQDMR
VPFKNLAYEYEKAKGRGQGKVSITFTKPIENMQKLENESQKIMSDEQKYLKILN
MKMLNQVFNYNDKLWQFNDDFNEFKIIAVELIRDEYENLNFQHMYFNAKNEQFQFF
KMIEFIRKGIR"

/translation="MSEKTKLQIAEHILKNCTWNBRGTMSFIVEHIQKDFKAKIFS
AIFQNSLTMFEDLKIDNEEWIEFISQNQRGLYHRFYEEERLDELIAHYGIKNAG
KRREVFHIA"

/orientation=forward
/translation_table=11
/product="replication initiation protein"
/protein_id="Prokka:JIMAIPOP_00008"
/translation="MSDIVKYHNDFNKIQLPNFSEQEQNLLFLIFAKIKEKGID
VNTIYANDFKINQKLNSREYLTENINSLYKFFKANFKQIETKTEIV
HYKNLVFETMEIHYVRKNPDGDYGTLLFRRIILKINPDFAVL
NYQLTNFTAELEEFIGSRLGRYAKTLYRLLQFQRTT
GTKRFEWEEFCRIMIDPODQYRQSEIDKRIKPAIKELK
ERNLFQDMRVPFKNLAYEYEKAKGRGQGKVSITFTKPIENMQKLE
NESQKIMSDEQKYLKILNMKMLNQVFNYNDKLWQFNDDFNEF
KIIAVELIRDEYENLNFQHMYFNAKNEQFQFFKMIEFIR
KGIR"

/ORIGIN

1 tcaaggcgga ttttatttg aagctgttaa ggtttagttg tcaatatttg tcccccttaat
61 acctacaatt tgtccccctta atacccctaa tttgccccct taatactcctc aattgttccc
121 cttaaatcct acacattttgc cccattaatt tccatattagc tcccccatac tagtgcttag
181 aaagatgctc aaaaataata aaaaaaaaaa aaaaaaaaaa aatatattc aatattttta ataatttcta
241 aatctataaa atatatattt gattttattg atcttctaa tgaataagta gtaaatctgag
301 atttttaata attttgatat taatatttaa gtttagacgc aagttgtatg aaaatacttg
361 aaaaagatttt tgacttatatt tgtaaaattt atattcattg gagaaagattc aataatattg
421 ttaaaaatatt tagttcagga tttctgtgatt tattttccag aatatttttt attttttttt
481 gctatgcttt caactataat tggaataaca ataacgaaac aggagatgct actagtgatt
541 cagttggaatt aatagaaaaa aagggcagctt ccaatatcct tagctgtatttt ccccttttttt
601 gcggcaaatc tgtaatttttt tggacttttt aagagattct gatattttat taggagggtt ttctaccaag
661 cttatatatta tgatttggaa ttaaatattg acaatttcca aatcctagt gtttaaagaa
721 aggaaactgtc tggatgcttt caacatcttt tggagttttt taaatatttt taatatttttt
781 atattttaa gaaagagatt gcgcggccag aattatattc tttatatatttt aatatttttt
841 ccccaataa aagaaagactg ttggcgtcata aacctttcct tttttaagac aagatgctgc
901 aattttata aagaaagatt ctccttttttt gcggcagtttatt ttagtttattt attttttcta
961 attttttctg ttttttttttt ttttttttttt ttttttttttt ttttttttttt
1021 ggttggactattttatatgttttag gctattttttttttttttttttttttttttttttttt tttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttttt
5221  tatccaatca  tattttataa  taaaaaaatg  attaataatt  tgcaccgcgt  ggctttgcat
5281  taattcgcaa  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga  tagaatttta
5341  tgcaccgcgt  ggctttgcat  taattcgcaa  gctcatttaa  tgtaaaagta  ttaaataaaa
5401  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
5461  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
5521  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
5581  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
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5941  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
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6241  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
6301  tttgacttcc  taattttata  gctcatttaa  tgtaaaagta  ttaaataaaa  ttatttatga
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