Xylella fastidiosa subsp. fastidiosa strain CFBP8073 chromosome, complete genome

GenBank: CP109886.1

FASTA Graphics

Go to:

LOCUS CP109886 513 bp DNA linear BCT 30-JAN-2023
DEFINITION Xylella fastidiosa subsp. fastidiosa strain CFBP8073 chromosome, complete genome.
ACCESSION CP109886 REGION: 102981..103493
VERSION CP109886.1
DBLINK BioProject: PRJNA891297
BioSample: SAMN31318977
KEYWORDS .
SOURCE Xylella fastidiosa subsp. fastidiosa
ORGANISM Xylella fastidiosa subsp. fastidiosa
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria; Lysobacterales; Lysobacteraceae; Xylella.
REFERENCE 1 (bases 1 to 513)
AUTHORS Velasco-Amo,M.D.P., Arias-Giraldo,L.F.F., Ecija,M.R., De La Fuente,L., Marco-Noales,E., Moralejo,E., Navas-Cort,J.A. and Landa,B.B.
TITLE Complete circularized genome resources of seven strains of Xylella fastidiosa subsp. fastidiosa using hybrid assembly reveals unknown plasmids
JOURNAL Phytopathology (2022) In press
PUBMED 36441872
REMARK Publication Status: Available-Online prior to print
REFERENCE 2 (bases 1 to 513)
AUTHORS Landa,B., Arias-Giraldo,L.F., Roman-Ecija,M., Velasco-Amo,M.P., De
La Fuente,L., Marco-Noales,E. and Moralejo,E.
TITLE Direct Submission
JOURNAL Submitted (17-OCT-2022) Crop Protection, Institute for Sustainable
Agriculture - CSIC, Av. Menendez Pidal SN, Cordoba 14004, Spain
COMMENT The annotation was added by the NCBI Prokaryotic Genome Annotation
Pipeline (PGAP). Information about PGAP can be found here:
https://www.ncbi.nlm.nih.gov/genome/annotation_prok/

##Genome-Assembly-Data-START##
Assembly Date :: SEP-2022
Assembly Method :: Canu v. 2.2
Genome Representation :: Full

```
     gene            1..513
                     /gene="rimM"
                     /locus_tag="OK117_00390"
     CDS             1..513
                     /gene="rimM"
                     /locus_tag="OK117_00390"
                     /inference="COORDINATES: similar to AA
                     sequence:RefSeq:WP_004085542.1"
                     /note="Essential for efficient processing of 16S rRNA;
                     Derived by automated computational analysis using gene
                     prediction method: Protein Homology.
                     GO_function: GO:0003723 - RNA binding [Evidence IEA];
                     GO_process: GO:0006364 - rRNA processing [Evidence IEA]"
                     /codon_start=1
                     /transl_table=11
                     /product="ribosome maturation factor RimM"
                     /protein_id="WCF28410.1"
                     /translation="MKDNERRILLGRVVGGFGLRGEIKIESWTEPRDAIFRYQPWLLR
                     SPTGTESMLNGARGYETGKRLIATFPGINDRNGVEAICGTEIYVPRSALPPPHPDEYY
                     WVDLEGLQVHTLEGVVLGSVSHLFSNGANDVIVIHGERERLIPFVQPDYVKSVDFEAE
                     RIVVDWDPEF"
ORIGIN
        1 atgaaagata atgagcgccg tatcctgcta ggaagggttg taggtggttt cgggttgcgt
       61 ggtgaaatca agatagagtc ttggactgag ccacgggatg cgatcttccg ttaccagccg
      121 tggttattac gttctcctac gggtaccgag tccatgttga atggtgcccg tggctacgag
      181 actggcaagc gtttgattgc aacctttcct ggcatcaatg atcgtaatgg agtcgaagcg
      241 atctgtggta cggaaatcta tgtgccacgc agcgccttgc ctccacctca ccccgacgag
      301 tattactggg tcgatttgga agggctgcaa gtacacaccc ttgaaggtgt ggttctcggt
      361 agcgtttccc atctgttttc caacggcgcc aatgatgtga tagtcatcca tggcgagcgc
      421 gagcgcttga tcccgtttgt acagcctgat tacgtgaagt cggttgattt tgaggctgag
      481 cgtattgttg tcgattggga tcctgagttc tga
//
```