Xylella fastidiosa subsp. sandyi strain OC8 chromosome, complete genome

GenBank: CP090547.1

FASTA Graphics

Go to:

LOCUS CP090547 1503 bp DNA linear BCT 15-JAN-2022

DEFINITION Xylella fastidiosa subsp. sandyi strain OC8 chromosome, complete genome.

ACCESSION CP090547 REGION: 1142594..1144096

VERSION CP090547.1

DBLINK BioProject: PRJNA672949
BioSample: SAMN24371056

KEYWORDS .

SOURCE Xylella fastidiosa subsp. sandyi

ORGANISM Xylella fastidiosa subsp. sandyi
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria; Lysobacterales; Lysobacteraceae; Xylella.

REFERENCE 1 (bases 1 to 1503)

AUTHORS O'Leary,M.L., Burbank,L.P., Chen,J. and Stenger,D.C.

TITLE Complete genome sequences of Xylella fastidiosa strains belonging to subspecies fastidiosa, morus, multiplex, and sandyi

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1503)

AUTHORS O'Leary,M.L., Burbank,L.P., Chen,J. and Stenger,D.C.

TITLE Direct Submission

JOURNAL Submitted (23-DEC-2021) ARS, USDA, 9611 S. Riverbend Ave, Parlier, CA 93648, USA

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 :: DEC-2021
Assembly Method :: Flye v. 2.9
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 813x
Sequencing Technology :: Oxford Nanopore MiniION, Illumina
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Date :: 01/06/2022 16:39:59
Annotation Pipeline :: NCBI Prokaryotic Genome Annotation Pipeline (PGAP)

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            Annotation Method               :: Best-placed reference protein
                                            set; GeneMarkS-2+
            Annotation Software revision     :: 5.3
            Features Annotated              :: Gene; CDS; rRNA; tRNA; ncRNA;
                                            repeat_region
            Genes (total)                   :: 2,661
            CDSs (total)                    :: 2,602
            Genes (coding)                  :: 2,515
            CDSs (with protein)              :: 2,515
            Genes (RNA)                     :: 59
            rRNAs                           :: 2, 2, 2 (5S, 16S, 23S)
            complete rRNAs                   :: 2, 2, 2 (5S, 16S, 23S)
            tRNAs                           :: 49
            ncRNAs                          :: 4
            Pseudo Genes (total)             :: 87
            CDSs (without protein)           :: 87
            Pseudo Genes (ambiguous residues) :: 0 of 87
            Pseudo Genes (frameshifted)      :: 47 of 87
            Pseudo Genes (incomplete)        :: 42 of 87
            Pseudo Genes (internal stop)     :: 19 of 87
            Pseudo Genes (multiple problems)  :: 16 of 87
            ##Genome-Annotation-Data-END##
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ORIGIN

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