Citrobacter braakii strain DY2019 chromosome, complete genome

GenBank: CP080539.1

FASTA Graphics

Go to:

LOCUS CP080539 1059 bp DNA linear BCT 10-AUG-2021
DEFINITION Citrobacter braakii strain DY2019 chromosome, complete genome.
ACCESSION CP080539 REGION: 3027684..3028742
VERSION CP080539.1
DBLINK BioProject: PRJNA751212
BioSample: SAMN20511720
KEYWORDS .
SOURCE Citrobacter braakii
ORGANISM Citrobacter braakii
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria;
Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter
freundii complex.
REFERENCE 1 (bases 1 to 1059)
AUTHORS Zheng,B.
TITLE pDY2019-NDM and pDY2019-OXA
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1059)
AUTHORS Xu,H.
TITLE Direct Submission
JOURNAL Submitted (03-AUG-2021) State Key Laboratory for Diagnosis and
Treatment of Infectious Diseases, The First Affiliated Hospital,
School of Medicine, Zhejiang University, Qingchun, Hangzhou 310000,
China
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 Method :: SPAdes v. 3.9.1
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 200X
Sequencing Technology :: Illumina NovaSeq
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Date :: 08/04/2021 12:33:13
Annotation Pipeline :: NCBI Prokaryotic Genome
Annotation Pipeline (PGAP)

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            Annotation Method               :: Best-placed reference protein
                                            set; GeneMarkS-2+
            Annotation Software revision     :: 5.2
            Features Annotated              :: Gene; CDS; rRNA; tRNA; ncRNA;
                                            repeat_region
            Genes (total)                   :: 5,152
            CDSs (total)                    :: 5,035
            Genes (coding)                  :: 4,928
            CDSs (with protein)              :: 4,928
            Genes (RNA)                     :: 117
            rRNAs                           :: 9, 8, 8 (5S, 16S, 23S)
            complete rRNAs                   :: 9, 8, 8 (5S, 16S, 23S)
            tRNAs                           :: 83
            ncRNAs                          :: 9
            Pseudo Genes (total)             :: 107
            CDSs (without protein)           :: 107
            Pseudo Genes (ambiguous residues) :: 0 of 107
            Pseudo Genes (frameshifted)      :: 34 of 107
            Pseudo Genes (incomplete)        :: 73 of 107
            Pseudo Genes (internal stop)     :: 20 of 107
            Pseudo Genes (multiple problems)  :: 16 of 107
            CRISPR Arrays                   :: 1
            ##Genome-Annotation-Data-END##
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                    /isolation_source="clinical"
                    /host="Homo sapiens"
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                    /collection_date="2019-05-23"
                    /collected_by="Hao Xu"
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     CDS            1..1059
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                    sequence:RefSeq:NP_460044.1"
                    /note="Derived by automated computational analysis using
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gene prediction method: Protein Homology."
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ORIGIN

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     121 gatattggta acaaccagat caacaacgct ggtcctaccc acgaaagcca actgggtgct
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     241 ttaggtcgta tgccgtacaa aggctacacc gacgctaccc atcaaaacgg cgctttcaaa
     301 gctcagggcg ttcagctgac cgctaaactg ggttacccaa tcactgacga tctggacgtt
     361 tatacccgtc tgggtggtat ggtttggcgt gcagacgcta aaaacaacga aggcttcaaa
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