Citrobacter amalonaticus isolate 2024CK-01695 chromosome, complete genome

GenBank: CP180152.1

FASTA Graphics

Go to:

LOCUS CP180152 1056 bp DNA linear BCT 11-FEB-2025
DEFINITION Citrobacter amalonaticus isolate 2024CK-01695 chromosome, complete genome.
ACCESSION CP180152 REGION: complement(1814822..1815877)
VERSION CP180152.1
DBLINK BioProject: PRJNA288601
BioSample: SAMN44510955
KEYWORDS .
SOURCE Citrobacter amalonaticus
ORGANISM Citrobacter amalonaticus
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter.
REFERENCE 1 (bases 1 to 1056)
AUTHORS Hergert,J., Casey,R., Wagner,J., Young,E.L. and Oakeson,K.F.
TITLE Pathogen: clinical or host-associated sample
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1056)
CONSRTM Clinical and Environmental Microbiology Branch: Whole genome sequencing antimicrobial resistance pathogens in the healthcare setting
TITLE Direct Submission
JOURNAL Submitted (30-OCT-2024) Division of Healthcare Quality Promotion, US Centers for Disease Control and Prevention, 1600 Clifton Rd, Atlanta, GA, USA
REFERENCE 3 (bases 1 to 1056)
AUTHORS Hergert,J., Casey,R., Wagner,J., Young,E.L. and Oakeson,K.F.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2025) Utah Public Health Laboratory, Utah Public Health Laboratory Infectious Disease submission group, 4431 S 2700 W, Salt Lake City, UT 84129, 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 Method :: Unicycler v. 0.5.0
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 100x
Sequencing Technology :: Oxford Nanopore GridION; Illumina MiSeq

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            ##Genome-Assembly-Data-END##

            ##Genome-Annotation-Data-START##
            Annotation Provider              :: NCBI
            Annotation Date                  :: 01/31/2025 13:30:43
            Annotation Pipeline              :: NCBI Prokaryotic Genome
                                               Annotation Pipeline (PGAP)
            Annotation Method                :: Best-placed reference protein
                                               set; GeneMarkS-2+
            Annotation Software revision     :: 6.9
            Features Annotated               :: Gene; CDS; rRNA; tRNA; ncRNA
            Genes (total)                    :: 4,547
            CDSs (total)                     :: 4,430
            Genes (coding)                   :: 4,356
            CDSs (with protein)              :: 4,356
            Genes (RNA)                      :: 117
            rRNAs                            :: 8, 7, 7 (5S, 16S, 23S)
            complete rRNAs                   :: 8, 7, 7 (5S, 16S, 23S)
            tRNAs                            :: 83
            ncRNAs                           :: 12
            Pseudo Genes (total)             :: 74
            CDSs (without protein)           :: 74
            Pseudo Genes (ambiguous residues) :: 0 of 74
            Pseudo Genes (frameshifted)      :: 24 of 74
            Pseudo Genes (incomplete)        :: 53 of 74
            Pseudo Genes (internal stop)     :: 7 of 74
            Pseudo Genes (multiple problems)  :: 9 of 74
            ##Genome-Annotation-Data-END##
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ORIGIN

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