Citrobacter freundii strain RHBSTW-00200 chromosome, complete genome

GenBank: CP055551.1

FASTA Graphics

Go to:

LOCUS CP055551 1662 bp DNA linear BCT 16-MAY-2022
DEFINITION Citrobacter freundii strain RHBSTW-00200 chromosome, complete genome.
ACCESSION CP055551 REGION: complement(1347555..1349216)
VERSION CP055551.1
DBLINK BioProject: PRJNA605147
BioSample: SAMN15148536
KEYWORDS .
SOURCE Citrobacter freundii
ORGANISM Citrobacter freundii
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria; Enterobacterales; Enterobacteriaceae; Citrobacter; Citrobacter freundii complex.
REFERENCE 1 (bases 1 to 1662)
AUTHORS AbuOun,M., Jones,H., Stubberfield,E., Gilson,D., Shaw,L.P., Hubbard,A.T.M., Chau,K.K., Sebra,R., Peto,T.E.A., Crook,D.W., Read,D.S., Gweon,H.S., Walker,A.S., Stoesser,N., Smith,R.P., Anjum,M.F. and On Behalf Of The Rehab,Consortium.
TITLE A genomic epidemiological study shows that prevalence of antimicrobial resistance in Enterobacterales is associated with the livestock host, as well as antimicrobial usage
JOURNAL Microb Genom 7 (10) (2021)
PUBMED 34609275
REFERENCE 2 (bases 1 to 1662)
AUTHORS Shaw,L.P.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2020) Nuffield Department of Medicine, University of Oxford, John Radcliffe Hospital, Oxford OX3 9DU, United Kingdom
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. v0.4.7
Assembly Name :: WTP1 T1-00200
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 92.8592821487567x
Sequencing Technology :: Hybrid: Illumina and OXFORD_NANOPORE
##Genome-Assembly-Data-END##

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            ##Genome-Annotation-Data-START##
            Annotation Provider              :: NCBI
            Annotation Date                  :: 06/18/2020 19:05:57
            Annotation Pipeline              :: NCBI Prokaryotic Genome
                                             Annotation Pipeline (PGAP)
            Annotation Method                :: Best-placed reference protein
                                             set; GeneMarkS-2+
            Annotation Software revision     :: 4.11
            Features Annotated               :: Gene; CDS; rRNA; tRNA; ncRNA;
                                             repeat_region
            Genes (total)                    :: 5,161
            CDSs (total)                     :: 5,043
            Genes (coding)                   :: 4,976
            CDSs (with protein)              :: 4,976
            Genes (RNA)                      :: 118
            rRNAs                            :: 9, 8, 8 (5S, 16S, 23S)
            complete rRNAs                   :: 9, 8, 8 (5S, 16S, 23S)
            tRNAs                            :: 83
            ncRNAs                           :: 10
            Pseudo Genes (total)             :: 67
            CDSs (without protein)           :: 67
            Pseudo Genes (ambiguous residues) :: 0 of 67
            Pseudo Genes (frameshifted)      :: 29 of 67
            Pseudo Genes (incomplete)        :: 35 of 67
            Pseudo Genes (internal stop)     :: 14 of 67
            Pseudo Genes (multiple problems) :: 9 of 67
            ##Genome-Annotation-Data-END##
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ORIGIN

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