Corynebacterium accolens strain CA1 chromosome

GenBank: CP100382.1

FASTA Graphics

Go to:

LOCUS CP100382 3495 bp DNA linear BCT 21-JUL-2023
DEFINITION Corynebacterium accolens strain CA1 chromosome.
ACCESSION CP100382 REGION: complement(2449934..2453428)
VERSION CP100382.1
DBLINK BioProject: PRJNA842591
BioSample: SAMN28690424
KEYWORDS .
SOURCE Corynebacterium accolens
ORGANISM Corynebacterium accolens
Bacteria; Bacillati; Actinomycetota; Actinomycetes;
Mycobacteriales; Corynebacteriaceae; Corynebacterium.
REFERENCE 1 (bases 1 to 3495)
AUTHORS Szabo,D., Ostorhazi,E., Stercz,B., Makra,N., Penzes,K., Kristof,K.,
Antal,I., Rethelyi,J.M., Zsigmond,R.I., Birtalan,E., Merkely,B. and
Tamas,L.
TITLE Specific nasopharyngeal Corynebacterium strains serve as gatekeepers against SARS-CoV2 infection
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3495)
AUTHORS Szabo,D., Ostorhazi,E., Stercz,B., Makra,N., Penzes,K., Kristof,K.,
Antal,I., Rethelyi,J.M., Zsigmond,R.I., Birtalan,E., Merkely,B. and
Tamas,L.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2022) Medical Microbiology, Semmelweis University, Ulloi street 26., Budapest 1085, Hungary
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. 3.13.1
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 26,48847x
Sequencing Technology :: Illumina MiSeq

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            ##Genome-Annotation-Data-START##
            Annotation Provider             :: NCBI
            Annotation Date                 :: 07/05/2022 10:43:12
            Annotation Pipeline             :: NCBI Prokaryotic Genome
                                               Annotation Pipeline (PGAP)
            Annotation Method               :: Best-placed reference protein
                                               set; GeneMarkS-2+
            Annotation Software revision     :: 6.1
            Features Annotated              :: Gene; CDS; rRNA; tRNA; ncRNA;
                                               repeat_region
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            CDSs (total)                    :: 2,369
            Genes (coding)                  :: 2,280
            CDSs (with protein)             :: 2,280
            Genes (RNA)                     :: 59
            rRNAs                           :: 3, 1, 1 (5S, 16S, 23S)
            complete rRNAs                  :: 3, 1, 1 (5S, 16S, 23S)
            tRNAs                           :: 51
            ncRNAs                          :: 3
            Pseudo Genes (total)             :: 89
            CDSs (without protein)          :: 89
            Pseudo Genes (ambiguous residues) :: 24 of 89
            Pseudo Genes (frameshifted)      :: 29 of 89
            Pseudo Genes (incomplete)        :: 48 of 89
            Pseudo Genes (internal stop)     :: 11 of 89
            Pseudo Genes (multiple problems)  :: 21 of 89
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