

Bacillus cereus strain FDAARGOS_799 chromosome, complete genome

GenBank: CP053951.1

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LOCUS CP053951 1209 bp DNA linear BCT 04-JUN-2020
DEFINITION Bacillus cereus strain FDAARGOS_799 chromosome, complete genome.
ACCESSION [CP053951](#) REGION: 1802701..1803909
VERSION CP053951.1
DBLINK BioProject: [PRJNA231221](#)
BioSample: [SAMN11056514](#)
KEYWORDS .
SOURCE Bacillus cereus
ORGANISM [Bacillus cereus](#)
Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus;
Bacillus cereus group.
REFERENCE 1 (bases 1 to 1209)
AUTHORS Nelson,B., Plummer,A., Tallon,L., Sadzewicz,L., Zhao,X.,
Vavikolanu,K., Mehta,A., Aluvathingal,J., Nadendla,S., Myers,T.,
Yan,Y. and Sichtig,H.
TITLE FDA dAtabase for Regulatory Grade micrObial Sequences (FDA-ARGOS):
Supporting development and validation of Infectious Disease Dx
tests
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1209)
AUTHORS Nelson,B., Plummer,A., Tallon,L., Sadzewicz,L., Zhao,X.,
Vavikolanu,K., Mehta,A., Aluvathingal,J., Nadendla,S., Myers,T.,
Yan,Y. and Sichtig,H.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-2020) Center for Devices and Radiological Health,
US Food and Drug Administration, 10903 New Hampshire Avenue, Silver
Spring, MD 20993-0002, 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 :: SMRT v. 2.3.0, HGAP v. 3
Genome Coverage :: 945.83x
Sequencing Technology :: Pacbio; Illumina
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Date :: 05/28/2020 20:32:58

```

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)           :: 6,172
CDSs (total)           :: 6,018
Genes (coding)         :: 5,823
CDSs (with protein)    :: 5,823
Genes (RNA)            :: 154
rRNAs                  :: 14, 14, 14 (5S, 16S, 23S)
complete rRNAs         :: 14, 14, 14 (5S, 16S, 23S)
tRNAs                  :: 107
ncRNAs                 :: 5
Pseudo Genes (total)   :: 195
CDSs (without protein) :: 195
Pseudo Genes (ambiguous residues) :: 0 of 195
Pseudo Genes (frameshifted) :: 95 of 195
Pseudo Genes (incomplete) :: 104 of 195
Pseudo Genes (internal stop) :: 59 of 195
Pseudo Genes (multiple problems) :: 55 of 195
##Genome-Annotation-Data-END##

```

```

FEATURES      Location/Qualifiers
    source      1..1209
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                /country="USA: MD"
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                /gene="nheB"
                /locus_tag="FOC93_12430"
    CDS         complement(1..1209)
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                /locus_tag="FOC93_12430"
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                sequence:RefSeq:WP_000162959.1"
                /note="Derived by automated computational analysis using
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                /codon_start=1

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GLTRLSSSINENKAQVDQLVEDLKKFRNKMTSDTQNFKGDNQITSILASQDAGIPLL
QNQITTYNEAISKYNAIIIGSSVATALGP IAIIGGAVVIATGAGTPLGVALIAGGAAA
VGGGTAGIVLAKKELDNAQAEIQKITGQITTAQLEVAGLTNIKTQTEYLTNTIDTAIT
ALQNISNQWYTMGSKYNSLLQNVD SISPNDLVFIKEDLNI AKDSWKNIKDYAEKIYAE
DIKVVDTKKA"
```

ORIGIN

```
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181 ccattgggttt gaaatgtttt gcaacgctgt aattgcagta tcaatcgatc ttgttaaata
241 ctgagtttgt gttttaatgt tcgttaaccc agctacttct aattgagcag ttgtaatttg
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481 tgtcgcaaca gatgaaccga taataattgc attatattta ctaattgcct cattgtacgt
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601 ttgatttgca tcacccttga agttttgcgt atccgacgtc attttatttc ggaatttttt
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