Bacillus subtilis subsp. subtilis str. 168 chromosome, complete genome

GenBank: CP053102.1

FASTA Graphics

Go to:

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LOCUS       CP053102               700 bp    DNA     linear   BCT 11-MAY-2020
DEFINITION  Bacillus subtilis subsp. subtilis str. 168 chromosome, complete
            genome.
ACCESSION   CP053102 REGION: 9810..10509
VERSION     CP053102.1
DBLINK      BioProject: PRJNA626600
            BioSample: SAMN14645747
KEYWORDS    .
SOURCE      Bacillus subtilis subsp. subtilis str. 168
  ORGANISM  Bacillus subtilis subsp. subtilis str. 168
            Bacteria; Firmicutes; Bacilli; Bacillales; Bacillaceae; Bacillus.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Dragos,A. and Kovacs,A.T.
  TITLE     Phage recombination drives evolution of spore-forming Bacilli
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 700)
  AUTHORS   Dragos,A. and Kovacs,A.T.
  TITLE     Direct Submission
  JOURNAL   Submitted (20-APR-2020) Department of Biotechnology and
            Biomedicine, Dansk: Universitet, Anker Engelunds Vej 101A, Kgs.
            Lyngby 2800, Denmark
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       :: HGAP v. 3
            Genome Representation  :: Full
            Expected Final Version :: Yes
            Genome Coverage       :: 189.95x
            Sequencing Technology  :: PacBio
            ##Genome-Assembly-Data-END##

            ##Genome-Annotation-Data-START##
            Annotation Provider            :: NCBI
            Annotation Date                :: 05/05/2020 12:34:33
            Annotation Pipeline            :: NCBI Prokaryotic Genome
                                           Annotation Pipeline (PGAP)
            Annotation Method              :: Best-placed reference protein
                                           set; GeneMarkS-2+
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           Annotation Software revision     :: 4.11
           Features Annotated               :: Gene; CDS; rRNA; tRNA; ncRNA;
                                            repeat_region
           Genes (total)                    :: 4,559
           CDSs (total)                     :: 4,438
           Genes (coding)                   :: 4,335
           CDSs (with protein)              :: 4,335
           Genes (RNA)                      :: 121
           rRNAs                            :: 10, 10, 10 (5S, 16S, 23S)
           complete rRNAs                   :: 10, 10, 10 (5S, 16S, 23S)
           tRNAs                            :: 86
           ncRNAs                           :: 5
           Pseudo Genes (total)             :: 103
           CDSs (without protein)           :: 103
           Pseudo Genes (ambiguous residues) :: 0 of 103
           Pseudo Genes (frameshifted)      :: 80 of 103
           Pseudo Genes (incomplete)        :: 29 of 103
           Pseudo Genes (internal stop)     :: 10 of 103
           Pseudo Genes (multiple problems)  :: 14 of 103
           ##Genome-Annotation-Data-END##
FEATURES             Location/Qualifiers
     source          1..700
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                     /mol_type="genomic DNA"
                     /strain="168"
                     /isolation_source="liquid-air interface biofilm"
                     /sub_species="subtilis"
                     /type_material="type strain of Bacillus subtilis"
                     /db_xref="taxon:224308"
                     /country="Germany: Jena"
                     /collection_date="2016"
                     /note="evolved population 4 of biofilm-deficient mutant;
                     genotype: rearrangements within prophage region"
     gene            2..>700
                     /locus_tag="HIR77_00040"
     rRNA            2..>700
                     /locus_tag="HIR77_00040"
                     /product="16S ribosomal RNA"
ORIGIN
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      121 cgtgggtaac ctgcctgtaa gactgggata actccgggaa accggggcta ataccggatg
      181 gttgtttgaa ccgcatggtt caaacataaa aggtggcttc ggctaccact tacagatgga
      241 cccgcggcgc attagctagt tggtgaggta acggctcacc aaggcgacga tgcgtagccg
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   301 acctgagagg gtgatcggcc acactgggac tgagacacgg cccagactcc tacgggaggc
   361 agcagtaggg aatcttccgc aatggacgaa agtctgacgg agcaacgccg cgtgagtgat
   421 gaaggttttc ggatcgtaaa gctctgttgt tagggaagaa caagtgccgt tcgaataggg
   481 cggtaccttg acggtaccta accagaaagc cacggctaac tacgtgccag cagccgcggt
   541 aatacgtagg tggcaagcgt tgtccggaat tattgggcgt aaagggctcg caggcggttt
   601 cttaagtctg atgtgaaagc ccccggctca accggggagg gtcattggaa actggggaac
   661 ttgagtgcag aagaggagag tggaattcca cgtgtagcgg
```