

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

GenBank: CP053102.1

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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JOURNAL Unpublished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

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set; GeneMarkS-2+
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
                        /organism="Bacillus subtilis subsp. subtilis str. 168"
                        /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 cgcgatggtt caaacataaa aggtggcttc ggctaccact tacagatgga

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241 cccgcggcgc attagctagt tggtagagta acggctcacc aaggcgacga tgcgtagccg
301 acctgagagg gtgatcggcc aactggggac tgagacacgg ccagactcc tacgggaggg
361 agcagtaggg aatcttccgc aatggacgaa agtctgacgg agcaacgccg cgtgagtgat
421 gaaggttttc ggatcgtaaa gctctgttgt tagggaagaa caagtgccgt tcgaataggg
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601 cttagctctg atgtgaaagc ccccggtca accggggagg gtcattggaa actggggaac
661 ttgagtgcag aagaggagag tggaattcca cgtgtagcgg