

Bordetella pertussis strain J029 chromosome, complete genome

GenBank: CP046995.1

[FASTA Graphics](#)

LOCUS CP046995 1002 bp DNA linear BCT 26-MAY-2020

DEFINITION Bordetella pertussis strain J029 chromosome, complete genome.

ACCESSION [CP046995](#) REGION: 121123..122124

VERSION CP046995.1

DBLINK BioProject: [PRJNA279196](#)

BioSample: [SAMN07352195](#)

KEYWORDS .

SOURCE Bordetella pertussis

ORGANISM [Bordetella pertussis](#)

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Alcaligenaceae; Bordetella.

REFERENCE 1 (bases 1 to 1002)

AUTHORS Weigand,M.R., Peng,Y., Tondella,M.L. and Williams,M.M.

TITLE Whole genome sequencing of Bordetella pertussis geographic and
temporal diversity in the United States

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1002)

AUTHORS Weigand,M.R., Peng,Y., Tondella,M.L. and Williams,M.M.

TITLE Direct Submission

JOURNAL Submitted (16-DEC-2019) NCIRD/DBD/MVPDB, Centers for Disease
Control and Prevention, 1600 Clifton Rd, Atlanta, GA 30029, 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 :: HGAP v. 3

Genome Coverage :: 173x

Sequencing Technology :: PacBio RSII; Illumina MiSeq

##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##

Annotation Provider :: NCBI

Annotation Date :: 12/17/2019 17:47:47

Annotation Pipeline :: NCBI Prokaryotic Genome

Annotation Pipeline (PGAP)

Annotation Method :: Best-placed reference protein
set; GeneMarkS-2+

Annotation Software revision :: 4.10

Features Annotated :: Gene; CDS; rRNA; tRNA; ncRNA;

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repeat_region
Genes (total)                :: 4,066
CDSs (total)                 :: 4,002
Genes (coding)               :: 3,688
CDSs (with protein)          :: 3,688
Genes (RNA)                  :: 64
rRNAs                        :: 3, 3, 3 (5S, 16S, 23S)
complete rRNAs               :: 3, 3, 3 (5S, 16S, 23S)
tRNAs                        :: 51
ncRNAs                       :: 4
Pseudo Genes (total)         :: 314
CDSs (without protein)       :: 314
Pseudo Genes (ambiguous residues) :: 0 of 314
Pseudo Genes (frameshifted)  :: 168 of 314
Pseudo Genes (incomplete)    :: 130 of 314
Pseudo Genes (internal stop)  :: 31 of 314
Pseudo Genes (multiple problems) :: 14 of 314
##Genome-Annotation-Data-END##

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```

FEATURES             Location/Qualifiers
     source            1..1002
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                        /strain="J029"
                        /host="Homo sapiens"
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                        /country="USA: CO"
                        /collection_date="2013"
     gene              complement(1..951)
                        /locus_tag="CG030_00650"
     CDS               complement(1..951)
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                        /inference="COORDINATES: similar to AA
                        sequence:RefSeq:NP_878985.1"
                        /note="Derived by automated computational analysis using
                        gene prediction method: Protein Homology."
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                        VEGAGWDFVFVAIDDHARVAFTDIHPDERFPSAVQFLKDAVAYYQRLGVTIQRLLTDN
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DAMKSWLHHYNWHRPHQGIGRAVPISRNLNDEYNLLTVHS"

ORIGIN

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```