Brucella melitensis BwIM_TUR_02 chromosome 2 sequence

GenBank: CP018539.1

FASTA Graphics PopSet

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LOCUS CP018539 2850 bp DNA linear BCT 13-JUN-2017
DEFINITION Brucella melitensis BwIM_TUR_02 chromosome 2 sequence.
ACCESSION CP018539 REGION: 787781..790630
VERSION CP018539.1
DBLINK BioProject: PRJNA347914
BioSample: SAMN05932989
KEYWORDS .
SOURCE Brucella melitensis
ORGANISM Brucella melitensis
Bacteria; Pseudomonadati; Pseudomonadota; Alphaproteobacteria;
Hyphomicrobiales; Brucellaceae; Brucella/Ochrobactrum group;
Brucella; Brucella melitensis group.
REFERENCE 1 (bases 1 to 2850)
AUTHORS Georgi,E., Walter,M.C., Pfalzgraf,M.T., Northoff,B.H.,
Holdt,L.M.,
Scholz,H.C., Zoeller,L., Zange,S. and Antwerpen,M.H.
TITLE Whole genome sequencing of Brucella melitensis isolated from 57
patients in Germany reveals high diversity in strains from Middle
East
JOURNAL PLoS ONE 12 (4), E0175425 (2017)
PUBMED 28388689
REFERENCE 2 (bases 1 to 2850)
AUTHORS Walter,M.C. and Georgi,E.
TITLE Direct Submission
JOURNAL Submitted (06-DEC-2016) Microbial Genomics, Bundeswehr Institute
of
Microbiology, Neuherbergstr. 11, Munich 80937, Germany
COMMENT Annotation was added by the NCBI Prokaryotic Genome Annotation
Pipeline (released 2013). Information about the Pipeline can be
found here: https://www.ncbi.nlm.nih.gov/genome/annotation_prok/

##Genome-Assembly-Data-START##
Assembly Method :: SPAdes v. 3.9.0
Genome Coverage :: 70.2
Sequencing Technology :: Illumina MiSeq
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Date :: 12/07/2016 15:01:29

Annotation Pipeline :: NCBI Prokaryotic Genome Annotation Pipeline
Annotation Method :: Best-placed reference protein set; GeneMarkS+
Annotation Software revision :: 4.0
Features Annotated :: Gene; CDS; rRNA; tRNA; ncRNA; repeat_region
Genes (total) :: 3,419
CDS (total) :: 3,351
Genes (coding) :: 3,177
CDS (coding) :: 3,177
Genes (RNA) :: 68
rRNAs :: 3, 3, 3 (5S, 16S, 23S)
complete rRNAs :: 3, 3, 3 (5S, 16S, 23S)
tRNAs :: 55
ncRNAs :: 4
Pseudo Genes (total) :: 174
Pseudo Genes (ambiguous residues) :: 1 of 174
Pseudo Genes (frameshifted) :: 122 of 174
Pseudo Genes (incomplete) :: 26 of 174
Pseudo Genes (internal stop) :: 38 of 174
Pseudo Genes (multiple problems) :: 13 of 174
##Genome-Annotation-Data-END##

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CDS 1..2850
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ORIGIN

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