

Bifidobacterium longum subsp. infantis strain Bi-26 chromosome

GenBank: CP054425.1

[FASTA Graphics](#)

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LOCUS CP054425 1437 bp DNA linear BCT 24-JUN-2020
DEFINITION Bifidobacterium longum subsp. infantis strain Bi-26 chromosome.
ACCESSION [CP054425](#) REGION: 822630..824066
VERSION CP054425.1
DBLINK BioProject: [PRJNA503890](#)
BioSample: [SAMN10380491](#)
KEYWORDS .
SOURCE Bifidobacterium longum subsp. infantis (Bifidobacterium infantis)
ORGANISM [Bifidobacterium longum subsp. infantis](#)
Bacteria; Actinobacteria; Bifidobacteriales; Bifidobacteriaceae;
Bifidobacterium.
REFERENCE 1 (bases 1 to 1437)
AUTHORS Zabel,B. and Huntley,S.
TITLE Bi-26 Re-sequencing
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1437)
AUTHORS Zabel,B.E.
TITLE Direct Submission
JOURNAL Submitted (06-NOV-2018) GEM, DuPont Nutrition and Health, 3329
Agriculture Dr, Madison, WI 53716, USA
REFERENCE 3 (bases 1 to 1437)
AUTHORS Zabel,B. and Huntley,S.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-2020) GEM, DuPont Nutrition and Health, 3329
Agriculture Dr, Madison, WI 53716, 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 Date :: 30-OCT-2019

Assembly Method :: SPAdes v. OCT-2019

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 100.0x

Sequencing Technology :: Illumina

##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##

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Annotation Provider      :: NCBI
Annotation Date          :: 06/05/2020 15:38:36
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)            :: 2,299
CDSs (total)            :: 2,227
Genes (coding)          :: 2,078
CDSs (with protein)     :: 2,078
Genes (RNA)             :: 72
rRNAs                   :: 4, 4, 4 (5S, 16S, 23S)
complete rRNAs          :: 4, 4, 4 (5S, 16S, 23S)
tRNAs                   :: 57
ncRNAs                  :: 3
Pseudo Genes (total)    :: 149
CDSs (without protein)  :: 149
Pseudo Genes (ambiguous residues) :: 0 of 149
Pseudo Genes (frameshifted) :: 77 of 149
Pseudo Genes (incomplete) :: 86 of 149
Pseudo Genes (internal stop) :: 21 of 149
Pseudo Genes (multiple problems) :: 30 of 149
CRISPR Arrays           :: 2
##Genome-Annotation-Data-END##

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FEATURES             Location/Qualifiers
    source            1..1437
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                        /strain="Bi-26"
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                        /host="Homo sapiens"
                        /sub_species="infantis"
                        /db_xref="taxon:1682"
                        /country="USA"
                        /collection_date="Aug-2012"
    gene              complement(1..1437)
                        /gene="purB"
                        /locus_tag="EE567_003695"
    CDS               complement(1..1437)
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/EC_number="4.3.2.2"
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gene prediction method: Protein Homology."
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SLLDTLSATLVESRWQRDLTDSTTQRNIGSALGYSLALTNLMGGLESIHFNTHVIER
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DPETAARLKALTPATYTGVASQLVAFDR"

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ORIGIN

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361 ctgggtggtc gaatcgttca gatcgcgctg ccaacgggat tccaccagcg tggcgagagc
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541 cagccgcgag gagatgtaca tccacacgct cagcacagc ttgtgcatga tgcggttggtc
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