

Bifidobacterium longum subsp. infantis strain PI_005 chromosome, complete genome

GenBank: CP054523.1

[FASTA Graphics](#)

LOCUS CP054523 1437 bp DNA linear BCT 02-MAY-2022
DEFINITION Bifidobacterium longum subsp. infantis strain PI_005 chromosome,
complete genome.
ACCESSION [CP054523](#) REGION: 784846..786282
VERSION CP054523.1
DBLINK BioProject: [PRJNA636403](#)
BioSample: [SAMN15077329](#)
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 Duar,R.M., Casaburi,G., Mitchell,R.D., Scofield,L.N.C., Ortega
Ramirez,C.A., Barile,D., Henrick,B.M. and Frese,S.A.
TITLE Comparative Genome Analysis of Bifidobacterium longum subsp.
infantis Strains Reveals Variation in Human Milk Oligosaccharide
Utilization Genes among Commercial Probiotics
JOURNAL Nutrients 12 (11), E3247 (2020)
PUBMED [33114073](#)
REMARK Publication Status: Online-Only
REFERENCE 2 (bases 1 to 1437)
AUTHORS Duar,R.
TITLE Direct Submission
JOURNAL Submitted (04-JUN-2020) R&D, Evolve Biosystems Inc., 2121 2nd St.
Suit B 101, Davis, CA 95618, 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 :: 03-MAR-2020

Assembly Method :: SPAdes v. 3.14.1

Genome Representation :: Full

Expected Final Version :: Yes

Genome Coverage :: 130x

Sequencing Technology :: Illumina NextSeq

##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##

```

Annotation Provider      :: NCBI
Annotation Date          :: 06/08/2020 12:02:25
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)            :: 2,309
CDSs (total)             :: 2,237
Genes (coding)           :: 2,083
CDSs (with protein)      :: 2,083
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)    :: 154
CDSs (without protein)   :: 154
Pseudo Genes (ambiguous residues) :: 0 of 154
Pseudo Genes (frameshifted) :: 76 of 154
Pseudo Genes (incomplete) :: 90 of 154
Pseudo Genes (internal stop) :: 23 of 154
Pseudo Genes (multiple problems) :: 30 of 154
CRISPR Arrays           :: 2
##Genome-Annotation-Data-END##

```

```

FEATURES             Location/Qualifiers
    source            1..1437
                        /organism="Bifidobacterium longum subsp. infantis"
                        /mol_type="genomic DNA"
                        /strain="PI_005"
                        /isolation_source="probiotic prodcut"
                        /host="Homo sapiens"
                        /sub_species="infantis"
                        /db_xref="taxon:1682"
                        /country="USA"
                        /collection_date="2018"
    gene              complement(1..1437)
                        /gene="purB"
                        /locus_tag="HUE64_03535"
    CDS               complement(1..1437)
                        /gene="purB"
                        /locus_tag="HUE64_03535"

```

```

/EC_number="4.3.2.2"
/inference="COORDINATES: similar to AA
sequence:RefSeq:WP_015439045.1"
/note="Derived by automated computational analysis using
gene prediction method: Protein Homology."
/codon_start=1
/transl_table=11
/product="adenylosuccinate lyase"
/protein_id="UPT32588.1"
/translation="MKLTDISPAIALTPLDGRYHKATAPLVEYMSEPALNRERMRVEV
EWMILLANGFEGNGNQPIVDGVKPFATAEEQAFLRAIPEDFGAEGIKQHAHEAITHHD
VKAVEYYIDDQIDKAPAEELTNINDELKTLVHFACTSEDINNLSIARCVKNAMEHVWTP
EFKRIIDHLGKAEEFKDMPLLSLTHGQPATPTTLGKELAVYVYRLNRQLKHIEHQEY
LGKINGATGTFGAHLAACPVDVDWVAVSREFVANRMGLTNWNLTTQIESHDWQAELYST
VSHANRIMHNLCVDVWMIYISRGVFAQVPVKGATGSSTMPHKVNPIRFENAEANFEISC
SLLDTLSATLVESRWQRDLTDSTTQRNIGSALGYSLALTNLMGGLESIHFNTHVIER
ELDENWEVLGEPIQTAMRACELKGLPGMDKPYEKVKELMRGHSIDKEQVEQFIDQSSF
DPETAARLKALTPATYTGVASQLVAFDR"

```

ORIGIN

```

1 tcaacggtcg aaagcgacga gctggctggc cacaccggtg tagtgggcgg gggtcagagc
61 cttcaagcga gcggcggttt ccgggtcgaa ggactgctgg tcgatgaact gctcgacctg
121 ctccctgtcg atggagtggc cgcgcataag ctccctgacc ttctcgtagc gtttgtccat
181 gccgggcagg cccttgagct cgcaggcgcg catggcggtc tggatcggtc cgccaagcac
241 ctcccagttc tcatccagct cagctcgat gacgtgggtg ttcgggtgga tggactcaag
301 gccgcccattg aggttggtca gggcgagcaa ggagtagccg agcgcggaac cgatgttgcg
361 ctgggtggtc gaatcgttca gatcgcgctg ccaacgggat tccaccagcg tggcgagagc
421 ggtgtcgagc agcgagcagc tgatctcgaa gttggcttcg gcgttctcga aacgaatcgg
481 gttgaccttg tgcggcatgg tggaggagcc ggtggcacc ttgaccggca cctgggcgaa
541 cagcccgcg gagatgtaca tccacacgtc cagcacagg ttgtgcatga tgcggttggc
601 gtgggagacg gtggagtaca gtcgggctg ccagtcgtgg ctttcgatct gcgtggtcag
661 cgggttccag gtcaggccca tgcggttggc gacgaattcg cgggagacgg cgaccagtc
721 gacatccggg catgcggcca ggtgggcgcc gaacgtgccg gtcgcgccgt tgatcttgcc
781 caagtactct tggttttcga tgtgcttgag ctgacggttc agacggtaga cgtagacggc
841 gagtccttg ccgagcgtgg tcggcgtggc cggctggccg tgagtgaggg agagcagcgg
901 catatccttg aattcctcgg ccttgccggc gaggtggtcg atgatgcgt tgaactccgg
961 ggtccacaag tggtccatcg cgttcttgac gcaacggcg atggagaggt tggtgatgtc
1021 ttcggacgtg caggcgaagt gtacgagggt cttcagctcg tcgttgatgt tggtcagctc
1081 ggccggagcc ttgtcgatct gatcgctgat gtagtactcc acggccttca catcggtgtg
1141 ggtgatggcc tcatgagcgg cgtgctgctt gatgccttcg gcgccgaagt cctcggaat
1201 ggcgcgcagg aaggcctgct cttcggcagt gaacggcttg acgccgtcaa cgatcggtcg
1261 gttgcccgtt cctcacaagg cgttggccag aaagaatcatc cattcgactt cgacacgcat
1321 gcgttcgcgg ttcagggcag gttcgctcat gtattcgacg agcggagcgg tggccttggtg
1381 gtaacggccg tcgagcgggg tcaatgcgat tgcgggggaa atatcggtaa gcttcat

```