

Porphyromonas gingivalis strain TDC 60 chromosome, complete genome

GenBank: CP025931.1

[FASTA Graphics](#)

LOCUS CP025931 670 bp DNA linear BCT 19-JAN-2018
DEFINITION Porphyromonas gingivalis strain TDC 60 chromosome, complete genome.
ACCESSION [CP025931](#) REGION: 880339..881008
VERSION CP025931.1
DBLINK BioProject: [PRJNA393092](#)
BioSample: [SAMN07315161](#)
KEYWORDS .
SOURCE Porphyromonas gingivalis
ORGANISM [Porphyromonas gingivalis](#)
Bacteria; Bacteroidetes; Bacteroidia; Bacteroidales;
Porphyromonadaceae; Porphyromonas.
REFERENCE 1 (bases 1 to 670)
AUTHORS Acuna-Amador,L., Primot,A., Cadieu,E., Roulet,A. and Barloy-Hubler,F.
TITLE Genomic repeats, misassembly and reannotation: a case study with long-read resequencing of Porphyromonas gingivalis reference strains
JOURNAL BMC Genomics 19 (1), 54 (2018)
PUBMED [29338683](#)
REMARK Publication Status: Online-Only
REFERENCE 2 (bases 1 to 670)
AUTHORS Acuna-Amador,L.A. and Barloy-Hubler,F.
TITLE Direct Submission
JOURNAL Submitted (12-JAN-2018) IGDR UMR6290-CNRS-UR1, 2 av Pr Leon Bernard, Rennes, France
COMMENT ##Genome-Assembly-Data-START##
Assembly Date :: JUN-2017
Assembly Method :: canu v. 1.3
Expected Final Version :: yes
Genome Coverage :: 30.4x
Sequencing Technology :: PacBio
##Genome-Assembly-Data-END##
FEATURES Location/Qualifiers
source 1..670
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/mol_type="genomic DNA"
/strain="TDC 60"
/isolation_source="Severe periodontal lesion"
/host="Homo sapiens"
/culture_collection="JCM:[19600](#)"

/db_xref="taxon:837"

gene <1..>670

/locus_tag="CF002_16SR1"

rRNA <1..>670

/locus_tag="CF002_16SR1"

/product="16S ribosomal RNA"

ORIGIN

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121  gttcggtaag tcagcggtag aacctgagcg ctcaacgttc agcctgccgt tgaaactacc
181  gggcttgagt tcagtggcgg caggcggaat tcgtggtgta gcggtgaaat gcatagatat
241  cacgaggaac tccgattgcg aaggcagctt gccatactgc gactgacact gaagcacgaa
301  ggcgtgggta tcaaacagga ttagataccc tggtagtcca cgcagtaaag gatgattact
361  aggagtttgc gatataccgt caagcttcca cagcgaaagc gttaagtaat ccacctgggg
421  agtacgccgg caacggtgaa actcaaagga attgacgggg gccgcacaa gcggaggaac
481  atgtggttta attcgatgat acgcgaggaa cttaccggg gattgaaatg tagatgacgg
541  atggtgaaaa ccgtcttccc ttcggggcctt ctatgtaggt gctgcatggt tgcgtcagc
601  tcgtgccgtg aggtgtcggc ttaagtcca taacgagcgc aaccacatc ggtagttgct
661  aacagttttc
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