Streptococcus salivarius strain KSS8 chromosome, complete genome

GenBank: CP145865.1

FASTA Graphics

Go to:

LOCUS CP145865 861 bp DNA linear BCT 07-JAN-2025
DEFINITION Streptococcus salivarius strain KSS8 chromosome, complete genome.
ACCESSION CP145865 REGION: complement(1677744..1678604)
VERSION CP145865.1
DBLINK BioProject: PRJNA1078522
BioSample: SAMN40004501
KEYWORDS .
SOURCE Streptococcus salivarius
ORGANISM Streptococcus salivarius
Bacteria; Bacillati; Bacillota; Bacilli; Lactobacillales;
Streptococcaceae; Streptococcus.
REFERENCE 1 (bases 1 to 861)
AUTHORS Lee,J.-H. and Moon,J.-H.
TITLE Complete genome sequence of Streptococcus salivarius KSS8
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 861)
AUTHORS Lee,J.-H. and Moon,J.-H.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-2024) Department of Oral Microbiology, Kyung Hee
University, 26, Kyungheedae-ro, Dongdaemun-gu, Seoul, NA 02447,
South Korea
COMMENT Bacteria and source DNA available from Ji-Hoi Moon, College of
Dentistry, Kyung Hee University, South Korea.
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 :: 21-DEC-2023
Assembly Method :: IPA HiFi genome assembler v. 2.0
Assembly Name :: KSS8
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 291.2x
Sequencing Technology :: PacBio Sequel
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI

```
            Annotation Date                :: 02/22/2024 10:21:26
            Annotation Pipeline            :: NCBI Prokaryotic Genome
                                           Annotation Pipeline (PGAP)
            Annotation Method              :: Best-placed reference protein
                                           set; GeneMarkS-2+
            Annotation Software revision    :: 6.6
            Features Annotated             :: Gene; CDS; rRNA; tRNA; ncRNA
            Genes (total)                  :: 1,996
            CDSs (total)                   :: 1,906
            Genes (coding)                 :: 1,853
            CDSs (with protein)            :: 1,853
            Genes (RNA)                    :: 90
            rRNAs                          :: 6, 6, 6 (5S, 16S, 23S)
            complete rRNAs                 :: 6, 6, 6 (5S, 16S, 23S)
            tRNAs                          :: 68
            ncRNAs                         :: 4
            Pseudo Genes (total)           :: 53
            CDSs (without protein)         :: 53
            Pseudo Genes (ambiguous residues) :: 0 of 53
            Pseudo Genes (frameshifted)    :: 22 of 53
            Pseudo Genes (incomplete)      :: 32 of 53
            Pseudo Genes (internal stop)   :: 18 of 53
            Pseudo Genes (multiple problems) :: 18 of 53
            CRISPR Arrays                  :: 1
            ##Genome-Annotation-Data-END##
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                   /note="Derived by automated computational analysis using
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ORIGIN

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      121 gaagagtatg tgcgccgtcg ttgtaaagaa gaaaatgttc ttcctcttca gattggagtt
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      301 ttgtcagaac ctattgataa gtcagtcctt gatgtgtcaa aattggactt tgacaatgtt
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      481 atgtaccttg gtattgaaca agcggtagtc ggtaaccgta tcggtgatat cggggcagct
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