Nitratidesulfovibrio vulgaris strain L2 chromosome, complete genome

NCBI Reference Sequence: NZ_CP116246.1

FASTA Graphics

Go to:

LOCUS NZ_CP116246 1146 bp DNA linear CON 30-AUG-2025
DEFINITION Nitratidesulfovibrio vulgaris strain L2 chromosome, complete genome.
ACCESSION NZ_CP116246 REGION: 768907..770052
VERSION NZ_CP116246.1
DBLINK BioProject: PRJNA224116
BioSample: SAMN32746340
Assembly: GCF_027947635.1
KEYWORDS RefSeq.
SOURCE Nitratidesulfovibrio vulgaris
ORGANISM Nitratidesulfovibrio vulgaris
Bacteria; Pseudomonadati; Thermodesulfobacteriota; Desulfovibrionia; Desulfovibrionales; Desulfovibrionaceae; Nitratidesulfovibrio.
REFERENCE 1 (bases 1 to 1146)
AUTHORS Karnachuk,O.V., Beletsky,A.V., Rakitin,A.L., Ikkert,O.P., Avakyan,M.R., Zyusman,V.S., Napilov,A., Mardanov,A.V. and Ravin,N.V.
TITLE An antibiotic-resistant Desulfovibrio produces H 2 S from supplements for animal farming
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1146)
AUTHORS Karnachuk,O.V., Beletsky,A.V., Rakitin,A.L., Ikkert,O.P., Avakyan,M.R., Zyusman,V.S., Napilov,A., Mardanov,A.V. and Ravin,N.V.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-2023) Department of molecular biology of microorganisms, Institute of Bioengineering, Research Center of Biotechnology of RAS, Prosp. 60-let Oktyabrya, bld 7-1, Moscow 117312, Russia
COMMENT REFSEQ INFORMATION: The reference sequence is identical to CP116246.1.
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 Method :: Flye v. 2.7b
Genome Representation :: Full
Expected Final Version :: Yes

Genome Coverage :: 435.0x
Sequencing Technology :: Illumina MiSeq; Oxford Nanopore MinION
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI RefSeq
Annotation Name :: GCF_027947635.1-RS_2025_08_29
Annotation Date :: 08/29/2025 13:02:22
Annotation Pipeline :: NCBI Prokaryotic Genome Annotation Pipeline (PGAP)
Annotation Method :: Best-placed reference protein set; GeneMarkS-2+
Annotation Software revision :: 6.10
Features Annotated :: Gene; CDS; rRNA; tRNA; ncRNA
Genes (total) :: 3,334
CDSs (total) :: 3,244
Genes (coding) :: 3,213
CDSs (with protein) :: 3,213
Genes (RNA) :: 90
rRNAs :: 6, 5, 5 (5S, 16S, 23S)
complete rRNAs :: 6, 5, 5 (5S, 16S, 23S)
tRNAs :: 68
ncRNAs :: 6
Pseudo Genes (total) :: 31
CDSs (without protein) :: 31
Pseudo Genes (ambiguous residues) :: 0 of 31
Pseudo Genes (frameshifted) :: 17 of 31
Pseudo Genes (incomplete) :: 20 of 31
Pseudo Genes (internal stop) :: 10 of 31
Pseudo Genes (multiple problems) :: 12 of 31
CRISPR Arrays :: 2
##Genome-Annotation-Data-END##
COMPLETENESS: full length.

FEATURES Location/Qualifiers
source 1..1146
/organism="Nitratidesulfovibrio vulgaris"
/mol_type="genomic DNA"
/strain="L2"
/isolation_source="swine finishing facility waste"
/db_xref="taxon:881"
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/gene="dsrB"
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/old_locus_tag="PH214_03265"

CDS 1..1146

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/locus_tag="PH214_RS03265"

/old_locus_tag="PH214_03265"

/EC_number="1.8.1.22"

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/GO_process="GO:0019420 - dissimilatory sulfate reduction [Evidence IEA]"

/note="Derived by automated computational analysis using gene prediction method: Protein Homology."

/codon_start=1

/transl_table=11

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/protein_id="WP_010937710.1"

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ORIGIN

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1141 ttctag
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