Yersinia enterocolitica strain Y177 chromosome, complete genome

GenBank: CP124246.1

FASTA Graphics

Go to:

LOCUS CP124246 1527 bp DNA linear BCT 07-MAR-2024
DEFINITION Yersinia enterocolitica strain Y177 chromosome, complete genome.
ACCESSION CP124246 REGION: 1624195..1625721
VERSION CP124246.1
DBLINK BioProject: PRJNA961371
BioSample: SAMN34359766
KEYWORDS .
SOURCE Yersinia enterocolitica
ORGANISM Yersinia enterocolitica
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria;
Enterobacterales; Yersiniaceae; Yersinia.
REFERENCE 1 (bases 1 to 1527)
AUTHORS Kittl,S., Frey,C.F., Brodard,I., Thomann,A., Vargas Amado,M.E.,
Scalisi,N., Schierack,P., Kuhnert,P., Staerk,K.D.C. and Jores,J.
TITLE Bacterial and parasite zoonotic pathogens carried in the guts of
foxes, racoons and other predators, Germany, 2021-2022
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1527)
AUTHORS Kittl,S. and Jores,J.
TITLE Direct Submission
JOURNAL Submitted (25-APR-2023) Department of Infectious Diseases and
Pathobiology, Institute of Veterinary Bacteriology, University of
Bern, Laengassstrasse 122, Bern 3012, Switzerland
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 Method :: Smrtlink v. v11
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 165x
Sequencing Technology :: PacBio
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Date :: 05/01/2023 12:01:52
Annotation Pipeline :: NCBI Prokaryotic Genome

Annotation Pipeline (PGAP)
Annotation Method :: Best-placed reference protein set; GeneMarkS-2+
Annotation Software revision :: 6.5
Features Annotated :: Gene; CDS; rRNA; tRNA; ncRNA
Genes (total) :: 4,240
CDSs (total) :: 4,118
Genes (coding) :: 4,061
CDSs (with protein) :: 4,061
Genes (RNA) :: 122
rRNAs :: 8, 7, 7 (5S, 16S, 23S)
complete rRNAs :: 8, 7, 7 (5S, 16S, 23S)
tRNAs :: 80
ncRNAs :: 20
Pseudo Genes (total) :: 57
CDSs (without protein) :: 57
Pseudo Genes (ambiguous residues) :: 0 of 57
Pseudo Genes (frameshifted) :: 34 of 57
Pseudo Genes (incomplete) :: 24 of 57
Pseudo Genes (internal stop) :: 10 of 57
Pseudo Genes (multiple problems) :: 10 of 57
##Genome-Annotation-Data-END##

FEATURES Location/Qualifiers
source 1..1527
/organism="Yersinia enterocolitica"
/mol_type="genomic DNA"
/strain="Y177"
/isolation_source="intestine"
/host="Procyon lotor"
/db_xref="taxon:630"
/geo_loc_name="Germany: Templin"
/collection_date="2022-02-17"
gene 1..1527
/locus_tag="QJR39_07460"
CDS 1..1527
/locus_tag="QJR39_07460"
/inference="COORDINATES: similar to AA sequence:RefSeq:WP_005161755.1"
/note="Derived by automated computational analysis using gene prediction method: Protein Homology."
/codon_start=1
/transl_table=11
/product="amino acid permease"
/protein_id="WWV04514.1"

```
                     /translation="MTQQNTKIPVQQGAQRLRRELKSRHLAMIAIGGSIGTGLFVASG
                     ATVSQAGPGGALLSYALIGLMVYFLMTSLGELAAFMPVSGSFSTYGSKYVEEGFGFAL
                     GWNYWYNWAVTIAVDLVAAQLVMNYWFPDAPGWIWSALFLALMFLLNYISVKGFGEAE
                     YWFSLIKVTTVIIFIIIGVMMISGIMKGGESAGWHNWTIGDAPFAGGFSAMIGVAMIV
                     GFSFQGTELIGIAAGESKDPGKNIPRAVRKVFWRILLFYIFAILIISLIIPYTDPSLL
                     RNDVKDISVSPFTLVFQNAGLLSAAAVMNAVILTAVLSAGNSGMYASTRMLFTLASEG
                     KAPRIFAKLSRGGVPRNALYATTVVAGLCFLSSMFGNQTVYLWLLNTSGMTGFIAWLG
                     IAISHYRFRRGYMMQGRDLNDLPYQSGFFPLGPIFAFVLCLIITLGQNYQAFLQDRID
                     WYGVTATYIGIPLFLVIWFGYKLSRGTKVIKYKDMEFPKWRDESHDDQEAKKTALIAD
                     "
ORIGIN
       1 atgactcagc aaaatactaa aatcccagtg caacagggtg cacagcgttt acgccgtgag
      61 cttaaatcac ggcatttagc catgattgct atcggtggct ccatcggtac cggtttgttt
     121 gtcgcctcag gcgcgacagt ttctcaggcc ggcccaggtg gagcattgct ctcctatgca
     181 ttgattggct tgatggttta cttcttgatg accagtctcg gtgaattggc ggcatttatg
     241 ccggtatctg gttcattttc gacttacggc tcaaaatatg ttgaggaagg cttcggcttc
     301 gcccttggct ggaactattg gtacaactgg gcggtgacta tcgctgttga cctggtcgcg
     361 gcacaattgg tgatgaatta ctggttcccg gatgcgccgg gctggatctg gagtgcgctg
     421 ttcctcgccc tgatgttttt actcaactac atatcagtga aaggttttgg tgaagcggaa
     481 tactggttct cactgattaa agtgaccaca gttattatct tcatcattat tggtgtgatg
     541 atgattagcg gcatcatgaa aggcggcgag agtgcagggt ggcacaactg gacaatcggt
     601 gatgcaccgt ttgccggagg gttctcggcg atgattggtg tggcgatgat tgtcggtttc
     661 tccttccagg gaactgagct gattggtatt gctgctggtg aatcaaaaga cccaggcaaa
     721 aacatccctc gtgcggtgcg caaggtattc tggcgtattc tgctgttcta tatctttgct
     781 atcctgatta tcagcctgat cattccgtat accgacccaa gtctgttacg taatgatgtt
     841 aaagatatta gcgtcagccc gttcacctta gtgttccaga atgcaggtct gctatctgcg
     901 gcagcggtga tgaatgcggt tattctgacc gcggtattgt cagcaggtaa ctcaggcatg
     961 tacgcctcta cccgtatgct atttaccttg gcttcagaag gtaaggctcc gcgtattttt
    1021 gccaaacttt ctcgcggtgg tgtaccccgt aatgcgctgt atgccaccac tgtagtcgcg
    1081 ggcttgtgct tcttaagttc gatgtttggt aatcaaactg tctatctgtg gttactgaat
    1141 acttcaggta tgacaggctt tatcgcctgg ttgggtattg ctatcagtca ttatcgtttc
    1201 cgtcgtggtt atatgatgca gggccgcgat ttgaacgatt taccgtatca gtcaggtttc
    1261 ttcccgctgg ggccaatctt tgcctttgtc ctgtgtttga tcattacttt gggtcaaaac
    1321 tatcaggcat tcctgcaaga tcgcattgat tggtatggcg tgaccgccac ttatatcggt
    1381 attccattat tcctggtgat ttggttcggc tataaactga gccgtggtac caaggtgatc
    1441 aaatacaaag atatggaatt cccgaaatgg cgtgatgaaa gtcatgatga tcaggaagct
    1501 aaaaaaacag cactgattgc tgactaa
//
```