Shigella flexneri strain FDAARGOS_716 chromosome

GenBank: CP050985.1

FASTA Graphics

Go to:

LOCUS CP050985 444 bp DNA linear BCT 12-APR-2020
DEFINITION Shigella flexneri strain FDAARGOS_716 chromosome.
ACCESSION CP050985 REGION: 3242303..3242746
VERSION CP050985.1
DBLINK BioProject: PRJNA231221
BioSample: SAMN11056431
KEYWORDS .
SOURCE Shigella flexneri
ORGANISM Shigella flexneri
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria;
Enterobacterales; Enterobacteriaceae; Shigella.
REFERENCE 1 (bases 1 to 444)
AUTHORS Fashae,K., Tallon,L., Sadzewicz,L., Vavikolanu,K., Mehta,A.,
Aluvathingal,J., Nadendla,S., Nandy,P., Geyer,C., Yan,Y. and
Sichtig,H.
TITLE FDA dAtabase for Regulatory Grade micrObial Sequences (FDA-ARGOS):
Supporting development and validation of Infectious Disease Dx
tests
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 444)
AUTHORS Fashae,K., Tallon,L., Sadzewicz,L., Vavikolanu,K., Mehta,A.,
Aluvathingal,J., Nadendla,S., Nandy,P., Geyer,C., Yan,Y. and
Sichtig,H.
TITLE Direct Submission
JOURNAL Submitted (25-NOV-2019) Center for Devices and Radiological
Health,
US Food and Drug Administration, 10903 New Hampshire Avenue,
Silver
Spring, MD 20993-0002, 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 Method :: canu v. 1.4
Genome Coverage :: 436.94x
Sequencing Technology :: Pacbio; Illumina
##Genome-Assembly-Data-END##

```
            ##Genome-Annotation-Data-START##
            Annotation Provider             :: NCBI
            Annotation Date                 :: 04/06/2020 10:23:52
            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)                   :: 5,062
            CDSs (total)                    :: 4,929
            Genes (coding)                  :: 4,156
            CDSs (with protein)             :: 4,156
            Genes (RNA)                     :: 133
            rRNAs                           :: 8, 7, 7 (5S, 16S, 23S)
            complete rRNAs                  :: 8, 7, 7 (5S, 16S, 23S)
            tRNAs                           :: 104
            ncRNAs                          :: 7
            Pseudo Genes (total)            :: 773
            CDSs (without protein)          :: 773
            Pseudo Genes (ambiguous residues) :: 0 of 773
            Pseudo Genes (frameshifted)      :: 379 of 773
            Pseudo Genes (incomplete)        :: 339 of 773
            Pseudo Genes (internal stop)     :: 164 of 773
            Pseudo Genes (multiple problems)  :: 102 of 773
            ##Genome-Annotation-Data-END##
FEATURES            Location/Qualifiers
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                    /geo_loc_name="Nigeria: Ibadan"
                    /collected_by="University of Ibadan"
    gene            1..444
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    CDS             1..444
                    /locus_tag="FOC24_17330"
                    /inference="COORDINATES: similar to AA
                    sequence:RefSeq:WP_004997737.1"
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/note="Derived by automated computational analysis using gene prediction method: Protein Homology."
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EIRSLSGRLHSAEKGSDFTQALLGHRSSSMTDKYRDGRGREWKDI"

ORIGIN

```
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     121 tctctcccca ccacgatttc cagattgaat ttaacacttg ccgatgtact ggataacttg
     181 aaaaaaataa acggtaaaaa cgaaaagtta ctcggaggga agacagccag gacaattgca
     241 gcacagttca ggattgcccg agacacatcc ggattgaaat gggaaggtga cccaccgcca
     301 tttcatgaaa tccgaagttt atccggtcgc ctgcactcag cagaaaaagg cagtgatttc
     361 actcaggcgc tccttggaca tcgttcatcc agcatgacgg ataaataccg tgacggacga
     421 gggagggaat ggaaagacat ttag
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