Staphylococcus aureus strain pt286 chromosome, complete genome

GenBank: CP049390.1

FASTA Graphics

Go to:

LOCUS CP049390 660 bp DNA linear BCT 24-SEP-2020

DEFINITION Staphylococcus aureus strain pt286 chromosome, complete genome.

ACCESSION CP049390 REGION: 40601..41260

VERSION CP049390.1

DBLINK BioProject: PRJNA470993
BioSample: SAMN12331103

KEYWORDS .

SOURCE Staphylococcus aureus

ORGANISM Staphylococcus aureus
Bacteria; Bacillati; Bacillota; Bacilli; Bacillales;
Staphylococcaceae; Staphylococcus.

REFERENCE 1 (bases 1 to 660)

AUTHORS Caban,A.B., Pak,T., Kumaresh,A., Dupper,A., Chacko,K.,
Sullivan,M.J., Altman,D.R. and van Bakel,H.

TITLE PathoSPOT genomic surveillance reveals prolonged under the radar outbreaks of nosocomial methicillin resistant S. aureus bloodstream infections

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 660)

AUTHORS Caban,A.B., Pak,T., Kumaresh,A., Dupper,A., Chacko,K.,
Sullivan,M.J., Altman,D.R. and van Bakel,H.

TITLE Direct Submission

JOURNAL Submitted (27-FEB-2020) Genetics and Genomic Sciences, Icahn School of Medicine, One Gustave L. Levy Place Box 1498, New York, NY 10029, 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 :: HGAP v. 2.3.0
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 384.687488612836x
Sequencing Technology :: PacBio
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##
Annotation Provider :: NCBI
Annotation Date :: 02/28/2020 15:22:01

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            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)                   :: 2,754
            CDSs (total)                    :: 2,672
            Genes (coding)                  :: 2,615
            CDSs (with protein)              :: 2,615
            Genes (RNA)                     :: 82
            rRNAs                           :: 7, 6, 6 (5S, 16S, 23S)
            complete rRNAs                   :: 7, 6, 6 (5S, 16S, 23S)
            tRNAs                           :: 59
            ncRNAs                          :: 4
            Pseudo Genes (total)             :: 57
            CDSs (without protein)           :: 57
            Pseudo Genes (ambiguous residues) :: 0 of 57
            Pseudo Genes (frameshifted)      :: 38 of 57
            Pseudo Genes (incomplete)        :: 12 of 57
            Pseudo Genes (internal stop)     :: 18 of 57
            Pseudo Genes (multiple problems)  :: 11 of 57
            ##Genome-Annotation-Data-END##
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ORIGIN

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