Staphylococcus aureus strain ER09690.3 plasmid pER09690.3A.1, complete sequence

GenBank: CP051964.1

FASTA Graphics

Go to:

LOCUS CP051964 767 bp DNA linear BCT 24-SEP-2020
DEFINITION Staphylococcus aureus strain ER09690.3 plasmid pER09690.3A.1, complete sequence.
ACCESSION CP051964 REGION: complement(13012..13778)
VERSION CP051964.1
DBLINK BioProject: PRJNA470993
BioSample: SAMN14669410
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Bacillati; Bacillota; Bacilli; Caryophanales; Staphylococcaceae; Staphylococcus.
REFERENCE 1 (bases 1 to 767)
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JOURNAL Unpublished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 767)
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 (22-APR-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 :: 429.792823264202x
Sequencing Technology :: PacBio
##Genome-Assembly-Data-END##

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

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            Annotation Date                :: 04/23/2020 09:56:49
            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)                  :: 2,821
            CDSs (total)                   :: 2,742
            Genes (coding)                 :: 2,668
            CDSs (with protein)            :: 2,668
            Genes (RNA)                    :: 79
            rRNAs                          :: 6, 5, 5 (5S, 16S, 23S)
            complete rRNAs                 :: 6, 5, 5 (5S, 16S, 23S)
            tRNAs                          :: 59
            ncRNAs                         :: 4
            Pseudo Genes (total)           :: 74
            CDSs (without protein)         :: 74
            Pseudo Genes (ambiguous residues) :: 0 of 74
            Pseudo Genes (frameshifted)    :: 52 of 74
            Pseudo Genes (incomplete)      :: 15 of 74
            Pseudo Genes (internal stop)   :: 17 of 74
            Pseudo Genes (multiple problems) :: 10 of 74
            ##Genome-Annotation-Data-END##
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                   /collected_by="Mount Sinai Hospital"
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                   /pseudo
     CDS           1..767
                   /gene="sed"
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/locus_tag="HIK70_14035"
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sequence:RefSeq:WP_128623913.1"
/note="frameshifted; Derived by automated computational
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/pseudo
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ORIGIN

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     121 tctgaattaa gtagtaccgc gctaaataat atgaaacatt cttatgcaga taaaaatcca
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     241 aaatttttta ctgaccttat caatttgaa gatttattaa taaacttcaa ttcaaaagaa
     301 atggctcaac atttcaaatc taaaaatgta gatgtttacg ctataagata tagcattaat
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     541 caaggcgcta tttgcaaaag gatttaaaat tgtataataa tgatactctc ggaggaaaaa
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     661 ttgatgttaa gggtgatttt cccgaaaaac aattacgaat atacagtgat aataaaacat
     721 tatccacaga gcaccttcat attgacatct atttatatga aaagtag
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//