Staphylococcus aureus strain NAS_NP_209 chromosome, complete genome

GenBank: CP062405.1

FASTA Graphics

Go to:

LOCUS CP062405 384 bp DNA linear BCT 28-FEB-2022
DEFINITION Staphylococcus aureus strain NAS_NP_209 chromosome, complete genome.
ACCESSION CP062405 REGION: 127814..128197
VERSION CP062405.1
DBLINK BioProject: PRJNA626345
BioSample: SAMN15567971
KEYWORDS .
SOURCE Staphylococcus aureus
ORGANISM Staphylococcus aureus
Bacteria; Bacillati; Bacillota; Bacilli; Bacillales; Staphylococcaceae; Staphylococcus.
REFERENCE 1 (bases 1 to 384)
AUTHORS Cella,E., Sutcliffe,C., Jubair,M., Weatherholtz,R.C., Reid,R., Reid,A., Quay,D., Azarian,T.H. and Hammitt,L.
TITLE Carriage prevalence and genomic epidemiology of Staphylococcus aureus among Native Americans in the southwest US
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 384)
AUTHORS Cella,E., Sutcliffe,C., Jubair,M., Weatherholtz,R.C., Reid,R., Reid,A., Quay,D., Azarian,T.H. and Hammitt,L.
TITLE Direct Submission
JOURNAL Submitted (30-JUL-2020) Burnett School of Biomedical Sciences, University of central Florida, 4111 Libra Dr, Orlando, FL 32816, 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 Date :: 2020
Assembly Method :: Uniclycler v. 0.4.8
Genome Representation :: Full
Expected Final Version :: Yes
Genome Coverage :: 50x
Sequencing Technology :: Illumina MiSeq; Oxford Nanopore
##Genome-Assembly-Data-END##

##Genome-Annotation-Data-START##

```
            Annotation Provider             :: NCBI
            Annotation Date                 :: 09/24/2020 19:17:56
            Annotation Pipeline             :: NCBI Prokaryotic Genome
                                               Annotation Pipeline (PGAP)
            Annotation Method               :: Best-placed reference protein
                                               set; GeneMarkS-2+
            Annotation Software revision     :: 4.13
            Features Annotated              :: Gene; CDS; rRNA; tRNA; ncRNA;
                                               repeat_region
            Genes (total)                   :: 2,832
            CDSs (total)                    :: 2,751
            Genes (coding)                  :: 2,657
            CDSs (with protein)             :: 2,657
            Genes (RNA)                     :: 81
            rRNAs                           :: 7, 6, 6 (5S, 16S, 23S)
            complete rRNAs                  :: 7, 6, 6 (5S, 16S, 23S)
            tRNAs                           :: 58
            ncRNAs                          :: 4
            Pseudo Genes (total)            :: 94
            CDSs (without protein)          :: 94
            Pseudo Genes (ambiguous residues) :: 0 of 94
            Pseudo Genes (frameshifted)     :: 57 of 94
            Pseudo Genes (incomplete)       :: 21 of 94
            Pseudo Genes (internal stop)    :: 32 of 94
            Pseudo Genes (multiple problems)  :: 13 of 94
            ##Genome-Annotation-Data-END##
FEATURES           Location/Qualifiers
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                    /strain="NAS_NP_209"
                    /host="Homo sapiens"
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                    /collected_by="UCF"
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     CDS            complement(1..384)
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                    /note="Derived by automated computational analysis using
                    gene prediction method: Protein Homology."
                    /codon_start=1
                    /transl_table=11
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SIILFISAIITLAIGGKSFDKNDSH"

ORIGIN

```
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       61 tatgaacaaa ataattgaag ttataaatga cgctaatgta aaaggtgtaa attgtgtgag
      121 cgataatatc aatgataaaa agaaccaaga gatagcccct agaaattgta aaatagcaga
      181 agaaattcta aaactcatat tattgaatat agctaaaata agtgcgggta atgcgactaa
      241 taccattata atgatgttga gtgtgaataa atatggctgt tcgaaagtta ctgtgtttgg
      301 acctgttgga tgcattgctg ctaagaacaa gcaaacaatc gtcgataaaa ttgctaaaat
      361 aataaaagtg attcgaactt tcat
```

//