Yersinia pestis CO92 plasmid pCD1, complete sequence

NCBI Reference Sequence: NC_003131.1

FASTA Graphics

LOCUS NC_003131 981 bp DNA linear CON 04-JUN-2026
DEFINITION Yersinia pestis CO92 plasmid pCD1, complete sequence.
ACCESSION NC_003131 REGION: complement(21935..22915)
VERSION NC_003131.1
DBLINK BioProject: PRJNA224116
BioSample: SAMEA1705942
Assembly: GCF_000009065.1
KEYWORDS RefSeq; chaperone; cytotoxic effector; IS100; IS1616; IS1617; lcr; low-calcium response; syc; targeted effector; transposase; type III secretion; V antigen; virulence; ylp; yop; ysc.
SOURCE Yersinia pestis CO92
ORGANISM Yersinia pestis CO92
Bacteria; Pseudomonadati; Pseudomonadota; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia.
REFERENCE 1 (bases 1 to 981)
AUTHORS Parkhill,J., Wren,B.W., Thomson,N.R., Titball,R.W., Holden,M.T., Prentice,M.B., Sebaihia,M., James,K.D., Churcher,C., Mungall,K.L., Baker,S., Basham,D., Bentley,S.D., Brooks,K., Cerdeno-Tarraga,A.M., Chillingworth,T., Cronin,A., Davies,R.M., Davis,P., Dougan,G., Feltwell,T., Hamlin,N., Holroyd,S., Jagels,K., Karlyshev,A.V., Leather,S., Moule,S., Oyston,P.C., Quail,M., Rutherford,K., Simmonds,M., Skelton,J., Stevens,K., Whitehead,S. and Barrell,B.G.
TITLE Genome sequence of Yersinia pestis, the causative agent of plague
JOURNAL Nature 413 (6855), 523-527 (2001)
PUBMED 11586360
REFERENCE 2 (bases 1 to 981)
AUTHORS James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1999) Yersinia pestis sequencing project, The Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge CB10 1SA E-mail:parkhill@sanger.ac.uk DNA supplied by Dr. Andrey Karlyshev and Prof. Brendan Wren, [3]. Department of Infectious and Tropical Diseases, London School of Hygiene and Tropical Medicine, Keppel Street, London WC1E 7HT
COMMENT REFSEQ INFORMATION: The reference sequence is identical to AL117189.1.
Notes:
Details of Y. pestis sequencing at the Sanger Centre are available on the World Wide Web.

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            (URL, http://www.sanger.ac.uk/Projects/Y_pestis/).
            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-Annotation-Data-START##
            Annotation Provider             :: NCBI RefSeq
            Annotation Name                 :: GCF_000009065.1-RS_2026_06_03
            Annotation Date                 :: 06/03/2026 19:48:37
            Annotation Pipeline             :: NCBI Prokaryotic Genome
                                               Annotation Pipeline (PGAP)
            Annotation Method               :: Best-placed reference protein
                                               set; GeneMarkS-2+
            Annotation Software revision     :: 6.11
            Features Annotated              :: Gene; CDS; rRNA; tRNA; ncRNA
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            CDSs (total)                    :: 4,317
            Genes (coding)                  :: 4,096
            CDSs (with protein)             :: 4,096
            Genes (RNA)                     :: 100
            rRNAs                           :: 7, 6, 6 (5S, 16S, 23S)
            complete rRNAs                  :: 7, 6, 6 (5S, 16S, 23S)
            tRNAs                           :: 69
            ncRNAs                          :: 12
            Pseudo Genes (total)            :: 221
            CDSs (without protein)          :: 221
            Pseudo Genes (ambiguous residues) :: 0 of 221
            Pseudo Genes (frameshifted)      :: 91 of 221
            Pseudo Genes (incomplete)        :: 144 of 221
            Pseudo Genes (internal stop)     :: 21 of 221
            Pseudo Genes (multiple problems)  :: 31 of 221
            CRISPR Arrays                   :: 2
            ##Genome-Annotation-Data-END##
            COMPLETENESS: full length.
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