

Yersinia pestis CO92 plasmid pMT1

GenBank: AL117211.1

[FASTA Graphics](#)

LOCUS AL117211 96210 bp DNA circular BCT 26-JUL-2016

DEFINITION Yersinia pestis CO92 plasmid pMT1.

ACCESSION AL117211

VERSION AL117211.1

DBLINK BioProject: [PRJNA34](#)

BioSample: [SAMEA1705942](#)

KEYWORDS ABC transporter; antirestriction; ATP-binding; bacteriophage; caf1R; capsule anchoring protein; chaperone; DNA methylase; DNA polymerase III; exonuclease; integrase; IS100; IS200; iteron; lipoprotein; murine toxin; parA; parB; partitioning; porphyrin; recombinase; repA; resolvase; tnpA; transcriptional regulator; transposase; ymt.

SOURCE Yersinia pestis CO92

ORGANISM [Yersinia pestis CO92](#)

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacterales; Yersiniaceae; Yersinia.

REFERENCE 1

AUTHORS Prentice,M.B., James,K.D., Parkhill,J., Baker,S.G., Stevens,K., Simmonds,M.N., Mungall,K.L., Churcher,C., Oyston,P.C., Titball,R.W., Wren,B.W., Wain,J., Pickard,D., Hien,T.T., Farrar,J.J. and Dougan,G.

TITLE Yersinia pestis pFra shows biovar-specific differences and recent common ancestry with a Salmonella enterica serovar Typhi plasmid

JOURNAL J. Bacteriol. 183 (8), 2586-2594 (2001)

PUBMED [11274119](#)

REFERENCE 2 (bases 1 to 96210)

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 3 (bases 1 to 96210)

AUTHORS James,K.D., Parkhill,J., Barrell,B.G. and Rajandream,M.A.

TITLE Direct Submission

JOURNAL Submitted (06-SEP-1999) Yersinia pestis sequencing project, The

Wellcome Trust Sanger Institute, Genome Campus, Hinxton, Cambridge
CB10 1SA E-mail: barrell@sanger.ac.uk DNA supplied by Dr. Andrey
Karlyshev and Prof. Brendan Wren, [3]. Department of Infectious &
Tropical Diseases, London School of Hygiene and Tropical Medicine,
Keppel Street, London WC1E 7HT

COMMENT Notes:

Details of *Y. pestis* sequencing at the Sanger Centre are available
on the World Wide Web.

(URL, http://www.sanger.ac.uk/Projects/Y_pestis/).

FEATURES Location/Qualifiers

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/mol_type="genomic DNA"

/strain="CO-92"

/db_xref="taxon:[214092](#)"

/plasmid="pMT1"

/note="biovar:Orientalis"

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/note="identical to *Y.pestis* KIM5 plasmid pMT1

(EMBL:AF053947) from 1 to 57331, except where noted"

misc_feature 1..48266

/note="identical to *Y.pestis* KIM5 plasmid pMT1

(EMBL:AF074611) from 48336 to 1, except where noted"

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/gene="YPMT1.84"

/gene_synonym="caf1"

CDS 85950..86462

/gene="YPMT1.84"

/gene_synonym="caf1"

/note="YPMT1.84, caf1, probable F1 capsule antigen, len:

170 aa; identical to CAF1_YERPE (EMBL:X61996) *Yersinia*

pestis F1 capsule antigen from plasmid pFRA (170 aa),

fasta scores; opt: 1050 z-score: 1191.5 E(): 0, 100.0%

identity in 170 aa overlap. Identical to caf1

(EMBL:AF074611) from *Y.pestis* KIM5 pMT1 (170 aa) (100.0%

identity in 170 aa overlap) / caf1 (EMBL:AF053947) from

Y.pestis KIM5 pMT1 (170 aa) (100.0% identity in 170 aa

overlap) "

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/transl_table=[11](#)

/product="putative F1 capsule antigen"

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/db_xref="PDB:1Z9S"
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/db_xref="PDB:4B0M"
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KEGAPITIMDNGNIDTELLVGTLTLGGYKTGTTSTSVNFTDAAGDPMYLTFTSQDGNN
HQFTTKVIGKDSRDFDISPKVNGENLVGDDVVLATGSQDFFVRSIGSKGGKLAAGKYT
DAVTVTVSNQ"
gene      87147..88325
          /gene="YPMT1.85"
CDS       87147..88325
          /gene="YPMT1.85"
          /note="YPMT1.85, possible integrase, len: 392 aa; weakly
similar to INTA_ECOLI (EMBL:U03737), intA, Escherichia
coli prophage CP4-57 integrase (413 aa), fasta scores;
opt: 210 z-score: 255.3 E(): 6.4e-07, 22.1% identity in
263 aa overlap. Identical to ORF Y1101 (EMBL:AF074611)
from Y.pestis KIM5 pMT1 (392 aa) (99.7% identity in 392 aa
overlap). Contains probable coiled-coil from 434 to 465
(32 residues) (Max score: 1.490, probability 0.94).
Contains Pfam match to entry PF00589 Phage_integrase,
'Phage' integrase family, score 29.10, E-value 7.9e-07"
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          /db_xref="InterPro:IPR011010"
          /db_xref="InterPro:IPR013762"
          /db_xref="InterPro:IPR023109"
          /db_xref="UniProtKB/TrEMBL:Q7ARA9"
          /translation="MIIQKLMPNILFMHTVKRASLSEWTMKNTFDKARAAENTSREAL
EYLERASGLSAVSTANFDGDMSSFSAFMLFTRLSELLITRRRPEIAVHCVLIHVMPHIS
EVKVS DISRVLVNQLVNPLILEGKIVQGRRVFSLMKQFLSWCAFQGLIDTSPLNDSML

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TPMSKVAIAQALRRILERPELMDLEPFTPRDLRRTARSYFPALGINQEVARKIMNHS
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                  /note="Pfam match to entry PF00589 Phage_integrase,
'Phage' integrase family, score 29.10, E-value 7.9e-07"
gene              complement(88320..88706)
                  /gene="YPMT1.86c"
CDS               complement(88320..88706)
                  /gene="YPMT1.86c"
                  /note="YPMT1.86c, hypothetical protein, len: 128 aa;
unknown function, identical to ORF Y1102 (EMBL:AF074611)
from Y.pestis KIM5 pMT1 (128 aa), fasta scores; opt: 801
z-score: 1004.7 E(): 0, 100.0% identity in 128 aa overlap"
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gene              88969..89181
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CDS               88969..89181
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unknown function"
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/note="YPMT1.87, possible porphyrin biosynthetic protein,
len: 788 aa; weakly similar to COBT_PSEDE (EMBL:M62869),
cobT, Pseudomonas denitrificans cobalamin biosynthesis
protein (631 aa), fasta scores; opt: 279 z-score: 262.6
E(): 2.5e-07, 26.3% identity in 407 aa overlap. Identical
to cobT (EMBL:AF074611) from Y.pestis KIM5 pMT1 (788 aa)
(100.0% identity in 788 aa overlap) / TR:068772
(EMBL:AF053947) from Y.pestis KIM5 pMT1 (784 aa) (100.0%
identity in 784 aa overlap) which has a different putative
start codon"
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/db_xref="InterPro:IPR025861"
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KFFLCPVVRWDGQSPFIDFMEEHWHLIDKPVALLEHGDVAVRNMSTEDCVKVAA
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DDKEEQEDDASEEEDSGDSDLPSLDKDLPIHDKEISDTE SKYTEAGEDESGDTPESD
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ESEGEDEGEEDVADHTDGE GKENEDAAEAPEDSESGFVPAPDEMTLEDALKALDEMEE
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HGANLYRLAMNDDR VFRKKEDHRAVNACVQQVIDLSGSMGGRKIQLALASAYTIADAL
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CETFPLNNVDGESVAQLATLFA GRMEDKKIMLVMSDGAPCAAGDGFHEHLRTVTKEI
ETLSDIDLMAIGVLTDA PRYYKKNYALVNSVEELGPSVVTELSRIILG"

misc_feature      91670..91671
/note="difference: A is present in EMBL:AF053947 and in
EMBL:AF074611"

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/gene="YPMT1.88"

CDS               91754..92989
/gene="YPMT1.88"
/note="YPMT1.88, possible porphyrin biosynthetic protein,
len: 411 aa; weakly similar to COBS_PSEDE (EMBL:M62869),
cobS, Pseudomonas denitrificans cobalamin biosynthesis
protein (332 aa), fasta scores; opt: 384 z-score: 453.4

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E(): 6e-18 28.6% identity in 308 aa overlap. Identical to
cobS (EMBL:AF074611) from Y.pestis KIM5 pMT1 (411 aa)
(100.0% identity in 411 aa overlap) / TR:O68771
(EMBL:AF053947) from Y.pestis KIM5 pMT1 (411 aa) (100.0%
identity in 411 aa overlap). Contains PS00017
ATP/GTP-binding site motif A (P-loop)"
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                /note="PS00017 ATP/GTP-binding site motif A (P-loop)"

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                /pseudo

CDS             93170..96208
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len: 3039 bp; identical to the N-terminal region of
putative DNA polymerase III, alpha subunit, ORF Y1106
(EMBL:AF074611) from Y.pestis KIM5 pMT1 (1174 aa) /
TR:O68770 (EMBL:AF053947) from Y.pestis KIM5 pMT1 (1135
aa). YPMT1.56c is the C-terminus of the same gene"
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ORIGIN

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   121 tcctgcacaa gcagggaatg agtagccggg cgattgccag agaactgggg atctcccgca

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