


Microbial Genomes (NCBI)
(Genome information)

Microbial Genomes URL

← → ↻ www.ncbi.nlm.nih.gov/genomes/MICROBES/microbial_taxtree.html ☆ RSS

 **Microbial Genomes**

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Microbial Genomes Resources presents public data from prokaryotic genome sequencing projects. The sequence collection contains data from finished genomes as well as draft assemblies.

Microbial Genome Annotation Tools: We are pleased to announce the availability of [GeneMark](#) and [Glimmer](#), gene prediction tools for microbial genome annotation.

Genome Annotation Pipeline: NCBI has developed a pipeline for annotation of prokaryotic genomes. This service is available to all users by request. If interested, please send an email to [NCBI Genomes](#).

Submission Check Tool: Microbial genome submission check is for the validation of genome submissions to Genbank.

The Concise BLAST database allows for faster calculation times and a broader taxonomic view by eliminating similar proteins within a genus.

Prokaryotes are the earliest forms of life, appearing on earth 4 billion years ago. During the course of their evolution they have extensively altered the biology and chemistry of our planet. More advanced organisms developed as once free-living bacteria took up symbiotic residence inside other cells. These organisms eventually became the organelles found in modern eukaryotes. Energy-producing mitochondria and chloroplasts are examples of organelles in eukaryotic cells.

The **Prokaryotes** include the **Archaea**, which include inhabitants of some of the most extreme environments on the planet, and the **Bacteria**, which include both important pathogens and producers of fermented food, antibiotics, and vitamins.

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Find a genome



Genome Information by organism

- Yersinia
- Yersinia (taxid:629)
- Yersinia pestis (taxid:632) **Select in list**
- Yersinia pseudotuberculosis subsp. pestis (taxid:632)
- Yersinia enterocolitica (taxid:630)
- Yersinia pestis subsp. pestis (taxid:385964)
- Yersinia pseudotuberculosis (taxid:633)
- Yersinia enterocolitica subsp. palearctica (taxid:150053)
- Yersinia pestis subsp. pestis bv. Orientalis (taxid:1234661)
- Yersinia pestis subsp. pestis bv. Antiqua (taxid:1234660)
- Yersinia pestis KIM (taxid:187410)
- Yersinia pestis KIM10+ (taxid:187410)
- Yersinia pestis Nepal516 (taxid:377628)
- Yersinia enterocolitica subsp. enterocolitica (taxid:150052)
- Yersinia pestis subsp. pestis bv. Medievalis (taxid:1234662)
- Yersinia enterocolitica (type O:9) (taxid:34055)
- Yersinia enterocolitica type O:9 (taxid:34055)
- Yersinia philomiragia (taxid:28110)
- Yersinia ruckeri (taxid:29486)

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Viruses [4046] Plasmids [4980]

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SubGroup	Size (Mb)	Chr	Organelles	Plasmids	Assemblies
Mollicutes	0.739592	-	-	-	1
Nanoviridae	0.006422	6	-	-	1
unclassified	0.211518	1	-	-	1
unclassified	0.034952	1	-	-	1
Retroviridae	0.005894	1	-	-	1
Bacilli	2.04344	-	-	-	1
Geminiviridae	0.005271	2	-	-	1
Geminiviridae	0.005399	2	-	-	1

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Genome

Genome Information by organism

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Organism/Name	Kingdom	Group	SubGroup	Size (Mb)	Chr	Organelles	Plasmids	Assemblies
 Yersinia pestis	Bacteria	Proteobacteria	Gammaproteobacteria	5.32207	1	-	9	228

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Detailed Information

Organism Overview ; Genome Assembly and Annotation report [228] ; Genome Groups report [21] ; ID: 153
 Plasmid Annotation Report [47]



Yersinia pestis

Causative agent of plague

Nice!

Taxonomy

Lineage: Bacteria[4861]; Proteobacteria[1879]; Gammaproteobacteria[796]; Enterobacteriales[161]; Enterobacteriaceae[161]; Yersinia[14]; Yersinia pestis[1]

Yersinia. This genus consists of 11 species, 3 of which are human pathogens. Specific virulence factors are encoded within pathogenicity islands (PAIs) that are required for the invasive phenotype associated with Yersinia infections. These PAIs may be carried on extrachromosomal plasmids or on the chromosome. One key virulence plasmid [More...](#)

Sequence data: genome assemblies: 228; sequence reads: 7 (See [Genome Assembly and Annotation report](#))
 genome groups: 21 (See [Genome Groups report](#))

Publications

1. Sylvatic plague in a Canadian black-tailed prairie dog (*Cynomys ludovicianus*). Antonation KS, et al. J Wildl Dis 2014 Jul
2. Historical variations in mutation rate in an epidemic pathogen, *Yersinia pestis*. Cui Y, et al. Proc Natl Acad Sci U S A 2013 Jun 8
3. A strain of *Yersinia pestis* ... [More...](#)

Click Drop Down Menu for gene Annotations..etc.

Representative (genome information for reference and representative genomes)

Reference genome: (see all organisms)

Yersinia pestis CO93

Submitter: Panzer Institute

Accession: F010981

Morphology: Gram Negative, Shape Bacilli

Enviro: Inhab: C, Type: Facultative, Optimum Temperature: 28-30, Temperature Range: Mesophilic, Habitat: Multiple

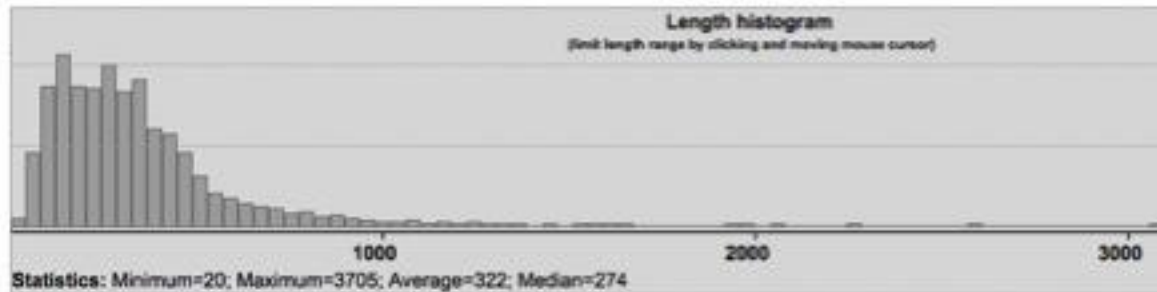
Phenotype: Disease: Bubonic plague

Table of Protein annotations

Type	Name	RefSeq	INSDC	Size (Mb)	GC%	Protein	rRNA	tRNA	Other RNA	Gene	Pseudogene
Chr	-	NC_003143.1	AL590842.1	4.65	47.6	3,708	19	70	14	4,012	112
Plasm	pPCP1	NC_003132.1	AL109969.1	0.009612	45.3	9	-	-	-	9	-
Plasm	pCD1	NC_003131.1	AL117189.1	0.070305	44.8	71	-	-	1	102	4
Plasm	pMT1	NC_003134.1	AL117211.1	0.09621	50.2	101	-	-	-	107	3

Search for particular protein sequences

Protein Details for *Yersinia pestis* CO92



Sequences: [chr](#) [pPCP1](#) [pCD1](#) [pMT1](#)

Search by locus, locus tag or protein name

toxin

Selected by toxin

Enter search term (points to text input)

Click (points to Search button)

Genbank File (points to Clear button)

Name	Accession	Start	Stop	Strand	GeneID	Locus	Locus tag	Protein product	Length
chr	NC_003143.1	1116620	1118110	-	1173840	-	YPO1002	YP_002346047.1	496
chr	NC_003143.1	2527832	2529970	+	1175083	-	YPO2252	YP_002347219.1	712
chr	NC_003143.1	2600645	2603269	+	1175144	-	YPO2312	YP_002347279.1	674
chr	NC_003143.1	2673209	2676163	-	1175212	sepC	YPO2380	YP_002347346.1	984
chr	NC_003143.1	4098633	4101491	-	1176494	-	YPO3673	YP_002348559.1	952
chr	NC_003143.1	4101516	4104551	-	1176495	-	YPO3674	YP_002348560.1	1011
chr	NC_003143.1	4105754	4110244	-	1176499	tcaC	YPO3676	YP_002348564.1	1496
chr	NC_003143.1	4113934	4116435	-	1176501	-	YPO3681	YP_002348565.1	833
pMT1	NC_003134.1	74447	76210	+	1172828	-	YPMT1.74	NP_395420.2	587