Resource Summary Report

Generated by dkNET on Apr 22, 2025

Bacterial Genomes

RRID:SCR_008141
Type: Tool

Proper Citation

Bacterial Genomes (RRID:SCR_008141)

Resource Information

URL: http://www.sanger.ac.uk/Projects/Microbes/

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Description: This website includes a list of projects that the Sanger Institute is currently working on or completed. All projects consist of the genomic sequencing of different bacteria. Each description of the bacteria includes its classification, a description, and the types of diseases that the bacteria is likely to cause. The Sanger Institute bacterial sequencing effort is concentrated on pathogens and model organisms. Data is accessible in a number of ways; for each organism there is a BLAST server, allowing users to search the sequences with their own query and retrieve the matching contigs. Sequences can also be downloaded directly by FTP. Data is accessible in a number of ways; for each organism there is a BLAST server, allowing you to search the sequences with your own query and retrieve the matching contigs. Sequences can also be downloaded directly by FTP. The primary sequence viewer and annotation tool, Artemis is available for download. This is a portable Java program which is used extensively within the Microbial Genomes group for the analysis and annotation of sequence data from cosmids to whole genomes. The Artemis Comparison Tool (ACT) is also useful for interactive viewing of the comparisons between large and small sequences.

Synonyms: Bacterial Genomes

Resource Type: data or information resource, data processing software, software application, data analysis software, database, software resource

Keywords: bacteria, bacterial, classification, description, disease, genomic, model, organism, pathogen, sequence, sequencing, model

Funding:

Resource Name: Bacterial Genomes

Resource ID: SCR_008141

Alternate IDs: nif-0000-20963

Record Creation Time: 20220129T080245+0000

Record Last Update: 20250421T053634+0000

Ratings and Alerts

No rating or validation information has been found for Bacterial Genomes.

No alerts have been found for Bacterial Genomes.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Mazandu GK, et al. (2011) Generation and Analysis of Large-Scale Data-Driven Mycobacterium tuberculosis Functional Networks for Drug Target Identification. Advances in bioinformatics, 2011, 801478.

Gu H, et al. (2009) Use of in vivo-induced antigen technology (IVIAT) for the identification of Streptococcus suis serotype 2 in vivo-induced bacterial protein antigens. BMC microbiology, 9, 201.

Badea L, et al. (2009) Secretion of flagellin by the LEE-encoded type III secretion system of enteropathogenic Escherichia coli. BMC microbiology, 9, 30.

Sim E, et al. (2008) Arylamine N-acetyltransferases in mycobacteria. Current drug metabolism, 9(6), 510.

Le Bourgeois P, et al. (2007) The unconventional Xer recombination machinery of Streptococci/Lactococci. PLoS genetics, 3(7), e117.

Chen Z, et al. (2006) Comparative analysis of tandem T7-like promoter containing regions in enterobacterial genomes reveals a novel group of genetic islands. Nucleic acids research, 34(4), 1133.

Wu H, et al. (2005) Prediction of functional modules based on comparative genome analysis and Gene Ontology application. Nucleic acids research, 33(9), 2822.

Delihas N, et al. (2003) Annotation and evolutionary relationships of a small regulatory RNA gene micF and its target ompF in Yersinia species. BMC microbiology, 3, 13.

Moran NA, et al. (2001) The process of genome shrinkage in the obligate symbiont Buchnera aphidicola. Genome biology, 2(12), RESEARCH0054.

Le Flèche P, et al. (2001) A tandem repeats database for bacterial genomes: application to the genotyping of Yersinia pestis and Bacillus anthracis. BMC microbiology, 1, 2.

Durell SR, et al. (2001) A family of putative Kir potassium channels in prokaryotes. BMC evolutionary biology, 1, 14.

Hoiczyk E, et al. (2000) Structure and sequence analysis of Yersinia YadA and Moraxella UspAs reveal a novel class of adhesins. The EMBO journal, 19(22), 5989.