Resource Summary Report

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JCVI CMR

RRID:SCR_005398
Type: Tool

Proper Citation

JCVI CMR (RRID:SCR_005398)

Resource Information

URL: http://cmr.jcvi.org/tigr-scripts/CMR/CmrHomePage.cgi

Proper Citation: JCVI CMR (RRID:SCR_005398)

Description: Database of all of the publicly available, complete prokaryotic genomes. In addition to having all of the organisms on a single website, common data types across all genomes in the CMR make searches more meaningful, and cross genome analysis highlight differences and similarities between the genomes. CMR offers a wide variety of tools and resources, all of which are available off of our menu bar at the top of each page. Below is an explanation and link for each of these menu options. * Genome Tools: Find organism lists as well as summary information and analyses for selected genomes. * Searches: Search CMR for genes, genomes, sequence regions, and evidence. * Comparative Tools: Compare multiple genomes based on a variety of criteria, including sequence homology and gene attributes. SNP data is also found under this menu. * Lists: Select and download gene, evidence, and genomic element lists. * Downloads: Download gene sequences or attributes for CMR organisms, or go to our FTP site. * Carts: Select genome preferences from our Genome Cart or download your Gene Cart genes. The Omniome is the relational database underlying the CMR and it holds all of the annotation for each of the CMR genomes, including DNA sequences, proteins, RNA genes and many other types of features. Associated with each of these DNA features in the Omniome are the feature coordinates, nucleotide and protein sequences (where appropriate), and the DNA molecule and organism with which the feature is associated. Also available are evidence types associated with annotation such as HMMs, BLAST, InterPro, COG, and Prosite, as well as individual gene attributes. In addition, the database stores identifiers from other centers such as GenBank and SwissProt, as well as manually curated information on each genome or each DNA molecule including website links. Also stored in the Omniome are precomputed homology data, called All vs All searches, used throughout the CMR for comparative analysis.

Abbreviations: JCVI_CMR, JCVI CMR, TIGR_CMR, TIGR CMR

Synonyms: JCVI Comprehensive Microbial Resource, J. Craig Venter Institute Comprehensive Microbial Resource, CMR, Comprehensive Microbial Resource

Resource Type: analysis service resource, production service resource, database, data or information resource, service resource, data analysis service

Keywords: microbial, prokaryotic, genome, annotation, dna sequence, protein, rna gene, blast, FASEB list

Funding: NSF ;
NIAID ;
DOE

Availability: Free

Resource Name: JCVI CMR

Resource ID: SCR_005398

Alternate IDs: nif-0000-03555

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250522T060235+0000

Ratings and Alerts

No rating or validation information has been found for JCVI CMR.

No alerts have been found for JCVI CMR.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 37 mentions in open access literature.

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

Mughal SR, et al. (2023) Genomic Diversity among Actinomyces naeslundii Strains and Closely Related Species. Microorganisms, 11(2).

Borisova M, et al. (2017) The N-Acetylmuramic Acid 6-Phosphate Phosphatase MupP Completes the Pseudomonas Peptidoglycan Recycling Pathway Leading to Intrinsic Fosfomycin Resistance. mBio, 8(2).

Ehebauer MT, et al. (2015) Characterization of the mycobacterial acyl-CoA carboxylase holo complexes reveals their functional expansion into amino acid catabolism. PLoS pathogens, 11(2), e1004623.

Slocum C, et al. (2014) Distinct lipid a moieties contribute to pathogen-induced site-specific vascular inflammation. PLoS pathogens, 10(7), e1004215.

P?oci?ski P, et al. (2014) Identification of protein partners in mycobacteria using a single-step affinity purification method. PloS one, 9(3), e91380.

Ramachandran VK, et al. (2014) The primary transcriptome of Salmonella enterica Serovar Typhimurium and its dependence on ppGpp during late stationary phase. PloS one, 9(3), e92690.

Zhang L, et al. (2014) The core proteome and pan proteome of Salmonella Paratyphi A epidemic strains. PloS one, 9(2), e89197.

Patton DL, et al. (2014) Whole genome identification of C. trachomatis immunodominant antigens after genital tract infections and effect of antibiotic treatment of pigtailed macaques. Journal of proteomics, 108, 99.

Fuchs S, et al. (2013) Aureolib - a proteome signature library: towards an understanding of staphylococcus aureus pathophysiology. PloS one, 8(8), e70669.

Charles RC, et al. (2013) Identification of immunogenic Salmonella enterica serotype Typhi antigens expressed in chronic biliary carriers of S. Typhi in Kathmandu, Nepal. PLoS neglected tropical diseases, 7(8), e2335.

Mahdavi J, et al. (2013) Pro-inflammatory cytokines can act as intracellular modulators of commensal bacterial virulence. Open biology, 3(10), 130048.

Ramachandran VK, et al. (2012) The architecture and ppGpp-dependent expression of the primary transcriptome of Salmonella Typhimurium during invasion gene expression. BMC genomics, 13, 25.

Zheng LL, et al. (2012) A comparison of computational methods for identifying virulence factors. PloS one, 7(8), e42517.

Phillips NJ, et al. (2012) Proteomic analysis of Neisseria gonorrhoeae biofilms shows shift to anaerobic respiration and changes in nutrient transport and outermembrane proteins. PloS one, 7(6), e38303.

Ricker N, et al. (2012) The limitations of draft assemblies for understanding prokaryotic adaptation and evolution. Genomics, 100(3), 167.

Arnvig K, et al. (2012) Non-coding RNA and its potential role in Mycobacterium tuberculosis pathogenesis. RNA biology, 9(4), 427.

Sycuro LK, et al. (2012) Multiple peptidoglycan modification networks modulate Helicobacter pylori's cell shape, motility, and colonization potential. PLoS pathogens, 8(3), e1002603.

Reichlen MJ, et al. (2012) MreA functions in the global regulation of methanogenic pathways in Methanosarcina acetivorans. mBio, 3(4), e00189.

Campanaro S, et al. (2012) The transcriptional landscape of the deep-sea bacterium Photobacterium profundum in both a toxR mutant and its parental strain. BMC genomics, 13, 567.

Cheng C, et al. (2012) Genome-wide analysis of the Pho regulon in a pstCA mutant of Citrobacter rodentium. PloS one, 7(11), e50682.