

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, data analysis service, data or information resource, database, production service resource, service resource

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: 20261017T203133+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 have not found any literature mentions for this resource.