Resource Summary Report

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Neisseria meningitidis MC58 Genome Page

RRID:SCR_002200
Type: Tool

Proper Citation

Neisseria meningitidis MC58 Genome Page (RRID:SCR_002200)

Resource Information

URL: http://microbes.ucsc.edu/cgi-bin/hgGateway?db=neisMeni_MC58_1

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Description: Portal contains detailed information for Neisseria meningitidis MC58. Information include DNA molecule summary, primary annotation summary, and taxonomy. It is a tool that allows the researcher to access all of the bacterial genome sequences completed to date. Users may access information on all of the bacterial genomes or any subset of them. Information in the website about its DNA molecule includes: total number of DNA molecules, total size of all DNA molecules, number of primary annotation coding bases, and number of G + C bases. Its primary annotation summary include: total genes, protein coding genes, tRNA genes, and rRNA genes. Sponsors: The CMR was previously funded by two grants, one from the U.S. Department of Energy (DOE) and one from the National Science Foundation (NSF). It is currently partially funded by a Microbial Sequence Center (MSC) grant from the National Institute of Allergy and Infectious Diseases (NIAID)

Synonyms: NMMGP

Resource Type: topical portal, data or information resource, database, portal

Keywords: gene, annotation, bacterial, coding, dna, genome, mc58, molecule, neisseria meningitidis, protein, rrna, taxonomy, trna

Availability: Free, Freely available

Resource Name: Neisseria meningitidis MC58 Genome Page

Resource ID: SCR_002200

Alternate IDs: nif-0000-20964

Old URLs: http://cmr.jcvi.org/tigr-scripts/CMR/GenomePage.cgi?database=gnm

Record Creation Time: 20220129T080212+0000

Record Last Update: 20260731T042628+0000

Ratings and Alerts

No rating or validation information has been found for Neisseria meningitidis MC58 Genome Page.

No alerts have been found for Neisseria meningitidis MC58 Genome Page.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 1 mentions in open access literature.

Listed below are recent publications. The full list is available at kravitz2 .

Ampattu BJ, et al. (2017) Transcriptomic buffering of cryptic genetic variation contributes to meningococcal virulence. BMC genomics, 18(1), 282.