Resource Summary Report

Generated by NIF on May 20, 2025

CCUG: Culture Collection; University of Goteborg; Sweden

RRID:SCR_006635
Type: Tool

Proper Citation

CCUG: Culture Collection; University of Goteborg; Sweden (RRID:SCR_006635)

Resource Information

URL: http://www.ccug.se/

Proper Citation: CCUG: Culture Collection; University of Goteborg; Sweden (RRID:SCR_006635)

Description: The CCUG holds a broad range of bacteria and the most demanded test strains of filamentous fungi and yeasts. We do not hold extremophils or intracellular organisms and we do not distribute hazard group 3 organisms. Cultures are freeze-dried and may be sent abroad promptly under controlled forms. Our identification service has been active for 43 years. CCUG has huge databases and they are pleased to share the information with you through their search engine.

Abbreviations: CCUG

Synonyms: Culture Collection, CCUG: Culture Collection; University of Gothenburg; Sweden, CCUG: Culture Collection

Resource Type: material resource, biomaterial supply resource

Keywords: bacteria, microorganisms, strains, taxonomic literature, fatty acids, sequences, 16 s rrna

Funding:

Resource Name: CCUG: Culture Collection; University of Goteborg; Sweden

Resource ID: SCR_006635

Alternate IDs: nif-0000-30239

Record Creation Time: 20220129T080237+0000

Record Last Update: 20250519T204918+0000

Ratings and Alerts

No rating or validation information has been found for CCUG: Culture Collection; University of Goteborg; Sweden.

No alerts have been found for CCUG: Culture Collection; University of Goteborg; Sweden.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 29 mentions in open access literature.

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

Srivastava A, et al. (2024) Draft genome sequence of Halobacillus campisalis strain ASL-17. Microbiology resource announcements, 13(2), e0069223.

Unitt A, et al. (2024) Characterizing the diversity and commensal origins of penA mosaicism in the genus Neisseria. Microbial genomics, 10(2).

Chen X, et al. (2023) Comparative Genomic Analysis Reveals Genetic Diversity and Pathogenic Potential of Haemophilus seminalis and Emended Description of Haemophilus seminalis. Microbiology spectrum, 11(4), e0477222.

Jaén-Luchoro D, et al. (2023) Knockout of Targeted Plasmid-Borne ?-Lactamase Genes in an Extended-Spectrum-?-Lactamase-Producing Escherichia coli Strain: Impact on Resistance and Proteomic Profile. Microbiology spectrum, 11(1), e0386722.

Marathe NP, et al. (2022) Novel Plasmid Carrying Mobile Colistin Resistance Gene mcr-4.3 and Mercury Resistance Genes in Shewanella baltica: Insights into Mobilization of mcr-4.3 in Shewanella Species. Microbiology spectrum, 10(6), e0203722.

Grevskott DH, et al. (2020) Nanopore sequencing reveals genomic map of CTX-M-type extended-spectrum ?-lactamases carried by Escherichia coli strains isolated from blue mussels (Mytilus edulis) in Norway. BMC microbiology, 20(1), 134.

Karlsson R, et al. (2020) Discovery of Species-unique Peptide Biomarkers of Bacterial

Pathogens by Tandem Mass Spectrometry-based Proteotyping. Molecular & cellular proteomics : MCP, 19(3), 518.

Tevell S, et al. (2020) Presence of the neonatal Staphylococcus capitis outbreak clone (NRCS-A) in prosthetic joint infections. Scientific reports, 10(1), 22389.

Moran A, et al. (2020) What works, why and how? A scoping review and logic model of rural clinical placements for allied health students. BMC health services research, 20(1), 866.

Williams G, et al. (2019) First report of infection with Pseudomonas citronellolis: a case of urosepsis. New microbes and new infections, 30, 100531.

Jin T, et al. (2019) A novel mouse model for septic arthritis induced by Pseudomonas aeruginosa. Scientific reports, 9(1), 16868.

Forster SC, et al. (2019) A human gut bacterial genome and culture collection for improved metagenomic analyses. Nature biotechnology, 37(2), 186.

Foster G, et al. (2019) Forensic microbiology reveals that Neisseria animaloris infections in harbour porpoises follow traumatic injuries by grey seals. Scientific reports, 9(1), 14338.

Brüggemann H, et al. (2018) Pan-genome analysis of the genus Finegoldia identifies two distinct clades, strain-specific heterogeneity, and putative virulence factors. Scientific reports, 8(1), 266.

Lindgren Å, et al. (2018) Development of a rapid MALDI-TOF MS based epidemiological screening method using MRSA as a model organism. European journal of clinical microbiology & infectious diseases : official publication of the European Society of Clinical Microbiology, 37(1), 57.

Karlsson R, et al. (2018) Proteotyping bacteria: Characterization, differentiation and identification of pneumococcus and other species within the Mitis Group of the genus Streptococcus by tandem mass spectrometry proteomics. PloS one, 13(12), e0208804.

Thofte O, et al. (2018) EF-Tu From Non-typeable Haemophilus influenzae Is an Immunogenic Surface-Exposed Protein Targeted by Bactericidal Antibodies. Frontiers in immunology, 9, 2910.

Carkaci D, et al. (2017) Genomic characterization, phylogenetic analysis, and identification of virulence factors in Aerococcus sanguinicola and Aerococcus urinae strains isolated from infection episodes. Microbial pathogenesis, 112, 327.

Aguilar-Ayala DA, et al. (2017) In vitro activity of bedaquiline against rapidly growing nontuberculous mycobacteria. Journal of medical microbiology, 66(8), 1140.

Johnning A, et al. (2016) Draft Genome Sequence of Extended-Spectrum-?-Lactamase-Producing Escherichia coli Strain CCUG 62462, Isolated from a Urine Sample. Genome announcements, 4(6).