

Resource Summary Report

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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: biomaterial supply resource, material resource

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

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: 20260919T195753+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 43 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Sokol D, et al. (2026) Metabolic interactions between bacterial co-isolates from catheter-associated urinary tract infections. *Scientific reports*, 16(1), 2061.

Golparian D, et al. (2026) Complete reference genomes of *Haemophilus ducreyi* isolates ITG3105, CIP76118, and TMA3542, using Oxford Nanopore and Illumina sequencing. *Microbiology resource announcements*, 15(6), e0142525.

Winterflood DM, et al. (2026) Whole-genome sequence analyses reveal cryptic species-level diversity among clinical *Actinotignum* isolates misidentified by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry. *Microbiology spectrum*, 14(4), e0219025.

Hamidi H, et al. (2026) High-resolution differentiation and identification of the clinically relevant pathogens *Haemophilus influenzae* and *Haemophilus aegyptius*: combined whole-cell MALDI-TOF MS and nano-LC-MS/MS proteotyping for defining protein biomarkers. *Microbiology spectrum*, 14(5), e0354225.

Yunda E, et al. (2026) Probing biofilm development, stress response and heterogeneity-spectroscopic characterization of single and multi-species consortia. *NPJ biofilms and microbiomes*, 12(1).

Jin C, et al. (2025) Seal milk oligosaccharides rival human milk complexity and exhibit functional dynamics during lactation. *Nature communications*, 16(1), 10067.

Qu T, et al. (2025) Laser-assisted microbial culturomics. *Nature communications*, 16(1), 10614.

Bachus A, et al. (2025) Pathogenicity of *Arcobacter cryaerophilus* in two human intestinal cell lines. *Gut pathogens*, 17(1), 48.

Sawada H, et al. (2025) *Afipia dichlorophenoxyacetatis* sp. nov., isolated from field soil in Japan, degrades 2,4-dichlorophenoxyacetic acid. *International journal of systematic and evolutionary microbiology*, 75(2).

Salvà-Serra F, et al. (2025) Description of *Pseudomonas imrae* sp. nov., carrying a novel class C β -lactamase gene variant, isolated from gut samples of Atlantic mackerel (*Scomber scombrus*). *Frontiers in microbiology*, 16, 1530878.

Svetlicic E, et al. (2025) Mass Spectrometry-Based Analysis of Surface Proteins in *Staphylococcus aureus* Clinical Strains: Identification of Promising k-mer Targets for Diagnostics. *Journal of proteome research*, 24(9), 4575.

Lin Y, et al. (2024) A case report of *Pseudomonas citronellolis* and *Escherichia coli* isolated from acute suppurative appendicitis: reveals the potential intestinal colonization and pathogenicity of *Pseudomonas citronellolis*. *Frontiers in cellular and infection microbiology*, 14, 1280188.

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

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

Buzzanca D, et al. (2023) *Arcobacteraceae* comparative genome analysis demonstrates genome heterogeneity and reduction in species isolated from animals and associated with human illness. *Heliyon*, 9(7), e17652.

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

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.

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.

Salvà-Serra F, et al. (2022) Responses of carbapenemase-producing and non-producing carbapenem-resistant *Pseudomonas aeruginosa* strains to meropenem revealed by quantitative tandem mass spectrometry proteomics. *Frontiers in microbiology*, 13, 1089140.

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