

Resource Summary Report

Generated by T1D on Sep 5, 2026

SuperCAT

RRID:SCR_004882

Type: Tool

Proper Citation

SuperCAT (RRID:SCR_004882)

Resource Information

URL: <http://mlstoslo.uio.no/>

Proper Citation: SuperCAT (RRID:SCR_004882)

Description: THIS RESOURCE IS NO LONGER IN SERVICE. Documented on January 11,2023. SuperCAT hosts typing databases for the Bacillus cereus group of bacteria. The databases contain MultiLocus Sequence Typing (MLST), MultiLocus Enzyme Electrophoresis (MLEE), and Amplified Fragment Length Polymorphism (AFLP) phylogenetic data. multilocus, sequence, Bacillus cereus, bacteria, Genomics, non-vertebrate, taxonomy, identification

Synonyms: SuperCAT

Resource Type: data or information resource, database

Defining Citation: [PMID:29568820](#), [PMID:20651034](#)

Keywords: bacillus cereus, bacteria, genomics, identification, multilocus, non-vertebrate, sequence, taxonomy

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: SuperCAT

Resource ID: SCR_004882

Alternate IDs: nif-0000-03509

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260904T000153+0000

Ratings and Alerts

No rating or validation information has been found for SuperCAT.

No alerts have been found for SuperCAT.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 15 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Bianco A, et al. (2020) Characterization of *Bacillus cereus* Group Isolates From Human Bacteremia by Whole-Genome Sequencing. *Frontiers in microbiology*, 11, 599524.

Liu C, et al. (2020) Assessment and molecular characterization of *Bacillus cereus* isolated from edible fungi in China. *BMC microbiology*, 20(1), 310.

Finke S, et al. (2019) *Bacillus thuringiensis* CbpA is a collagen binding cell surface protein under c-di-GMP control. *Cell surface (Amsterdam, Netherlands)*, 5, 100032.

Carter L, et al. (2018) Analysis of enterotoxigenic *Bacillus cereus* strains from dried foods using whole genome sequencing, multi-locus sequence analysis and toxin gene prevalence and distribution using endpoint PCR analysis. *International journal of food microbiology*, 284, 31.

Carter L, et al. (2017) Draft Genome Sequences of Enterotoxigenic *Bacillus cereus* Strains Obtained from Powdered Infant Formula. *Genome announcements*, 5(8).

Raymond B, et al. (2017) In defense of *Bacillus thuringiensis*, the safest and most successful microbial insecticide available to humanity - a response to EFSA. *FEMS microbiology ecology*, 93(7).

Fiedoruk K, et al. (2017) Genetic Environment of *cry1* Genes Indicates Their Common Origin. *Genome biology and evolution*, 9(9), 2265.

Liu Y, et al. (2017) Genetic diversity and population structure of the *Bacillus cereus* group bacteria from diverse marine environments. *Scientific reports*, 7(1), 689.

Blackburn MB, et al. (2014) Crystalliferous *Bacillus cereus* group bacteria from a Maryland hardwood forest are dominated by psychrotolerant strains. *MicrobiologyOpen*, 3(4), 578.

Blackburn MB, et al. (2013) Phylogenetic distribution of phenotypic traits in *Bacillus thuringiensis* determined by multilocus sequence analysis. *PloS one*, 8(6), e66061.

Agren J, et al. (2012) Gegenees: fragmented alignment of multiple genomes for determining phylogenomic distances and genetic signatures unique for specified target groups. *PloS one*, 7(6), e39107.

Tourasse NJ, et al. (2011) Diversity, mobility, and structural and functional evolution of group II introns carrying an unusual 3' extension. BMC research notes, 4, 564.

Enersen M, et al. (2011) Porphyromonas gingivalis: a clonal pathogen?: Diversities in housekeeping genes and the major fimbriae gene. Journal of oral microbiology, 3.

Tourasse NJ, et al. (2010) HyperCAT: an extension of the SuperCAT database for global multi-scheme and multi-datatype phylogenetic analysis of the Bacillus cereus group population. Database : the journal of biological databases and curation, 2010, baq017.

Fagerlund A, et al. (2007) Toxin production in a rare and genetically remote cluster of strains of the Bacillus cereus group. BMC microbiology, 7, 43.