

Resource Summary Report

Generated by T1D on Jul 31, 2026

ICEberg

RRID:SCR_006026

Type: Tool

Proper Citation

ICEberg (RRID:SCR_006026)

Resource Information

URL: <http://db-mml.sjtu.edu.cn/ICEberg/>

Proper Citation: ICEberg (RRID:SCR_006026)

Description: ICEberg is an integrated database that provides comprehensive information about integrative and conjugative elements (ICEs) found in bacteria. ICEs are conjugative self-transmissible elements that can integrate into and excise from a host chromosome. An ICE contains three typical modules, integration and excision, conjugation, and regulation modules, that collectively promote vertical inheritance and periodic lateral gene flow. Many ICEs carry likely virulence determinants, antibiotic-resistant factors and/or genes coding for other beneficial traits. ICEberg offers a unique, highly organized, readily explorable archive of both predicted and experimentally supported ICE-relevant data. It currently contains details of 428 ICEs found in representatives of 124 bacterial species, and a collection of >400 directly related references. A broad range of similarity search, sequence alignment, genome context browser, phylogenetic and other functional analysis tools are readily accessible via ICEberg. ICEberg will facilitate efficient, multidisciplinary and innovative exploration of bacterial ICEs and be of particular interest to researchers in the broad fields of prokaryotic evolution, pathogenesis, biotechnology and metabolism. The ICEberg database will be maintained, updated and improved regularly to ensure its ongoing maximum utility to the research community.

Abbreviations: ICEberg

Synonyms: ICEberg: a web-based resource for integrative and conjugative elements found in Bacteria

Resource Type: service resource, data analysis service, data or information resource, database, production service resource, analysis service resource

Defining Citation: [PMID:22009673](#)

Keywords: dna, protein, sequence, chromosome, element, gene, similarity search, sequence alignment, genome, phylogenetic, functional analysis, bio.tools, FASEB list

Funding: National Natural Science Foundation of China 973 program 2009CB118901;
National Natural Science Foundation of China 973 program 2012CB721002;
National Natural Science Foundation of China 863 program 2011BAD23B05-3;
Ministry of Science and Technology China ;
Ministry of Education China NCET-10-0572;
Shanghai Jiaotong University ;
Shanghai Municipality ;
Action Medical Research SP4255;
Innovation Fellowship ;
East Midlands Development Agency

Resource Name: ICEberg

Resource ID: SCR_006026

Alternate IDs: nlx_151424, biotools:iceberg

Alternate URLs: <https://bio.tools/iceberg>

Record Creation Time: 20220129T080233+0000

Record Last Update: 20260731T042717+0000

Ratings and Alerts

No rating or validation information has been found for ICEberg.

No alerts have been found for ICEberg.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 77 mentions in open access literature.

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

Loo RTJ, et al. (2025) Interpretable Machine Learning for Cross-Cohort Prediction of Motor Fluctuations in Parkinson's Disease. *Movement disorders : official journal of the Movement Disorder Society*, 40(8), 1604.

Soto-Serrano A, et al. (2025) "Expanding the Lactococcal Cell Wall Polysaccharide Paradigm: Novel Structures and Metabolic Pathways in the Emerging Dairy Species *Pseudolactococcus laudensis* and *Pseudolactococcus raffinolactis*". *MicrobiologyOpen*, 14(6), e70133.

Krutova M, et al. (2025) Genomic islands and molecular mechanisms relating to drug-resistance in *Clostridioides (Clostridium) difficile* PCR ribotype 176. *Emerging microbes &*

infections, 14(1), 2482698.

Bellotti G, et al. (2025) Comprehensive genome-wide analysis for the safety assessment of microbial biostimulants in agricultural applications. *Microbial genomics*, 11(4).

De Maayer P, et al. (2025) Pan-genome analysis of the *Enterobacter hormaechei* complex highlights its genomic flexibility and pertinence as a multidrug resistant pathogen. *BMC genomics*, 26(1), 408.

Filali Razzouki A, et al. (2025) Explaining facial action units' correlation with hypomimia and clinical scores in Parkinson's disease. *NPJ Parkinson's disease*, 11(1), 53.

Pan T, et al. (2025) Mobile genetic elements in *Klebsiella pneumoniae*. *Journal of bacteriology*, 207(5), e0001225.

Li Y, et al. (2025) Population Genomics, Virulence Traits, and Antimicrobial Resistance of *Streptococcus suis* Isolated in China. *Microorganisms*, 13(6).

Stefan M, et al. (2025) Recurrence following invasive GAS infections in adults: Triumph of virulence or failure of immunity? *Virulence*, 16(1), 2563765.

Pérez-García C, et al. (2025) The rise of serotype 8 is associated with lineages and mutations in the capsular operon with different potential to produce invasive pneumococcal disease. *Emerging microbes & infections*, 14(1), 2521845.

Zheng L, et al. (2024) Comparative genomics of Tn6411 transposons carrying the blaIMP-1 gene in *Pseudomonas aeruginosa*. *PloS one*, 19(7), e0306442.

Contarin R, et al. (2024) The interplay between mobilome and resistome in *Staphylococcus aureus*. *mBio*, 15(10), e0242824.

Zhou N, et al. (2024) Metagenomic insights into the resistome, mobilome, and virulome of dogs with diverse lifestyles. *Animal microbiome*, 6(1), 76.

Slizovskiy IB, et al. (2024) Factors impacting target-enriched long-read sequencing of resistomes and mobilomes. *Genome research*, 34(11), 2048.

Li X, et al. (2024) Population genetic analysis of clinical *Mycobacterium abscessus* complex strains in China. *Frontiers in cellular and infection microbiology*, 14, 1496896.

Cataldo PG, et al. (2024) Comprehensive characterization of γ -aminobutyric acid (GABA) production by *Levilactobacillus brevis* CRL 2013: insights from physiology, genomics, and proteomics. *Frontiers in microbiology*, 15, 1408624.

Roy Chowdhury P, et al. (2024) Identification and evolution of ICE-PmuST394: a novel integrative conjugative element in *Pasteurella multocida* ST394. *The Journal of antimicrobial chemotherapy*, 79(4), 851.

Carneiro DG, et al. (2024) Genome sequencing and analysis of *Salmonella enterica* subsp. *enterica* serotype Enteritidis PT4 578: insights into pathogenicity and virulence. *Access microbiology*, 6(11).

Ayyappan MV, et al. (2024) Emergence of multidrug resistant, ctx negative seventh pandemic *Vibrio cholerae* O1 El Tor sequence type (ST) 69 in coastal water of Kerala, India. *Scientific reports*, 14(1), 2031.

Uruén C, et al. (2023) Invasive *Streptococcus suis* isolated in Spain contain a highly promiscuous and dynamic resistome. *Frontiers in cellular and infection microbiology*, 13, 1329632.