

Resource Summary Report

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ICEberg

RRID:SCR_006026

Type: Tool

Proper Citation

ICEberg (RRID:SCR_006026)

Resource Information

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

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

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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: 20260905T132546+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 89 mentions in open access literature.

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

de Almeida LN, et al. (2026) Comparative genomic analyses reveal key traits for biocontrol and the promotion of plant growth in *Paenibacillus* strains. *World journal of microbiology & biotechnology*, 42(3).

Rodriguez S, et al. (2026) Genomic plasticity and mobilome architecture of *Vibrio europaeus* reveal key mechanisms of evolutionary adaptation. *Microbial genomics*, 12(1).

Hassan F, et al. (2026) Genomic analysis identifies candidate SOS-associated and EPS/envelope-remodeling islands in a drinking-water *Stenotrophomonas maltophilia* complex isolate. *Scientific reports*, 16(1).

Tao J, et al. (2026) Identification of a novel SXT/R391 integrative and conjugative element harboring bla NDM-1 in a clinical *Providencia huaxiensis* isolate. *Frontiers in microbiology*, 17, 1818759.

Luo R, et al. (2026) Pan-genomic insights into resistance, virulence, and stress adaptation in *Clostridium perfringens* from the Tibetan Plateau. *mSphere*, 11(5), e0079225.

Tran E, et al. (2026) Ecological context structures duplication and mobilization of antibiotic and metal resistance genes in bacteria. *bioRxiv* : the preprint server for biology.

Zajmi A, et al. (2026) Identification of novel prophages and variants of integrative and conjugative elements in *Elizabethkingia anophelis* clinical isolates from Seremban, Malaysia. *BMC microbiology*, 26(1).

Bongulto K, et al. (2026) Nested mobile genetic elements mediating antimicrobial resistance genes mobility within and between *Acinetobacter* isolates. *iScience*, 29(5), 115648.

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.

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.

Zheng L, et al. (2025) Genomic features and fitness cost of co-existence of bla KPC-2 and bla VIM-2 plasmids in ICU-derived pan-drug resistant *Pseudomonas aeruginosa*. *Frontiers in cellular and infection microbiology*, 15, 1617614.

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.

Vezina B, et al. (2025) The rise and global spread of IMP carbapenemases (1996-2023): a genomic epidemiology study. *Nature communications*, 17(1), 183.

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

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.

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

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.

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

Slizovskiy IB, et al. (2025) Reducing skin microbiome exposure impacts through swine farm biosecurity. *GigaScience*, 14.

Perez-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.