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, production service resource, service resource, database, data or information 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: 20250407T215559+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 66 mentions in open access literature.

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

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.

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.

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.

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

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.

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).

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Huang J, et al. (2023) Emergence of Tigecycline and Carbapenem-Resistant Citrobacter freundii Co-Carrying tmexCD1-toprJ1, blaKPC-2, and blaNDM-1 from a Sepsis Patient. Infection and drug resistance, 16, 5855.

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Forster SC, et al. (2022) Strain-level characterization of broad host range mobile genetic elements transferring antibiotic resistance from the human microbiome. Nature communications, 13(1), 1445.

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Gluck-Thaler E, et al. (2022) Giant Starship Elements Mobilize Accessory Genes in Fungal Genomes. Molecular biology and evolution, 39(5).

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Cave R, et al. (2022) An Emerging Lineage of Uropathogenic Extended Spectrum ?-Lactamase Escherichia coli ST127. Microbiology spectrum, 10(6), e0251122.

Wheatley RM, et al. (2021) CRISPR-Cas systems restrict horizontal gene transfer in Pseudomonas aeruginosa. The ISME journal, 15(5), 1420.

Mbanga J, et al. (2021) Genomic Analysis of Enterococcus spp. Isolated From a Wastewater Treatment Plant and Its Associated Waters in Umgungundlovu District, South Africa. Frontiers in microbiology, 12, 648454.

Camarillo-Guerrero LF, et al. (2021) Massive expansion of human gut bacteriophage diversity. Cell, 184(4), 1098.