Resource Summary Report

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ISFinder

RRID:SCR_003020
Type: Tool

Proper Citation

ISFinder (RRID:SCR_003020)

Resource Information

URL: http://www-is.biotoul.fr

Proper Citation: ISFinder (RRID:SCR_003020)

Description: Database of a list of insertion sequences isolated from eubacteria and archaea. It is organized into individual files containing their general features (name, size, origin, family.....) as well as their DNA and potential protein sequences. Although most of the entries have been identified as individual elements, a growing number are included from their description in sequenced bacterial genomes. The search engine permits the retrieval and display of individual and groups of ISs based on a combination of their general features. Two levels of search are available. The simple search option enables the user to sort elements using a limited number of basic items whereas the extensive search offers an additional set of possibilities such as comparisons of the sequences of terminal inverted repeats and a variety of different layout displays. Built in links are provided to: the EMBL sequence database, the NCBI taxonomy database and to the ESF plasmid database. At present, only individual sequences can be downloaded one by one for comparison. An on-line BLAST facility is available and in future versions direct access to additional analytical tools will be provided on line. Direct submission of ISs is encouraged using the on-line form provided.

Abbreviations: ISFinder

Synonyms: IS Finder, Isfinder

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

Defining Citation: PMID:22367867, PMID:19906702

Keywords: insertion sequence, insertion, sequence, blast, dna, protein sequence, bio.tools, FASEB list

Funding: CNRS

Resource Name: ISFinder

Resource ID: SCR_003020

Alternate IDs: biotools:isfinder, nif-0000-03050

Alternate URLs: https://bio.tools/isfinder

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250501T080535+0000

Ratings and Alerts

No rating or validation information has been found for ISFinder.

No alerts have been found for ISFinder.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 945 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Hirabayashi A, et al. (2025) Emergence of the mobile RND-type efflux pump gene cluster tmexCD1-toprJ1 in Klebsiella pneumoniae clinical isolates in Japan. The Journal of antimicrobial chemotherapy, 80(1), 192.

Liu F, et al. (2025) Uneven distribution of prokaryote-derived horizontal gene transfer in fungi: a lifestyle-dependent phenomenon. mBio, 16(1), e0285524.

Haenni M, et al. (2025) Distinct molecular epidemiology of resistances to extended-spectrum cephalosporins and carbapenems in Enterobacter hormaechei in cats and dogs versus horses in France. The Journal of antimicrobial chemotherapy, 80(2), 567.

Alcántara C, et al. (2025) Holzapfeliella saturejae sp. nov. isolated from flowers of winter savoury Satureja montana L. International journal of systematic and evolutionary

microbiology, 75(1).

Li J, et al. (2025) "Sichuanvirus", a novel bacteriophage viral genus, able to lyse carbapenem-resistant Klebsiella pneumoniae. BMC microbiology, 25(1), 17.

Xie Y, et al. (2025) The prevalence of optrA-carrying Enterococci in the vaginal micro-ecology of pregnant women in late pregnancy. Microbiology spectrum, 13(1), e0213524.

Jian Z, et al. (2025) Prevalence and molecular characteristics of colistin-resistant isolates among carbapenem-resistant Klebsiella pneumoniae in Central South China: a multicenter study. Annals of clinical microbiology and antimicrobials, 24(1), 1.

Nong Y, et al. (2024) Emergence and clonal expansion of a qacA-harbouring sequence type 45 lineage of methicillin-resistant Staphylococcus aureus. Communications biology, 7(1), 349.

Schwartzman JA, et al. (2024) Global diversity of enterococci and description of 18 previously unknown species. Proceedings of the National Academy of Sciences of the United States of America, 121(10), e2310852121.

Yao Y, et al. (2024) Predominant transmission of KPC-2 carbapenemase in Germany by a unique IncN plasmid variant harboring a novel non-transposable element (NTE KPC -Y). Microbiology spectrum, 12(1), e0256423.

Shang B, et al. (2024) A Novel Transposon Tn7709 Harbors Multidrug Resistance Genes in a Pathogenic Aeromonas media Strain QST31. Microorganisms, 12(3).

Tong CH, et al. (2024) Core and variable antimicrobial resistance genes in the gut microbiomes of Chinese and European pigs. Zoological research, 45(1), 189.

Vázquez X, et al. (2024) Insights into the Evolution of IncR Plasmids Found in the Southern European Clone of the Monophasic Variant of Salmonella enterica Serovar Typhimurium. Antibiotics (Basel, Switzerland), 13(4).

Ba X, et al. (2024) Global emergence of a hypervirulent carbapenem-resistant Escherichia coli ST410 clone. Nature communications, 15(1), 494.

Vlkova K, et al. (2024) Simultaneous PCR detection of Paenibacillus larvae targeting insertion sequence IS256 and Melissococcus plutonius targeting pMP1 plasmid from hive specimens. Folia microbiologica, 69(2), 415.

Kim E, et al. (2024) Genomic characteristics of cfr and fexA carrying Staphylococcus aureus isolated from pig carcasses in Korea. Veterinary research, 55(1), 21.

Wang X, et al. (2024) Inter-plasmid transfer of antibiotic resistance genes accelerates antibiotic resistance in bacterial pathogens. The ISME journal, 18(1).

Martino F, et al. (2024) New insights on mcr-1-harboring plasmids from human clinical Escherichia coli isolates. PloS one, 19(2), e0294820.

Park JH, et al. (2024) The Transposition of Insertion Sequences in Sigma-Factor- and LysR-Deficient Mutants of Deinococcus geothermalis. Microorganisms, 12(2).

Xu A, et al. (2024) Multicenter retrospective genomic characterization of carbapenemase-producing Acinetobacter baumannii isolates from Jiangxi patients 2021-2022: identification of a novel international clone, IC11. mSphere, 9(6), e0027624.