

Resource Summary Report

Generated by [NIF](#) on Jul 31, 2026

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: service resource, data repository, data analysis service, data or information resource, database, storage service resource, analysis service resource, production 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: 20260731T042646+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 1047 mentions in open access literature.

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

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

Xu X, et al. (2025) Ecological connectivity of genomic markers of antimicrobial resistance in *Escherichia coli* in Hong Kong. *Nature communications*, 16(1), 7319.

Leonildi A, et al. (2025) Phenotypic and Molecular Characterization of Pyomelanin-Producing *Acinetobacter baumannii* ST2Pas;ST1816/ST195Oxf Causing the First European Nosocomial Outbreak. *Microorganisms*, 13(3).

Gomi R, et al. (2025) Quinolone Resistance Genes *qnr*, *aac(6')-Ib-cr*, *oqxAB*, and *qepA* in Environmental *Escherichia coli*: Insights into Their Genetic Contexts from Comparative Genomics. *Microbial ecology*, 88(1), 6.

Xin X, et al. (2025) Genomic Insights into Carbapenem-Resistant Organisms Producing New Delhi Metallo- β -Lactamase in Live Poultry Markets. *Microorganisms*, 13(6).

Feng Y, et al. (2025) Genetic characterization and transmission of the multidrug resistance gene *cfr* in fecal and environmental pathways on a chicken farm in China. *Poultry science*, 104(6), 105079.

Davidovich C, et al. (2025) Occurrence of "under-the-radar" antibiotic resistance in anthropogenically affected produce. *The ISME journal*, 19(1).

Rosenberg M, et al. (2025) Experimental evolution of *Escherichia coli* on semi-dry silver, copper, stainless steel, and glass surfaces. *Microbiology spectrum*, 13(4), e0217324.

Wang K, et al. (2025) Genomic and phenotypic insights into ST164 blaNDM-1-positive *Acinetobacter baumannii* from intestinal colonization in China. *BMC microbiology*, 25(1), 272.

Teixeira M, et al. (2025) Circling in on plasmids: benchmarking plasmid detection and reconstruction tools for short-read data from diverse species. *Briefings in bioinformatics*, 26(6).

Liu H, et al. (2025) New resistance threat in difficult-to-treat resistance *Pseudomonas aeruginosa* co-producing AFM and KPC carbapenemases: plasmid dynamic transfer and global phylogeography perspective. *Emerging microbes & infections*, 14(1), 2585632.

Huo B, et al. (2025) Mechanistic insights into the formation and spread of carbapenem-resistant hypervirulent *Klebsiella pneumoniae* via an IncHI1B/repB hybrid virulence plasmid. *Microbial genomics*, 11(10).

Kruasuan W, et al. (2025) Clinical long-read metagenomic sequencing of culture-negative infective endocarditis reveals genomic features and antimicrobial resistance. *BMC infectious diseases*, 25(1), 1299.

Li P, et al. (2025) Characterization of bla NDM-5-carrying plasmids in two clinical *Salmonella* isolates from Jiaying city, China. *Frontiers in microbiology*, 16, 1620907.

Wirbel J, et al. (2025) Discovering Broader Host Ranges and an IS-bound Prophage Class Through Long-Read Metagenomics. *bioRxiv : the preprint server for biology*.

Lu X, et al. (2025) Plasmids of two novel incompatibility groups IncFIIpPROV114-NR and IncpCHS4.1-3 from Providencia. *Virulence*, 16(1), 2512034.

Fritz B, et al. (2025) Influence of Different Transposon Families on Genomic Stability of *Shewanella oneidensis* MR1. *Microbial biotechnology*, 18(7), e70188.

Kumavath R, et al. (2025) Unraveling the role of mobile genetic elements in antibiotic resistance transmission and defense strategies in bacteria. *Frontiers in systems biology*, 5, 1557413.

O'Ferrall AM, et al. (2025) Freshwater snail faecal metagenomes reveal environmental reservoirs of antimicrobial resistance genes across two continents. *Microbial genomics*, 11(8).

Bello A, et al. (2025) Genomic analysis of multidrug-resistant *Escherichia coli* isolated from dairy cows in Shihezi city, Xinjiang, China. *Frontiers in microbiology*, 16, 1527546.