

# Resource Summary Report

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## ISFinder

RRID:SCR\_003020

Type: Tool

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### Proper Citation

ISFinder (RRID:SCR\_003020)

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### 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, data analysis service, data or information resource, data repository, database, production service resource, service 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:** 20260821T193658+0000

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## Ratings and Alerts

No rating or validation information has been found for ISFinder.

No alerts have been found for ISFinder.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 1181 mentions in open access literature.

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

Begmatov S, et al. (2026) Plasmids of the multidrug-resistant *Citrobacter portucalensis* KOS1-1 strain isolated from a wastewater treatment plant harbor antibiotic resistance genes and gene clusters involved in carbon metabolism. *Microbiology spectrum*, 14(3), e0203825.

Zhang Y, et al. (2026) Pivotal plasmids drive the global spread of CTX-M-27 in *Escherichia coli*. *Infection*, 54(1), 315.

Yang D, et al. (2026) Global genomic landscape of *Staphylococcus lugdunensis*: population structure, antimicrobial resistance, and virulence determinants. *Applied and environmental microbiology*, 92(3), e0189325.

Royer M, et al. (2026) The mecillinam resistome in *Klebsiella pneumoniae*: how resistance to a one-target  $\beta$ -lactam triggers a diversity of responses. *Antimicrobial agents and chemotherapy*, 70(3), e0120725.

Liu X, et al. (2026) Characterization of a conjugative IncFII/IncR plasmid harboring blaKPC-2 in a clinical ST91 *Citrobacter freundii* isolate. *BMC microbiology*, 26(1).

Graham CI, et al. (2026) Widespread macrolide resistance among rapidly growing mycobacteria due to plasmids containing erm(55). *Scientific reports*, 16(1), 2358.

Rathna V, et al. (2026) Pan-genome and antibiotic resistance insights into *Xanthomonas citri* pv. *punicae* pathotypes. *BMC microbiology*, 26(1).

Bloemen B, et al. (2026) Recovery and microbial host assignment of mobile genetic elements in complex microbiomes: insights from a spiked gut sample. *mSystems*, 11(2), e0128225.

El Halfawy NM, et al. (2026) Genomic characterization of multidrug-resistant *Escherichia coli* strains identified from patients with urinary tract infection in Egypt. *Scientific reports*, 16(1).

Hassan F, et al. (2026) Comparative genomics reveals synteny-guided remodeling of carbohydrate-foraging and intrinsic resistance in an ocular *Chryseobacterium* isolate, NG-CE01. *BMC microbiology*, 26(1).

Amer MA, et al. (2026) WGS reveals high-risk clones of *Pseudomonas aeruginosa* harbouring extensive antimicrobial and predicted anti-phage defense systems recovered from diabetic foot ulcer patients in Egypt. *BMC microbiology*, 26(1).

Zhang J, et al. (2026) Clinical Characteristics and Whole-Genome Sequencing Analysis of Carbapenem- and Colistin-Resistant Hypervirulent *Klebsiella pneumoniae*. *Infection and drug resistance*, 19, 582373.

Sadaqat M, et al. (2026) Molecular evaluation of colistin resistance in *Klebsiella pneumoniae* strains isolated from patients in hospitals of Qom province. *Iranian journal of microbiology*, 18(2), 244.

Puigsech-Boixeda G, et al. (2026) Emerging reservoirs of metallo- $\beta$ -lactamase genes among non-aeruginosa *Pseudomonas* and *Stutzerimonas* species in a Spanish tertiary hospital. *Frontiers in microbiology*, 17, 1810036.

Wirbel J, et al. (2026) Long-read metagenomics reveals phage dynamics in the human gut microbiome. *Nature*, 649(8098), 982.

Xu B, et al. (2026) Enhanced SfaTnpB enables single-base-specific, one-pot nucleic acid detection for high-sensitivity diagnostics. *Nucleic acids research*, 54(1).

Yan Z, et al. (2026) Dissemination of antimicrobial resistance in *Klebsiella* spp. from urban aquatic environments: a multi-country genomic perspective. *Journal of advanced research*, 84, 737.

Li D, et al. (2026) Plasmid-mediated convergence of multidrug resistance and hypervirulence in community-acquired *Klebsiella pneumoniae* in Tianjin, China. *BMC microbiology*, 26(1).

Wang Z, et al. (2026) Emergence of a multidrug-resistant *Pseudomonas fulva* clinical isolate co-harboring *tmexCD3-toprJ3*, *bla* OXA-1, and *bla* IMP-45 on a transferable megaplasmid. *Frontiers in cellular and infection microbiology*, 16, 1722020.

Chen D, et al. (2026) Analysis of mobile genetic elements carrying *mcr* genes in clinical *Leclercia* spp. isolates. *BMC microbiology*, 26(1).