

Resource Summary Report

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MacSyFinder

RRID:SCR_024106

Type: Tool

Proper Citation

MacSyFinder (RRID:SCR_024106)

Resource Information

URL: <https://github.com/gem-pasteur/macsyfinder>

Proper Citation: MacSyFinder (RRID:SCR_024106)

Description: Software tool to mine genomes for molecular systems with Application to CRISPR-Cas Systems. Detection of macromolecular systems in protein datasets using systems modelling and similarity search.

Synonyms: macsyfinder

Resource Type: software resource, software application

Defining Citation: [PMID:25330359](#)

Keywords: Detection of macromolecular system, protein datasets, mine genomes, molecular systems,

Availability: Free, Available for download, Freely available,

Resource Name: MacSyFinder

Resource ID: SCR_024106

Alternate IDs: OMICS_20116

Alternate URLs: <https://sources.debian.org/src/macsyfinder/>

License: GPL-3.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260731T043154+0000

Ratings and Alerts

No rating or validation information has been found for MacSyFinder.

No alerts have been found for MacSyFinder.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Das J, et al. (2025) Genomic insights into novel predatory myxobacteria isolated from human feces. *Microbiology spectrum*, 13(7), e0214724.

Kurilenko V, et al. (2025) Description and Genome-Based Analysis of *Vibrio chaetopteri* sp. nov., a New Species of the Mediterranei Clade Isolated from a Marine Polychaete. *Microorganisms*, 13(3).

Serna C, et al. (2025) Integrative and conjugative elements associated with antimicrobial resistance in multidrug resistant *Pasteurella multocida* isolates from bovine respiratory disease (BRD)-affected animals in Spanish feedlots. *The veterinary quarterly*, 45(1), 1.

Henriques WS, et al. (2025) Structures reveal how the Cas1-2/3 integrase captures, delivers, and integrates foreign DNA into CRISPR loci. *bioRxiv : the preprint server for biology*.

Velo-Suarez L, et al. (2025) Genomic diversity in *Porphyromonas*: evidence of *Porphyromonas catoniae* commensality in lungs. *Microbial genomics*, 11(6).

Henriques WS, et al. (2025) Structures reveal how the Cas1-2/3 integrase captures, delivers, and integrates foreign DNA into CRISPR loci. *Structure (London, England : 1993)*, 33(12), 2058.

Briand M, et al. (2025) The hidden life of *Xylella*: mining the NCBI Sequence Read Archive reveals potential new species, host plants, and infected areas for this elusive bacterial plant pathogen. *Applied and environmental microbiology*, 91(10), e0091325.

Santhosh A, et al. (2025) Genomic characterization of an environmental *Burkholderia thailandensis* strain from Kerala, India reveals virulence and antimicrobial resistance signatures. *BMC genomics*, 26(1), 1146.

Toribio-Celestino L, et al. (2024) A plasmid-chromosome crosstalk in multidrug resistant enterobacteria. *Nature communications*, 15(1), 10859.

Wang H, et al. (2024) Pangenome analysis of *Shewanella xiamenensis* revealed important genetic traits concerning genetic diversity, pathogenicity and antibiotic resistance. *BMC genomics*, 25(1), 216.

Vizzarro G, et al. (2024) *Vibrio cholerae* pathogenicity island 2 encodes two distinct types of restriction systems. *Journal of bacteriology*, 206(9), e0014524.

Barcia-Cruz R, et al. (2024) Phage-inducible chromosomal minimalist islands (PICMIs), a novel family of small marine satellites of virulent phages. *Nature communications*, 15(1), 664.

Mancilla-Rojano J, et al. (2024) A bioinformatic approach to identify confirmed and probable CRISPR-Cas systems in the *Acinetobacter calcoaceticus*-*Acinetobacter baumannii* complex genomes. *Frontiers in microbiology*, 15, 1335997.

Alonso-Del Valle A, et al. (2023) Antimicrobial resistance level and conjugation permissiveness shape plasmid distribution in clinical enterobacteria. *Proceedings of the National Academy of Sciences of the United States of America*, 120(51), e2314135120.

de Sousa JAM, et al. (2023) Identification and characterization of thousands of bacteriophage satellites across bacteria. *Nucleic acids research*, 51(6), 2759.

Dittmer J, et al. (2023) The terrestrial isopod symbiont '*Candidatus Hepatincola porcellionum*' is a potential nutrient scavenger related to Holosporales symbionts of protists. *ISME communications*, 3(1), 18.

K??stlbacher S, et al. (2021) Pangenomics reveals alternative environmental lifestyles among chlamydiae. *Nature communications*, 12(1), 4021.

Delgado-Blas JF, et al. (2021) Population genomics and antimicrobial resistance dynamics of *Escherichia coli* in wastewater and river environments. *Communications biology*, 4(1), 457.

Liu Z, et al. (2020) Comparative Genomic Analysis Provides Insights into the Phylogeny, Resistome, Virulome, and Host Adaptation in the Genus *Ewingella*. *Pathogens (Basel, Switzerland)*, 9(5).

Wuyts S, et al. (2019) Comparative genome analysis of *Lactobacillus mudanjiangensis*, an understudied member of the *Lactobacillus plantarum* group. *Microbial genomics*, 5(9).