

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 12, 2026

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 application, software resource

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: 20260912T200307+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 28 mentions in open access literature.

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

Ercole TG, et al. (2026) Integrated genome mining and phytohormone profiling of six plant growth-promoting elite bacterial strains. Archives of microbiology, 208(3), 152.

Tagg KA, et al. (2026) Pangenome dynamics and population structure of the zoonotic pathogen Salmonella enterica serotype Hadar. Nature communications, 17(1), 1270.

Payne CJ, et al. (2026) Are the genomes of motile Aeromonas species from the aquatic environment shaped by local geography and host species? Microbial genomics, 12(4).

Takei S, et al. (2026) Isolation and identification of Pseudoxanthomonas winnipegensis from blood culture by MALDI-MS. Frontiers in cellular and infection microbiology, 16, 1755501.

Liang J, et al. (2026) Complex temporal dynamics of phage-bacteria populations in an animal-associated marine system. Nature communications, 17(1).

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).

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

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).

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.

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.

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.

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.