

# Resource Summary Report

Generated by [FDI Lab - SciCrunch.org](https://fdi-lab.sci-crunch.org) on Apr 24, 2025

## PlasmidSeeker

RRID:SCR\_024167

Type: Tool

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### Proper Citation

PlasmidSeeker (RRID:SCR\_024167)

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### Resource Information

**URL:** <https://github.com/bioinfo-ut/PlasmidSeeker>

**Proper Citation:** PlasmidSeeker (RRID:SCR\_024167)

**Description:** Software tool as k-mer based program for identification of known plasmids from whole genome sequencing reads. Used for identification of known plasmids from bacterial whole genome sequencing reads.

**Synonyms:** plasmidseeker

**Resource Type:** data analysis software, data processing software, software resource, software application

**Defining Citation:** [PMID:29629246](https://pubmed.ncbi.nlm.nih.gov/29629246/)

**Keywords:** k-mer based program, identification of known plasmids, whole genome sequencing reads,

**Funding:**

**Availability:** Free, Available for download, Freely available,

**Resource Name:** PlasmidSeeker

**Resource ID:** SCR\_024167

**Alternate IDs:** OMICS\_28371

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

**License:** BSD-3-Clause license

**Record Creation Time:** 20230824T050212+0000

**Record Last Update:** 20250423T061313+0000

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## Ratings and Alerts

No rating or validation information has been found for PlasmidSeeker.

No alerts have been found for PlasmidSeeker.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 14 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch.org](#).

Sun Z, et al. (2025) The pivotal role of IncFIB(Mar) plasmid in the emergence and spread of hypervirulent carbapenem-resistant *Klebsiella pneumoniae*. *Science advances*, 11(5), eado9097.

Peñil-Celis A, et al. (2024) Mobile genetic elements define the non-random structure of the *Salmonella enterica* serovar Typhi pangenome. *mSystems*, 9(8), e0036524.

Nusrin S, et al. (2022) Multiple Mechanisms Confer Resistance to Azithromycin in *Shigella* in Bangladesh: a Comprehensive Whole Genome-Based Approach. *Microbiology spectrum*, 10(4), e0074122.

Okdah L, et al. (2022) Genomic Characterization of Colistin-Resistant Isolates from the King Fahad Medical City, Kingdom of Saudi Arabia. *Antibiotics (Basel, Switzerland)*, 11(11).

Castro-Gutierrez V, et al. (2022) Dissemination of metaldehyde catabolic pathways is driven by mobile genetic elements in Proteobacteria. *Microbial genomics*, 8(10).

Bravo V, et al. (2021) Genomic analysis of the diversity, antimicrobial resistance and virulence potential of clinical *Campylobacter jejuni* and *Campylobacter coli* strains from Chile. *PLoS neglected tropical diseases*, 15(2), e0009207.

Teo JQ, et al. (2021) Genomic characterization of carbapenem-non-susceptible *Pseudomonas aeruginosa* in Singapore. *Emerging microbes & infections*, 10(1), 1706.

Mageiros L, et al. (2021) Genome evolution and the emergence of pathogenicity in avian *Escherichia coli*. *Nature communications*, 12(1), 765.

Kulecka M, et al. (2021) Higher genome variability within metabolism genes associates with recurrent *Clostridium difficile* infection. *BMC microbiology*, 21(1), 36.

Tshibangu-Kabamba E, et al. (2020) Next-Generation Sequencing of the Whole Bacterial Genome for Tracking Molecular Insight into the Broad-Spectrum Antimicrobial Resistance of *Helicobacter pylori* Clinical Isolates from the Democratic Republic of Congo. *Microorganisms*, 8(6).

Mwangi C, et al. (2020) Whole Genome Sequencing Reveals Virulence Potentials of *Helicobacter pylori* Strain KE21 Isolated from a Kenyan Patient with Gastric Signet Ring Cell Carcinoma. *Toxins*, 12(9).

Martins FH, et al. (2020) EspFu-Mediated Actin Assembly Enhances Enteropathogenic *Escherichia coli* Adherence and Activates Host Cell Inflammatory Signaling Pathways. *mBio*, 11(2).

Kiu R, et al. (2019) Phylogenomic analysis of gastroenteritis-associated *Clostridium perfringens* in England and Wales over a 7-year period indicates distribution of clonal toxigenic strains in multiple outbreaks and extensive involvement of enterotoxin-encoding (CPE) plasmids. *Microbial genomics*, 5(10).

Kiu R, et al. (2019) Genomic analysis on broiler-associated *Clostridium perfringens* strains and exploratory caecal microbiome investigation reveals key factors linked to poultry necrotic enteritis. *Animal microbiome*, 1, 12.