

Resource Summary Report

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PlasmidSeeker

RRID:SCR_024167

Type: Tool

Proper Citation

PlasmidSeeker (RRID:SCR_024167)

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 processing software, data analysis software, software application, software resource

Defining Citation: [PMID:29629246](#)

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

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: 20260801T190825+0000

Ratings and Alerts

No rating or validation information has been found for PlasmidSeeker.

No alerts have been found for PlasmidSeeker.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Linn KZ, et al. (2025) Impact of standard precautions and unrestricted movements of carbapenemase-producing Enterobacterales (CPE) carriers on CPE transmission in a nursing home in Singapore: a prospective cohort study. *Antimicrobial resistance and infection control*, 14(1), 38.

Bui PH, et al. (2025) Identification of genetic determinants of antibiotic resistance in *Helicobacter pylori* isolates in Vietnam by high-throughput sequencing. *BMC microbiology*, 25(1), 264.

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.

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

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).

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.

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

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

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.

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.