

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Kaptive

RRID:SCR_024046

Type: Tool

Proper Citation

Kaptive (RRID:SCR_024046)

Resource Information

URL: <https://github.com/klebgenomics/Kaptive>

Proper Citation: Kaptive (RRID:SCR_024046)

Description: Software tool to report information about surface polysaccharide loci for *Klebsiella pneumoniae* species complex and *Acinetobacter baumannii* genome assemblies.

Synonyms: kaptive

Resource Type: software application, software resource

Defining Citation: [PMID:28348840](#)

Keywords: report information, surface polysaccharide loci, genome assemblies,

Availability: Free, Available for download, Freely available,

Resource Name: Kaptive

Resource ID: SCR_024046

Alternate IDs: OMICS_27932

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

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260905T133316+0000

Ratings and Alerts

No rating or validation information has been found for Kaptive.

No alerts have been found for Kaptive.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

Li S, et al. (2026) Genomic dissection of the clonal background and global dissemination of hypervirulent *Klebsiella pneumoniae* CG23-KL57 lineage. *Nature communications*, 17(1), 1451.

Boattini M, et al. (2026) Emergence of resistance to novel β -lactam/ β -lactamase inhibitor combinations in KPC-producing *Klebsiella pneumoniae*: clinical and genomic insights from consecutive bloodstream infections. *Infection*, 54(2), 841.

Pariona JGM, et al. (2026) Whole-genome analysis of extensively drug-resistant *Acinetobacter baumannii* isolates from a Peruvian tertiary hospital reveals the emergence of OXA-23-producing ST79 and ST1079 clones. *Microbiology spectrum*, 14(3), e0341525.

Watanabe A, et al. (2026) Carriage of hypervirulent and ESBL-producing *Klebsiella pneumoniae* complex among community-dwelling individuals in Japan. *Applied and environmental microbiology*, 92(2), e0168725.

Maqbool M, et al. (2026) Exploration of the genomic diversity of third-generation cephalosporin-resistant *Escherichia coli* in Australian clinical settings. *Microbial genomics*, 12(1).

Sharar NS, et al. (2026) Multiple prophage acquisition events over the course of an outbreak drive lysogenic conversion of capsular polysaccharides produced by carbapenem-resistant *Acinetobacter baumannii* isolates. *Microbiology spectrum*, 14(6), e0408425.

Tsolakidou P, et al. (2025) Epidemiological and Microbiological Characterization of Carbapenemase-Producing *Klebsiella pneumoniae* Isolates in a Regional Greek Hospital: A Retrospective Study. *Microorganisms*, 13(9).

Lean SS, et al. (2025) The Road Less Traveled: Exploring the Genomic Characteristics and Antimicrobial Resistance Potential of *Acinetobacter baumannii* From the Indigenous Orang Asli Community in Peninsular Malaysia. *MicrobiologyOpen*, 14(5), e70073.

Jiang X, et al. (2025) The global genomic landscape of hypervirulent *Klebsiella pneumoniae* from 1932 to 2021. *mLife*, 4(4), 378.

Stanton TD, et al. (2025) Fast and accurate in silico antigen typing with Kaptive 3. *Microbial genomics*, 11(6).

Boeckaerts D, et al. (2024) Prediction of *Klebsiella* phage-host specificity at the strain level. *Nature communications*, 15(1), 4355.

Feng Y, et al. (2024) Population genomics uncovers global distribution, antimicrobial resistance, and virulence genes of the opportunistic pathogen *Klebsiella aerogenes*. *Cell reports*, 43(8), 114602.

Slarve MJ, et al. (2024) Clinical assays rapidly predict bacterial susceptibility to monoclonal antibody therapy. *JCI insight*, 9(2).

Amadesi S, et al. (2024) Complete Genome Sequence of a *Klebsiella pneumoniae* Strain Carrying Novel Variant blaKPC-203, Cross-Resistant to Ceftazidime/Avibactam and Cefiderocol, but Susceptible to Carbapenems, Isolated in Italy, 2023. *Pathogens (Basel, Switzerland)*, 13(6).

Shpirt AM, et al. (2024) An *Acinetobacter baumannii* nasal carriage isolate recovered from an asymptomatic patient in Vietnam is extensively antibiotic resistant and produces a rare K71 type capsule. *Microbiology spectrum*, 12(12), e0183824.

Yang Y, et al. (2024) Large-scale genomic survey with deep learning-based method reveals strain-level phage specificity determinants. *GigaScience*, 13.

Koncz M, et al. (2024) Genomic surveillance as a scalable framework for precision phage therapy against antibiotic-resistant pathogens. *Cell*, 187(21), 5901.

Dey S, et al. (2023) Unravelling the Evolutionary Dynamics of High-Risk *Klebsiella pneumoniae* ST147 Clones: Insights from Comparative Pangenome Analysis. *Genes*, 14(5).