

Resource Summary Report

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Kleborate

RRID:SCR_024051

Type: Tool

Proper Citation

Kleborate (RRID:SCR_024051)

Resource Information

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

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Description: Software tool to screen genome assemblies of *Klebsiella pneumoniae* and the *Klebsiella pneumoniae* species complex (KpSC) for MLST sequence type, species (e.g. *K. pneumoniae*, *K. quasipneumoniae*, *K. variicola*, etc.), ICEKp associated virulence loci (yersiniabactin (ybt), colibactin (clb), salmochelin (iro), hypermucoidy (rmpA)), virulence plasmid associated loci (salmochelin (iro), aerobactin (iuc), hypermucoidy (rmpA, rmpA2)), antimicrobial resistance determinants (acquired genes, SNPs, gene truncations and intrinsic β -lactamases), and K (capsule) and O antigen (LPS) serotype prediction, via wzi alleles and Kaptive.

Synonyms: KLEBORATE, kleborate

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

Keywords: screen genome assemblies, *Klebsiella pneumoniae*, *Klebsiella pneumoniae* species complex, genome assemblies,

Availability: Free, Available for download, Freely available,

Resource Name: Kleborate

Resource ID: SCR_024051

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

License: GPL-3.0 license

Record Creation Time: 20230824T050211+0000

Record Last Update: 20260803T040900+0000

Ratings and Alerts

No rating or validation information has been found for Kleborate.

No alerts have been found for Kleborate.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 11 mentions in open access literature.

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

González-Espinosa F, et al. (2025) Outbreak of NDM-5-producing *Klebsiella variicola* in intensive care units: an overlooked pathogen in Argentina? *Microbiology spectrum*, 13(8), e0067225.

Li Z, et al. (2025) Characterization of OXA232-Producing Carbapenem-Resistant *Klebsiella pneumoniae*: Genomic Analysis and Virulence Assessment. *Polish journal of microbiology*, 74(1), 82.

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

Hsu CR, et al. (2025) A novel *Klebsiella pneumoniae* diguanylate cyclase contributes to intestinal cell adhesion, biofilm formation, iron utilization, and in vivo virulence by gastrointestinal infection. *Virulence*, 16(1), 2544882.

Ni Y, et al. (2025) Emergence of Tigecycline-Nonsusceptible Carbapenem-Resistant *Klebsiella pneumoniae* with Metallo- β -Lactamase and Transferable Ceftazidime-Avibactam Resistance in China. *Pathogens (Basel, Switzerland)*, 14(3).

Lam MMC, et al. (2025) Genomic and functional analysis of *rmp* locus variants in *Klebsiella pneumoniae*. *Genome medicine*, 17(1), 36.

Concha-Eloko R, et al. (2025) Unlocking data in *Klebsiella* lysogens to predict capsular type-specificity of phage depolymerases. *Nature communications*, 16(1), 8798.

Itoga M, et al. (2024) Severe co-infection caused by difficult-to-diagnose hypermucoviscous *Klebsiella pneumoniae* K1-ST82 in a patient with COVID-19: a case report. *BMC infectious diseases*, 24(1), 1215.

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.

Yang Y, et al. (2024) CRISPR-Cas3 and type I restriction-modification team up against blaKPC-IncF plasmid transfer in *Klebsiella pneumoniae*. *BMC microbiology*, 24(1), 240.

DeLeo FR, et al. (2023) Interaction of multidrug-resistant hypervirulent *Klebsiella pneumoniae* with components of human innate host defense. *mBio*, 14(5), e0194923.