

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 wzj alleles and Kaptive.

Synonyms: KLEBORATE, kleborate

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

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: 20260912T200045+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 27 mentions in open access literature.

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

Ayzanoa B, et al. (2026) Genomic surveillance of multidrug-resistant *Escherichia coli* and *Klebsiella* in clinical and wastewater isolates from a paediatric hospital in Lima, Peru. *Access microbiology*, 8(1).

Zenati K, et al. (2026) The oral cavity as a reservoir for resistance- and hypervirulence-associated genes of *Klebsiella pneumoniae* in hospitalized patients. *Frontiers in microbiology*, 17, 1751947.

Jaidane N, et al. (2026) Carbapenem and colistin-resistant *Klebsiella pneumoniae* co-producing NDM-5 and OXA-48 in a teaching hospital from Tunisia. *JAC-antimicrobial resistance*, 8(2), dlaf043.

Meyer J, et al. (2026) Pandemic SHV-106-producing *Klebsiella pneumoniae* ST231 isolated from Brazilian hedgehog (*Coendou spinosus*) reveals an emerging environmental circulation of a high-risk multidrug-resistant lineage. *Antonie van Leeuwenhoek*, 119(5).

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.

Boral J, et al. (2026) Activity of cefepime/enmetazobactam against highly multidrug-resistant bacterial isolates recovered from war-associated wounds in Ukraine. *JAC-antimicrobial resistance*, 8(1), dlaf256.

Centner CM, et al. (2026) Antimicrobial resistance databases: opportunities and challenges for public health. *npj antimicrobials and resistance*, 4(1), 1.

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.

He Y, et al. (2026) Molecular epidemiology of antimicrobial resistance and virulence of carbapenem-resistant *Klebsiella pneumoniae* in South China. *Frontiers in microbiology*, 17, 1817833.

Aga ONL, et al. (2026) Evolutionary inference reveals global natural histories and predicted pathways of antimicrobial resistance in *Klebsiella pneumoniae*. PLoS biology, 24(6), e3003848.

Li Y, et al. (2026) Repeated insertions at positions 261-280 in KPC-2 highlight a ceftazidime-avibactam resistance hotspot. iScience, 29(7), 116514.

Aiddi A, et al. (2026) Global High-Risk *Escherichia coli* Clones in Moroccan Aquatic Settings: Genomic Evidence of Environmental Dissemination. International journal of microbiology, 2026, 6271074.

Mbwana JR, et al. (2026) Molecular characterisation of extended-Spectrum-Beta-lactamase-producing *Klebsiella pneumoniae* among children and chicken in the rural Korogwe District, Tanzania. One health (Amsterdam, Netherlands), 23, 101472.

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.

S?kowska A, et al. (2025) Whole Genome Sequencing of *Klebsiella variicola* Strains Isolated from Patients with Cancer. Antibiotics (Basel, Switzerland), 14(8).

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.

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.

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

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.