

Resource Summary Report

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

Antibiotic Resistance Genes Database

RRID:SCR_007040

Type: Tool

Proper Citation

Antibiotic Resistance Genes Database (RRID:SCR_007040)

Resource Information

URL: <http://ardb.cbcb.umd.edu>

Proper Citation: Antibiotic Resistance Genes Database (RRID:SCR_007040)

Description: The goals of Antibiotic Resistance Genes Database (ARGB) are to provide a centralized compendium of information on antibiotic resistance, to facilitate the consistent annotation of resistance information in newly sequenced organisms, and also to facilitate the identification and characterization of new genes. ARGB contains six types of database groups: - Resistance Type: This database contains information, such as resistance profile, mechanism, requirement, epidemiology for each type. - Resistance Gene: This database contains information, such as resistance profile, resistance type, requirement, protein and DNA sequence for each gene. This database only includes NON-REDUNDANT, NON-VECTOR, COMPLETE genes. - Antibiotic: This database contains information, such as producer, action mechanism, resistance type, for each gene. - Resistance Gene(NonRD): This database contains the same information as Resistance Gene. It does NOT include NON-REDUNDANT, NON-VECTOR genes, but includes INCOMPLETE genes. - Resistance Gene(ALL): This database contains the same information as Resistance Gene. It includes all REDUNDANT, VECTOR AND INCOMPLETE genes. - Resistance Species: This database contains resistance profile and corresponding resistance genes for each species. Furthermore, ARDB also contains three types BLAST database: - Resistance Genes Complete: Contains only NON-REDUNDANT, NON-VECTOR, COMPLETE genes sequences. - Resistance Genes Non-redundant: Contains NON-REDUNDANT, NON-VECTOR, COMPLETE, INCOMPLETE genes sequences. - Resistance Genes All: Contains all REDUNDANT, VECTOR, COMPLETE, INCOMPLETE genes sequences. Lastly, ARDB provides four types of Analytical tools: - Normal BLAST: This function allows an user to input a DNA or protein sequence, and find similar DNA (Nucleotide BLAST) or protein (Protein BLAST) sequences using blastn, blastp, blastx, tblastn, tblastx - RPS BLAST: A web RPSBLAST (RPS BLAST) interface is provided to align a query sequence against the Position Specific Scoring Matrix (PSSM) for each type. Normally, this will give the same annotation information as using regular BLAST mentioned above. - Multiple Sequences BLAST (Genome Annotation): This function allows an user to annotate multiple (less than 5000) query sequences in FASTA format. -

Mutation Resistance Identification: This function allows an user to identify mutations that will cause potential antibiotic resistance, for 12 genes (16S rRNA, 23S rRNA, gyrA, gyrB, parC, parE, rpoB, katG, pncA, embB, folP, dfr). :Sponsors: ARDB is funded by Uniformed Services University of the Health Sciences, administered by the Henry Jackson Foundation. :

Synonyms: ARDB

Resource Type: data computation service, data or information resource, database

Keywords: genome, antibiotic, antibiotic resistance gene, dna, metagenome, mutation resistance, prokaryotic genomic database, protein, FASEB list

Resource Name: Antibiotic Resistance Genes Database

Resource ID: SCR_007040

Alternate IDs: nif-0000-02565

Record Creation Time: 20220129T080239+0000

Record Last Update: 20260905T132606+0000

Ratings and Alerts

No rating or validation information has been found for Antibiotic Resistance Genes Database.

No alerts have been found for Antibiotic Resistance Genes Database.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 124 mentions in open access literature.

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

Tan ZW, et al. (2026) Complete genome sequencing of *Lactobacillus pentosus* HP-B1718 and identification of the key enzyme for liquiritin biotransformation. *Frontiers in microbiology*, 17, 1840719.

Lai Y, et al. (2026) Comparative genomics reveals the molecular basis for divergent algicidal strategies in two *Alteromonas macleodii* strains. *Applied and environmental microbiology*, 92(1), e0196525.

Zhen Z, et al. (2026) Genome-wide characteristics, antibiotic resistance, and pathogenicity analysis of *Streptococcus parasuis* strains isolated from diseased pigs. *BMC microbiology*,

26(1).

Wang Y, et al. (2025) Bacteriophage-based control of Salmonella on table eggs and breeding eggs in poultry. *Poultry science*, 104(4), 104969.

Du H, et al. (2025) Thermophilic microbial agents promote the fermentation progression of spent mushroom compost and pig manure. *Frontiers in microbiology*, 16, 1575397.

Xie Q, et al. (2025) Molecular epidemiology of carbapenem-resistant *Klebsiella pneumoniae* ST15-KL19 isolates from ICU patients in a Chinese tertiary hospital. *Frontiers in microbiology*, 16, 1673965.

Basu U, et al. (2025) Longitudinal metagenomics reveals continuous restructuring of soil pathobiome under persistent *Phytophthora* pressure. *Frontiers in plant science*, 16, 1749879.

Wang L, et al. (2025) Metagenomic analysis reveals distinct patterns of gut microbiota features with diversified functions in *C. difficile* infection (CDI), asymptomatic carriage and non-CDI diarrhea. *Gut microbes*, 17(1), 2505269.

Ste Marie J, et al. (2025) Longitudinal replicated metagenomic analysis of biosolids-amended soils reveals enrichment of ARGs, virulence factors, and ESKAPE pathogens. *npj antimicrobials and resistance*, 3(1), 96.

Li L, et al. (2024) The effects of food provisioning on the gut microbiota community and antibiotic resistance genes of Yunnan snub-nosed monkey. *Frontiers in microbiology*, 15, 1361218.

Yang L, et al. (2024) Genomic and Transcriptomic Analyses Reveal Multiple Strategies for *Vibrio parahaemolyticus* to Tolerate Sub-Lethal Concentrations of Three Antibiotics. *Foods (Basel, Switzerland)*, 13(11).

Bertrans-Tubau L, et al. (2024) Nature-based bioreactors: Tackling antibiotic resistance in urban wastewater treatment. *Environmental science and ecotechnology*, 22, 100445.

Liu Y, et al. (2024) Bacterial isolation and genome analysis of a novel *Klebsiella quasipneumoniae* phage in southwest China's karst area. *Virology journal*, 21(1), 56.

Gao Y, et al. (2024) Different artificial feeding strategies shape the diverse gut microbial communities and functions with the potential risk of pathogen transmission to captive Asian small-clawed otters (*Aonyx cinereus*). *mSystems*, 9(12), e0095424.

Rafiei S, et al. (2024) Genomic analysis of vB_PaS-HSN4 bacteriophage and its antibacterial activity (in vivo and in vitro) against *Pseudomonas aeruginosa* isolated from burn. *Scientific reports*, 14(1), 2007.

Zhao Y, et al. (2024) Exploring Alashan Ground Squirrel (*Spermophilus alashanicus*) Diversity: Metagenomic and Transcriptomic Datasets from the Helan Mountains. *Scientific data*, 11(1), 517.

Wu C, et al. (2024) Clinical manifestations, antimicrobial resistance and genomic feature analysis of multidrug-resistant *Elizabethkingia* strains. *Annals of clinical microbiology and*

antimicrobials, 23(1), 32.

Ren J, et al. (2024) Impacts of sulfamethoxazole stress on vegetable growth and rhizosphere bacteria and the corresponding mitigation mechanism. *Frontiers in bioengineering and biotechnology*, 12, 1303670.

Chen T, et al. (2024) Genome sequence and evaluation of safety and probiotic potential of *Lactocaseibacillus paracasei* LC86 and *Lactocaseibacillus casei* LC89. *Frontiers in microbiology*, 15, 1501502.

Fanelli F, et al. (2023) Probiotic Potential and Safety Assessment of Type Strains of *Weissella* and *Periweissella* Species. *Microbiology spectrum*, 11(2), e0304722.