

Resource Summary Report

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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>

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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 or information resource, data computation service, 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: 20260729T044140+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 109 mentions in open access literature.

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

Wang Y, et al. (2025) Bacteriophage-based control of Salmonella on table eggs and breeding genes 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.

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.
- Bertrans-Tubau L, et al. (2024) Nature-based bioreactors: Tackling antibiotic resistance in urban wastewater treatment. *Environmental science and ecotechnology*, 22, 100445.
- 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.
- 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.
- 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.
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- Fanelli F, et al. (2023) Probiotic Potential and Safety Assessment of Type Strains of *Weissella* and *Periweissella* Species. *Microbiology spectrum*, 11(2), e0304722.
- Lin C, et al. (2023) A Rapid Antimicrobial Resistance Diagnostic Platform for *Staphylococcus aureus* Using Recombinase Polymerase Amplification. *Microbiology spectrum*, 11(2), e0447622.
- Shin H, et al. (2023) Resistome Study in Aquatic Environments. *Journal of microbiology and biotechnology*, 33(3), 277.
- Dwiyanto J, et al. (2023) Social demographics determinants for resistome and microbiome variation of a multiethnic community in Southern Malaysia. *NPJ biofilms and microbiomes*, 9(1), 55.
- Chen X, et al. (2023) Comparative Genomic Analysis Reveals Genetic Diversity and Pathogenic Potential of *Haemophilus seminalis* and Emended Description of *Haemophilus seminalis*. *Microbiology spectrum*, 11(4), e0477222.

Xu M, et al. (2022) Metagenomic insights into the spatiotemporal responses of antibiotic resistance genes and microbial communities in aquaculture sediments. *Chemosphere*, 307(Pt 1), 135596.

Ye Y, et al. (2022) Characterization and Genomic Analysis of Novel *Vibrio* parahaemolyticus Phage vB_VpaP_DE10. *Viruses*, 14(8).

Shuai M, et al. (2022) Human Gut Antibiotic Resistome and Progression of Diabetes. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 9(11), e2104965.