

Anti-Microbial Resistance DB (AMR-DB) User Manual

The AMR-DB is a Centers for Disease Control and Prevention (CDC)-funded database resource. It started as a comprehensive non-redundant database of anti-microbial resistance gene and protein sequences derived from 5 major AMR databases (CARD, Resfinder, ARG-ANNOT, Lahey/NCBI and MEGARes), which was used to query GenBank to enable global analysis of AMR from sequenced bacterial genomes. The layout of the website consists of 5 main sections: Home, Analysis, Primer, Support, and Contact.

1. Home

The AMR-DB home page dashboard provides a high-level summary of AMR-DB contents. Menu and submenus provide functionality to browse and search data, AMR information on world map, AMR-Finder that allows users to find AMR genes in AMR-DB reference database. Primer menu allow users to browse and search catalog of AMR primers loaded in AMR-DB, and it allow users to primer finder on existing AMR-DB reference database. Secure admin menu is only available to registered users with admin role, and it allow users to edit data in AMR-DB.

1.1. Header Menu

The right corner of menu allows the user to sign-up or sign-in into AMR-DB (see below). Only registered users can sign-in (1). The horizontal menu across the top of the page has four sections in addition to the (A) home button: B) Analysis, C) Primer D) “support”, E) “contact” page, and F) Admin (only appears when signed in as a registered user).

Not signed in:



Signed in:



1. **Sign In/Sign Up:** The user must register and sign in to edit AMR-DB.

A. **Home:** goes to the home page

B. **Analysis:** The location of all the tools to view, browse and search the AMR-DB. Tools available from this page include:

2.2. Sequence Similarity Search Module

The AMR-Finder tool allows users to find homologous AMR genes based on user-provided input multi-FASTA sequences (**A**) and allows users to access the gene information pages (see Section B.3) and sequence alignments for the best hits and download results and AMR sequences (**B**).

A

Sequence Similarity Search Module

Perform a nucleotide or protein search using AMR-Finder against the AMRdb. Paste protein or nucleotide sequences in FASTA format. For more information see [AMRdb help page](#)

Please paste your sequence in FASTA format to be searched:

[USE AN EXAMPLE PROTEIN SEQUENCE](#)

[USE AN EXAMPLE NUCLEOTIDE SEQUENCE](#)

Select File to upload:

[Browse...](#) No file selected.

SUBMIT

BLAST OUTPUT AGAINST AMRDB

The best hit based on AMR-Finder result is shown for each query sequence combined with the metadata of the AMRdb hit. All the columns of the table are sortable and searchable. To display the alignment between the query sequence and the AMRdb best hit sequence, click on the (+) sign in front of Identity ID.

[Download Alignment](#)

Show 10 entries

[Copy](#)

[CSV](#)

[Excel](#)

[PDF](#)

[Print](#)

Search:

Identity ID	User ID	Identity	E_Value	Gene Symbol	Allele	Protein Name	Protein ID	Drug Family
12604	Test_Sequence_1	100.0	0.0	rpoB2		DNA-directed RNA polymerase	BAD59497.1	peptide antibiotic, rifamycin antibiotic

Sequence Alignment

```
Query|Test_Sequence_1|1-1162 VLEGRIVTS SRTESPLAAP GVPGAPRRLS FARIREPLAV PGLLDIQTES
Hit|rpoB2 MLEGRIVTS SRTESPLAAP GVPGAPRRLS FARIREPLAV PGLLDIQTES

FGWLIGAPDW CARAAARGTE PVAGLAEVLA EISPIEDFAG TMSLTLSOPR
FGWLIGAPDW CARAAARGTE PVAGLAEVLA EISPIEDFAG TMSLTLSOPR

FEEVKASVEE CKDKDLTYAA PWFVTAEFVN NNTGEIKSQT VFMGDFPHMT
FEEVKASVEE CKDKDLTYAA PWFVTAEFVN NNTGEIKSQT VFMGDFPHMT
```

B

BLAST OUTPUT AGAINST AMRDB

The best hit based on AMR-Finder result is shown for each query sequence combined with the metadata of the AMRdb hit. All the columns of the table are sortable and searchable. To display the alignment between the query sequence and the AMRdb best hit sequence, click on the (+) sign in front of Identity ID.

Download Alignment

Show 10 entries

Copy CSV Excel PDF Print

Search:

Identity ID	User ID	Identity	E_Value	Gene Symbol	Allele	Protein Name	Protein ID	Drug Family
12604	Example_1	100.0	0.0	rpoB2		DNA-directed RNA polymerase	BAD59497.1	peptide antibiotic, rifamycin antibiotic

Sequence Alignment

Query_1|Example_1|1-1162

Hit|rpoB2

VLEGRIVTS SRTESPLAAP GVPGAPRRLS FARIREPLAV PGLLDIQTES
MLEGRIVTS SRTESPLAAP GVPGAPRRLS FARIREPLAV PGLLDIQTES

FGWLIGAPDW CARAAARGTE PVAGLAEVLA EISPIEDFAG TMSLTLSQPR
FGWLIGAPDW CARAAARGTE PVAGLAEVLA EISPIEDFAG TMSLTLSQPR

FEEVKASVEE CKDKDLTYAA PWFVTAEFVN NNTGEIKSQT VFMGDFPMMT
FEEVKASVEE CKDKDLTYAA PWFVTAEFVN NNTGEIKSQT VFMGDFPMMT

2.3. Browse and Search

The Browse and Search tool enables users to view, search, and export the data contained within the AMR-DB based on different classifications such as gene name, drug targets, threat level and organism names. Users can perform a global search (**A**) across all data fields using the search function or can tailor their search to specific data fields using the advanced search (**B**) option. The results of both a global (**A**) and advanced (**B**) search are displayed in tabular format with the most commonly searched data types preferentially displayed. Users can display detailed information about each gene by clicking on the Identity ID link to open a detailed gene information page (**C**)

A

AMRdb Browse/Search Module

Browse and search the data contained within the AMRdb. Commonly searched data types are preferentially displayed. Each data type is also sortable.

Example search function: To display all *Escherichia coli* genes of the beta-lactam drug family, enter "Escherichia coli beta-lactam" in the main search bar. AMRdb data will be filtered and only those AMR genes found in *Escherichia coli* AND that belong to the beta-lactam drug family are displayed. For more information see [help page](#).

Show entries

Export

Advanced Search

Search:

Identity ID	Gene Symbol	Allele	Protein/Product Name	Protein ID	Drug Family	Organism
11116	blaNDM	1	beta-lactamase	CAZ39946.1	penam, cephamycin, carbapenem, cephalosporin	Klebsiella pneumoniae
11117	blaNDM	10	beta-lactamase	AGT37351.1	penam, carbapenem, cephalosporin, cephamycin	Klebsiella pneumoniae
11118	blaNDM	11	beta-lactamase	AJE61443.1		Escherichia coli
11119	blaNDM	12	beta-lactamase	BAQ79439.1	penam, carbapenem, cephalosporin, cephamycin	Escherichia coli
11120	blaNDM	13	beta-lactamase	BAQ02518.1	penam, carbapenem, cephalosporin, cephamycin	Escherichia coli

B

Advance Search

Field Name	Operator	Values	And / Or	+ Add
<input type="text" value="Gene Symbol"/>	<input "="" type="text" value="="/>	<input type="text" value="aac(6')"/>	<input type="text" value="AND"/>	Delete Row
<input type="text" value="Taxon Genus"/>	<input "="" type="text" value="="/>	<input type="text" value="Escherichia"/>	<input type="text" value="AND"/>	Delete Row
<input type="text" value="Taxon Species"/>	<input "="" type="text" value="="/>	<input type="text" value="coli"/>	<input type="text" value="AND"/>	Delete Row
<input type="text" value="Mol Type"/>	<input "="" type="text" value="="/>	<input type="text" value="Plasmid"/>	<input type="text" value="AND"/>	Delete Row
<input type="text" value="Specimen Collection Date"/>	<input "="" type="text" value=">="/>	<input type="text" value="2005"/>	<input type="text" value="AND"/>	Delete Row

Submit

C

The detailed gene page displays identification, metadata, antibiogram, taxonomy, and sequence information for a selected AMR gene. Toggle between the different sets of information to display the associated data.

Gene details of AMR gene ID # 11116

IDENTITY

CLASSIFICATION

ANTIBIOGRAM

THREAT LEVEL

TAXONOMY

SEQUENCE

METADATA

HIT

Gene Symbol:	blaNDM
Gene Alternative Names:	blaNDM-1 NDM-1
Gene Family:	NDM beta-lactamase
Gene Class:	-
Allele:	1
Parent Allele Family:	-
Parent Allele:	NDM
Product/Protein Name:	beta-lactamase
Product/Protein Alternative Names:	cephalosporinase, penicillinase
Protein ID:	CAZ39946.1
EC Number:	3.5.2.6

3. Primer

3.1. Primer Catalog

The primer catalog tool provides a listing of all primers stored in the AMR-DB. Users can perform a global search of the available primers using the search function to identify specific primers of interest.

Primer Catalog

Primer Catalog provides listing and advance search of all primers available in the system. For more information see [help page](#).

Show entries

Search:

Primer	Target	FWD	REV
ACC	Screening of AmpC	CCTCCGTCAGCTCAGATACA	TTTACTAGGTGCAAGCCAGACA
ACT	Screening of AmpC	CGTTACGCCGCTGATGAAAG	CCAGGGTAAGGCCTTTCCTG
AIM	Screening of MBL	ATGAAACGTCGCTTCACCCTGCTG	TCAAGGCCGCGCGCCGCTGGA
CMY	Screening of AmpC	GGGGCATATGATGAAAAATCGTTA	CCGGATCCTCAACCGGCAACTG
CMY	Screening of AmpC	AACACACTGATTGCGTCTGA	TCCTGGGCCTCATCGTCAGTTAT
CTX	Screening of ESBL	CGCTTGCGATGTGCAG	ACCGCGATATCGTTGGT
DHA	Screening of AmpC	GCAAAGCCAGTATGCGTACG	CAGTTGTTGCGCCCGTTTTA
FOX	Screening of AmpC	TAGTCTGGGCCAGCCATTTG	GTAACCGGATTGGCCTGGAA
GES	Screening of Carbapenemases	CTTCATTCAGCGCACTATTAC	TAACTTGACCGACAGAGG
GIM	Screening of MBL	AACCTCCAACCTTGCCATGC	TCGACACACCTTGGTCTGAA

Showing 1 to 10 of 24 entries

Previous 2 3 Next

3.2. Primer Finder

The Primer Finder is a web-based tool that enables *in silico* testing of the performance of PCR and RT-PCR primers used for ARG diagnostics. It will support multiple use cases (ARG-specific primers and flanking gene-specific primers). Unless the user specifies an input sequence or GenBank accession to test (see screenshot below), Primer Finder will first check primer-binding to ARGs internal to the AMR-DB (default) from a user-provided multi-FASTA sequence of primers or pasted sequence of forward and reverse primers. Primer Finder will produce an output report of the predicted binding sites, target(s) hit, amplicon sequence, length, position, number of degenerate bases and mismatches per primer, strand, gene annotations overlapping the amplicon and amplicon FASTA file. If the user specifies an input sequence or GenBank accession to query primer-binding sites, possibly to check primers external to ARGs (a.k.a., flanking primers), Primer Finder will first find the ARGs on the input sequence using our newly-developed AMR-Finder, and annotate ARGs within the input sequence, search for primer-binding sites and generate a report. The produced report displays multiple binding sites for primers on the specified genome(s). When using user-supplied sequences to query, it's critical to have as much of the target genome (in the case of single isolate screening by PCR) provided so that primer-binding specificity and amplicon length can be verified.

Primary Finder

PCR primer finder assesses the specificity of primers on AMR genes or a target genome. PCR primer finder uses open source [Simulate_PCR](#) tools for predicting both desired and off-target amplification products.

For more information see AMRdb [help page](#)

Primer Forward Sequence:

[USE AN EXAMPLE PRIMER FORWARD SEQUENCE](#)

Select File to upload:

No file selected.

Primer Reverse Sequence:

[USE AN EXAMPLE PRIMER REVERSE SEQUENCE](#)

Select File to upload:

No file selected.

Reference:

☒ AMR-DB(default)

☐ No file selected.

☐ GenBank Accession

4. Support

Access the user and admin manuals through this tab.


5. Contact

Contact page allows user to submit questions, comments or issues to the AMR-DB Team.


Contact Us

If you have questions about or would like assistance using the ARMdb, please contact us using the form below.


Name*





Email*



Subject*



Message*



6. Admin

After the user signs into the AMR-DB, a new menu will be shown (F) “ADMIN”, which has three sub-menus: F.1.) Submit New Data, and F.2.) Edit Data, and F.3.) Submit New Primer.

6.1. Submit Data.

When the user submits a new entry in the database, the system will automatically assign a unique Identity ID for the new submission. The user needs to provide the identity details in the IDENTITY tab, taxonomy information in the CLASSIFICATION tab, any antibiogram data under the ANTIBIOGRAM tab, CDC antibiotic threat level under the THREAT LEVEL tab, sequence information in their respective fields of the SEQUENCE tab, and other metadata information under the METADATA tab.

Some of the data (e.g., “gene symbol”) is required, while some are optional (e.g., “antibiogram data”). Once the user completes data entry, clicking on the “next” button at the bottom of the tab will shift to the next tab. The data submission button is in the last tab.

Submit new data to the AMRdb

This page allows the user to submit new AMR data into the AMRdb. The page is split into six different sections or tabs: 1) Identification details of the AMR entry, 2) drug classification and SNP variant information, 3) antibiogram data if any, 4) threat level of the organism, 5) taxonomy of the organism, 6) protein and nucleotide sequence, and 7) any metadata associated with the AMR sequence. For more information see the [help page](#).

IDENTITY	CLASSIFICATION	ANTIBIOGRAM	THREAT LEVEL	TAXONOMY	SEQUENCE	METADATA
<p>Identity ID</p> <input type="text" value="148950"/>						
<p>Gene Symbol</p> <input type="text" value="e.g. AAC(1)"/>						
<p>Product/Protein Name</p> <input type="text" value="e.g. CMY-7 bla<sub>CMY-7</sub>"/>						
<p>Source</p> <input type="text" value="e.g. GenBank"/>						
<p>Source ID</p> <input type="text" value="e.g. AJ011291.1"/>						
<p>Gene Alternative Names</p> <input type="text" value="e.g. Names"/>						
<p>Gene Family</p> <input type="text" value="e.g. AAC(1)"/>						
<p>Gene Class</p> <input type="text" value="e.g."/>						
<p>Protein Alternative Names</p> <input type="text" value="e.g. Alternative Names"/>						

6.2. Edit Data.

The second sub-menu option from the Admin menu, “Edit Data”, with similar appearance to the Browse and Search Page, allows the user to edit any existing ID in the AMR-DB. The page layout is like the ID description page except all the fields are editable and there is a submit button after the last tab.

Show entries

Search:

Identity ID	Gene Symbol	Allele	Protein/Product Name	Protein ID	Drug Family	Organism
10001	aac(1)	I	aminoglycoside N-acetyltransferase	ADH03009.1		Acinetobacter baumannii
10002	aac(2')	I lb	aminoglycoside 2'-N-acetyltransferase	APB03221.1	aminoglycoside antibiotic	Paenibacillus sp.
10003	aac(2')	I a	aminoglycoside 2'-N-acetyltransferase	AAA03550.1	aminoglycoside antibiotic	Providencia stuartii
10004	aac(2')	I b	aminoglycoside 2'-N-acetyltransferase	AAC44793.1	aminoglycoside antibiotic	Mycolicibacterium fortuitum
10005	aac(2')	I c	aminoglycoside 2'-N-acetyltransferase	CCP42991.1	aminoglycoside antibiotic	Mycobacterium tuberculosis
10006	aac(2')	I d	aminoglycoside 2'-N-acetyltransferase	AAB41701.1	aminoglycoside antibiotic	Mycolicibacterium smegmatis
10007	aac(2')	I e	aminoglycoside 2'-N-acetyltransferase	NP_302635.1	aminoglycoside antibiotic	Mycobacterium leprae
10008	aac(3)	I lla	aminoglycoside N(3)-acetyltransferase	CAA39184.1	aminoglycoside antibiotic	Pseudomonas aeruginosa
10009	aac(3)	I llb	aminoglycoside N(3)-acetyltransferase	AAA25682.1	aminoglycoside antibiotic	Bosea sp.
10010	aac(3)	I llc	aminoglycoside N(3)-acetyltransferase	AAA25683.1	aminoglycoside antibiotic	Pseudomonas aeruginosa

Showing 1 to 10 of 2,876 entries

Previous 2 3 4 5 ... 288 Next

6.3. Submit New Primer.

This page enables the registered user to add new primer sequences to the Primer Catalog. The four data fields are: Primer (e.g., IMP), Target (e.g., Screening of MBL), FWD (i.e., forward primer sequence), and REV (i.e., reverse primer sequence). Sequence of primers is the conventional 5'→3' orientation. Hit "SUBMIT" when completed.

6.4. Rebuild Reference Database

This page enables the registered user to rebuild reference database by pulling data from MySQL database. During build, all new reference sequences added in the MySQL database will be added to AMR-Finder reference database. Hit "REBUILD" to initiate the reference database build process