

DATABASES, RESOURCES AND TOOLS
FOR ANTIMICROBIAL RESEARCH

AMR WORKSHOP

15th October 2021

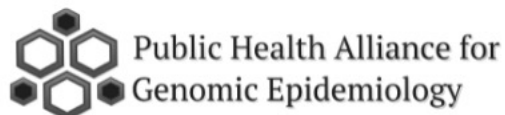
3-7:30 PM London Time

7-11:30 AM Vancouver Time

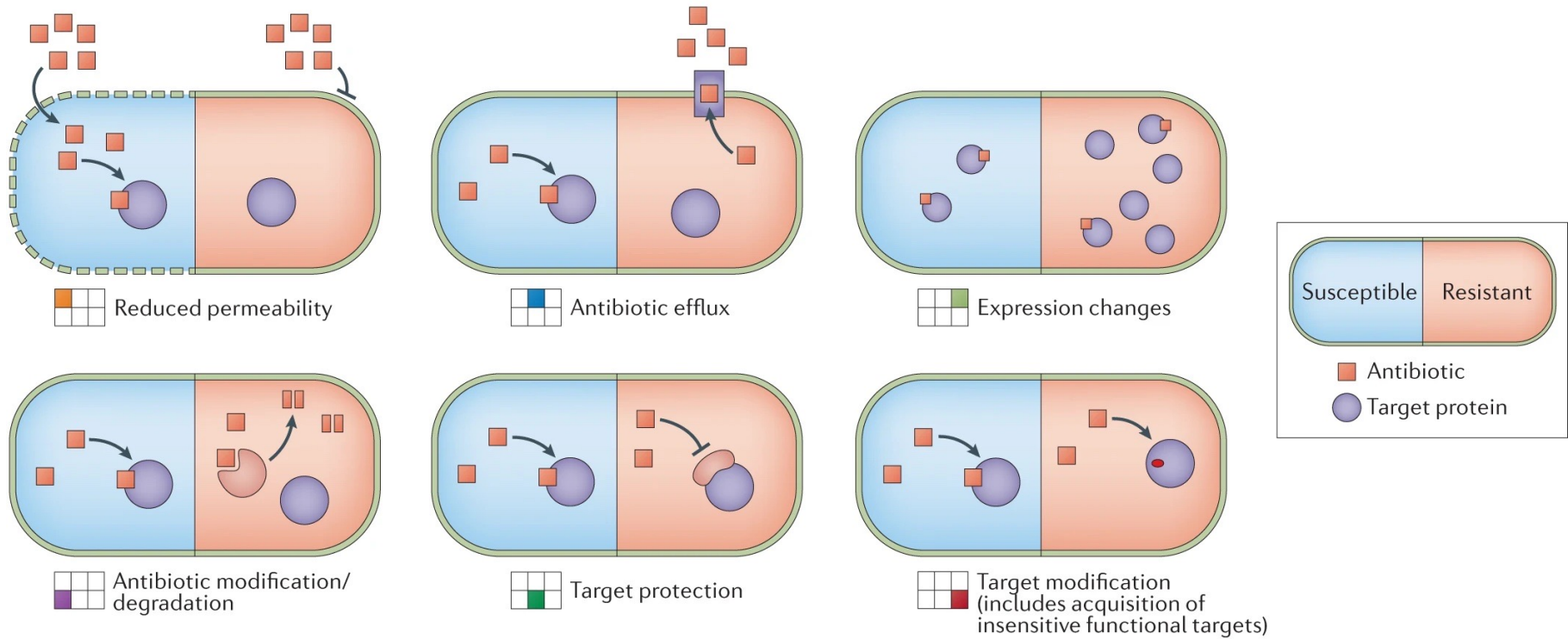
Introduction to databases and resources for AMR genomics

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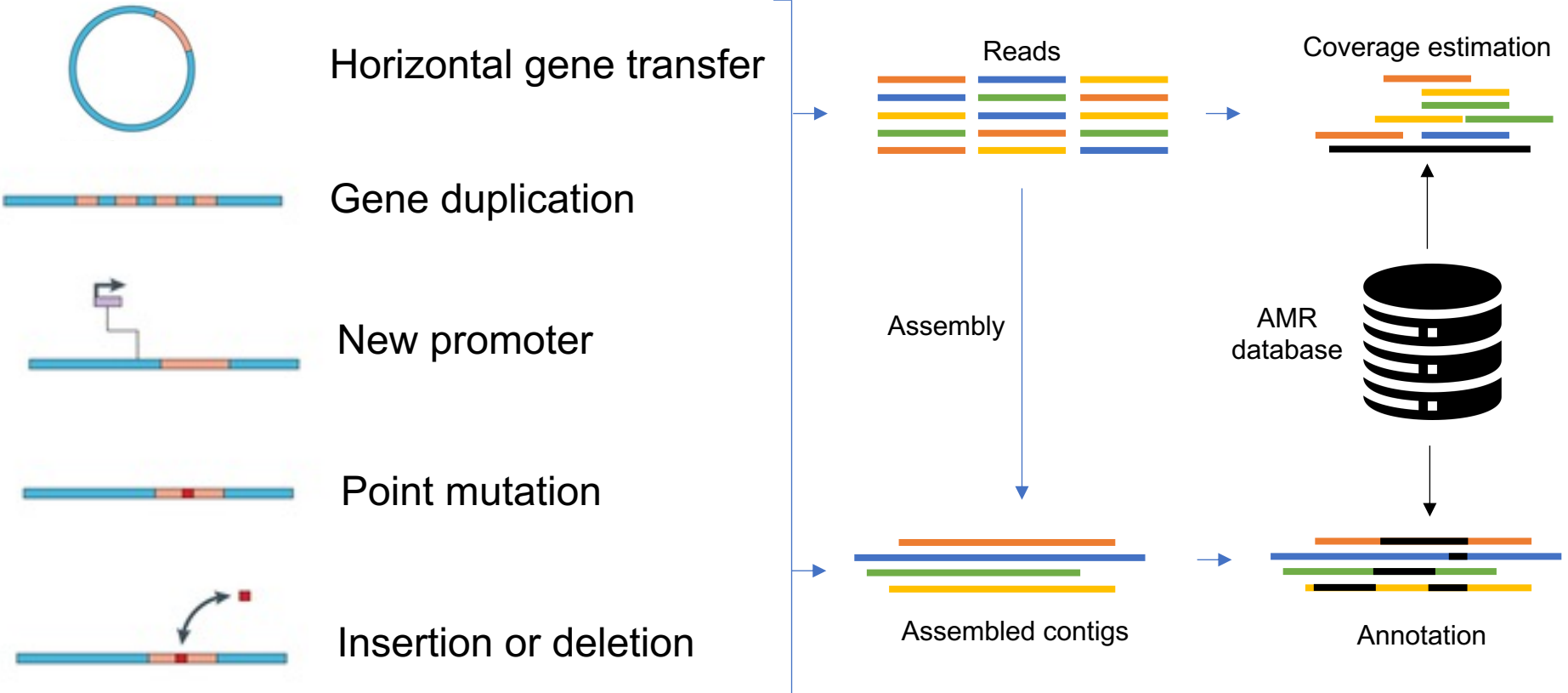


Antimicrobial resistance (AMR) mechanisms



Genetic determinants of AMR

Resistance / target gene
Promoter



AMR databases: overview

Database	Description	Link	Status
General databases			
CARD ⁶⁷	<ul style="list-style-type: none"> • Ontology-based database that provides comprehensive information of AR genes and their resistance mechanisms • Currently contains >2,200 protein homologues and includes a curated set of resistance-conferring chromosomal mutations in protein-coding genes 	https://card.mcmaster.ca/	Active; launched in 2013; updated monthly
Resfinder ⁷²	Collation of AR genes involved in HGT events	https://cge.cbs.dtu.dk//services/ResFinder/	Active; started in 2012; update regularly; last update in February 2019
ResfinderFG ⁸⁴	Collection of resistance gene variants identified in multiple functional metagenomics studies	https://cge.cbs.dtu.dk/services/ResFinderFG/	Active; last update in November 2016
Resfams ²⁶	A profile HMM-based curated database confirmed for AR function	http://www.dantaslab.org/resfams/	Active; last update in January 2015
ARDB ⁶⁵	<ul style="list-style-type: none"> • First centralized resource of AR gene information • Manually curated; contains >4,500 AR sequences 	https://ardb.cbcb.umd.edu/	Archived; last updated in 2009
MEGARes ¹⁷⁸	<ul style="list-style-type: none"> • Collation of multiple databases (CARD, ARG-ANNOT and ResFinder) to avoid redundancy between entries • For high-throughput screening and statistical analysis 	https://megares.meglab.org/	Active; last update in December 2016
NDARO	<ul style="list-style-type: none"> • Collated and curated data from multiple databases (CARD, Lahey, Pasteur Institute β-Lactamases and ResFinder) • Contains 4,500 AR sequences 	https://www.ncbi.nlm.nih.gov/bioproject/PRJNA313047	Active; started in 2016
ARG-ANNOT ⁶⁶	<ul style="list-style-type: none"> • Repository of >1,800 AR sequences collated from scientific literature and online resources • Also includes point mutation data for select AR-associated chromosomal genes 	Not available	Archived; last update in May 2018
Mustard ⁸⁵	Resource containing 6,095 AR determinants from 20 families, including curated sets of AR genes identified in functional metagenomics studies	http://mgps.eu/Mustard/	Active; last update in November 2018
FARME database ⁸³	Curated set of microbial sequences functionally screened to confer resistance in various functional metagenomics studies of different habitats	http://staff.washington.edu/jwallace/farme/	Active; last update in 2017
SARG (v2) ⁷⁴	<ul style="list-style-type: none"> • Hierarchical structured database derived from ARDB, CARD and NCBI-NR database • Contains >12,000 AR genes; also includes profile HMMs for 189 AR genes subtypes 	http://smile.hku.hk/SARGs	Active
Lahey list of β -lactamases ⁷⁰	First initiative to compile known β -lactamases and assign nomenclature to novel ones	http://www.lahey.org/Studies/	Archived; last update in 2015
BLDB ¹⁷⁹	Manually curated database for AR enzymes classified by class, family and subfamily	http://bldb.eu/	Active; last update in November 2018
LacED ^{68,69}	Curated database of TEM and SHV β -lactamases, including a curated set of known TEM and SHV variants	http://www.laced.uni-stuttgart.de/	TEMLacED active; last update in 2017; SHVED archived; last update in April 2010
CBMAR ⁷¹	Database that identifies and characterizes novel β -lactamases on the basis of Ambler classification	http://proteininformatics.org/mkumar/lactamasedb/	Last update in September 2014

AMR databases: focus



ResFinder 4.1

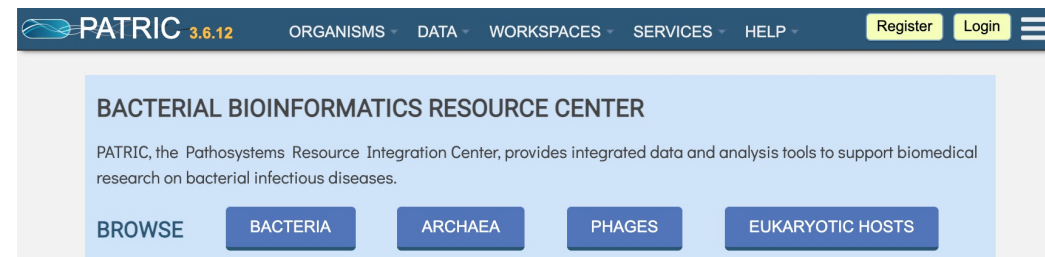


The Comprehensive Antibiotic Resistance Database
A bioinformatic database of resistance genes, their products and associated phenotypes.
6453 Ontology Terms, 4937 Reference Sequences, 1788 SNPs, 2775 Publications, 4983 AMR Detection Models
Resistome predictions: 263 pathogens, 14795 chromosomes, 2675 genomic islands, 30591 plasmids, 105556 WGS assemblies, 231629 alleles
[CARD Bait Capture Platform 1.0.0](#) | [State of the CARD 2021 Presentations & Demonstrations](#)



[Health](#) > [Pathogen Detection](#) > National Database of Antibiotic Resistant Organisms (NDARO) ^ v

National Database of Antibiotic Resistant Organisms (NDARO)



- Broad in scope (species, AMR families, antibiotics)
- Build upon each other and add expertise
- Custom annotation tools
- Regularly updated and active

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ResFinder 4.1

Service

Instructions

Output

Article abstract

Citations

Overview of genes

Database history

ResFinder identifies acquired genes and/or finds chromosomal mutations mediating antimicrobial resistance in total or partial DNA sequence of bacteria.

ResFinder and PointFinder software: [\(2021-06-30\)](#)

ResFinder database: [\(2021-09-23\)](#)

PointFinder database: [\(2021-02-01\)](#)

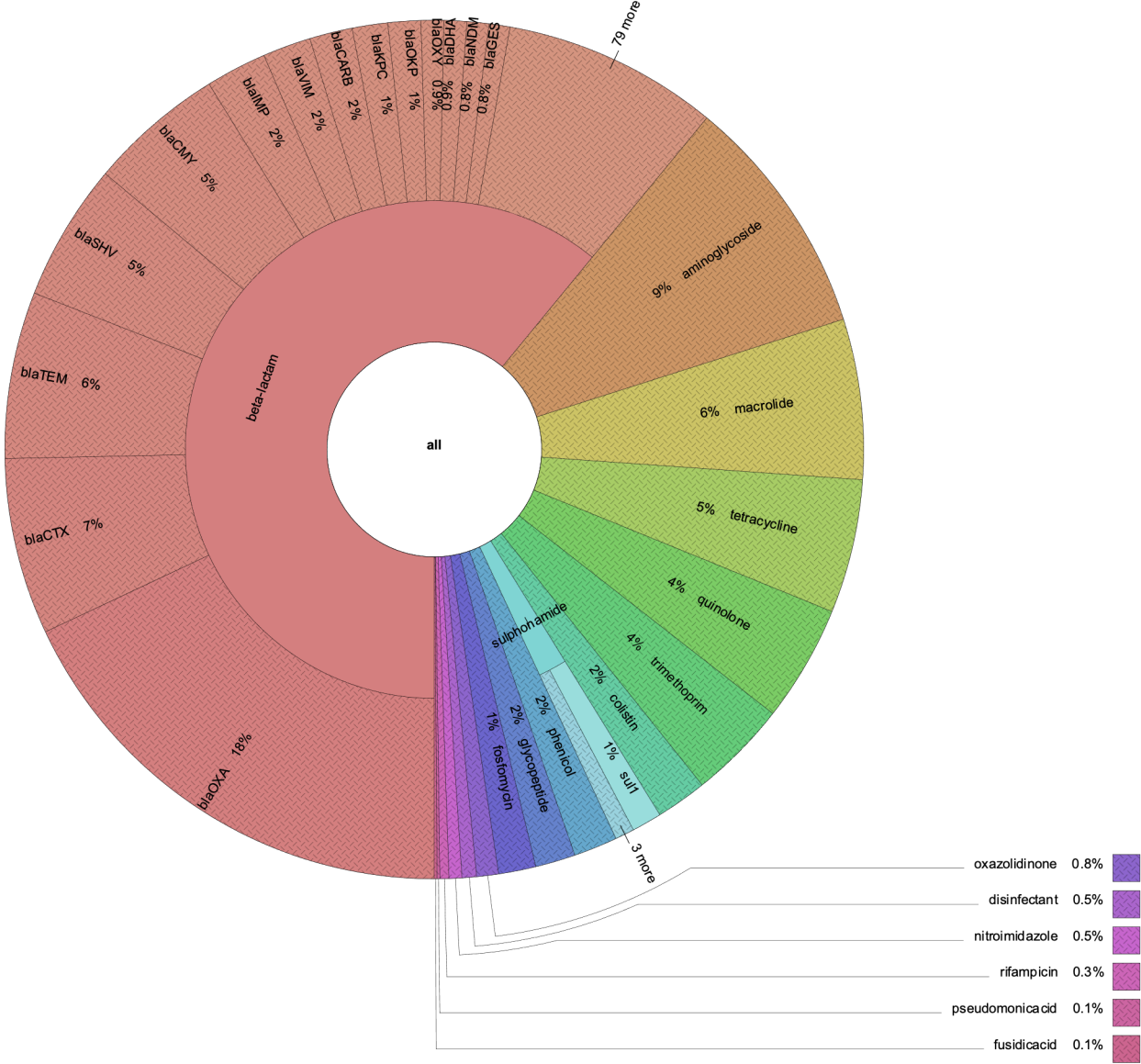
The database is curated by:

Frank Møller Aarestrup

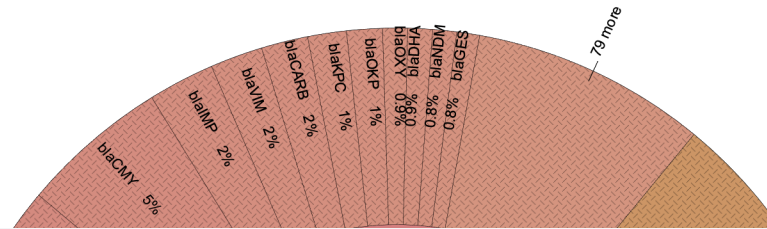
[\(click to contact\)](#)

- Acquired genes (n=2919) and/or chromosomal mutations
 - *Campylobacter* spp.
 - *Campylobacter jejuni*
 - *Campylobacter coli*
 - *Escherichia coli*
 - *Salmonella* spp.
 - *Plasmodium falciparum*
 - *Neisseria gonorrhoeae*
 - *Mycobacterium tuberculosis*
 - *Enterococcus faecalis*
 - *Enterococcus faecium*
 - *Klebsiella*
 - *Helicobacter pylori*
 - *Staphylococcus aureus*

ResFinder: Distribution of gene database

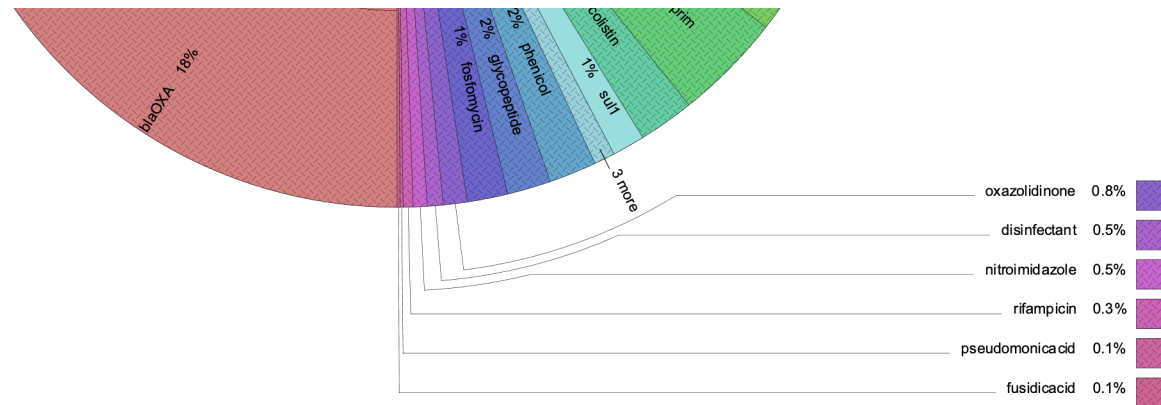


ResFinder: Distribution of gene database



genomicepidemiology/resfinder_db

pseudomonicacid.fsa	9.21 KB	2021-03-09	added aac(3)-IIa_6_CP023555, blaCMY-150_...
quinolone.fsa	91.63 KB	2021-06-12	Fixed oqxA and oqxB gene names
rifampicin.fsa	4.77 KB	2020-08-28	Updated with genes ARR-8,blaIMI-4,ant(3'')-I...
sulphonamide.fsa	45.76 KB	2018-05-24	Reformat phenicol, rifampicin and sulphonami...
tetracycline.fsa	226.64 KB	2020-06-02	Update db with blaVMB-1,blaLMB-1,blaCMY-1...
trimethoprim.fsa	51.95 KB	2021-04-13	fixed dfra19_2 bug



ResFinder: AMR phenotype prediction results

ceftriaxone	beta-lactam	Resistant	blaCTX-M-15 (blaCTX-M-15_AY044436)
ceftazidime	beta-lactam	Resistant	blaCTX-M-15 (blaCTX-M-15_AY044436), blaNDM-1 (blaNDM-1_FN396876)
fortimicin	aminoglycoside	No resistance	
carbomycin	macrolide	No resistance	
ticarcillin	beta-lactam	Resistant	blaCTX-M-15 (blaCTX-M-15_AY044436)
azithromycin	macrolide	No resistance	
chlorhexidine	quaternary ammonium compound	No resistance	
kasugamycin	aminoglycoside	No resistance	
chloramphenicol	amphenicol	Resistant	catB3 (catB3_AJ009818), catA1 (catA1_V00622), catB3 (catB3_U13880)
cetylpyridinium chloride	quaternary ammonium compound	No resistance	
ampicillin+clavulanic acid	beta-lactam	Resistant	blaNDM-1 (blaNDM-1_FN396876), blaOXA-1 (blaOXA-1_HQ170510)
cefotaxime	beta-lactam	Resistant	blaCTX-M-15 (blaCTX-M-15_AY044436), blaNDM-1 (blaNDM-1_FN396876)

ResFinder: AMR genotype results (genes and chromosomal mutations)

Aminoglycoside									
Resistance gene	Identity	Alignment Length/Gene Length	Position in reference	Contig or Depth	Position in contig	Phenotype	PMID	Accession no.	Notes
aac(6')-Ib-cr	100.0	600/600	1..600	JN420336.1 Klebsiella pneumoniae plasmid pNDM-MAR, complete sequence	2361..2960	ciprofloxacin	unpublished	DQ303918	MIC of ciprofloxacin does not always increase above ECOFF PMID 16369542
Beta-lactam									
Resistance gene	Identity	Alignment Length/Gene Length	Position in reference	Contig or Depth	Position in contig	Phenotype	PMID	Accession no.	Notes
blaNDM-1	100.0	813/813	1..813	JN420336.1 Klebsiella pneumoniae plasmid pNDM-MAR, complete sequence	9726..10538	amoxicillin, amoxicillin+clavulanic acid, ampicillin, ampicillin+clavulanic acid, cefepime, cefixime, cefotaxime, cefoxitin, ceftazidime, ertapenem, imipenem, meropenem, piperacillin, piperacillin+tazobactam	19770275	FN396876	Subclass B1
blaCTX-M-15	100.0	876/876	1..876	JN420336.1 Klebsiella pneumoniae plasmid pNDM-MAR, complete sequence	263730..264605	amoxicillin, ampicillin, aztreonam, cefepime, cefotaxime, ceftazidime, ceftriaxone, piperacillin, ticarcillin	11470367, 26169409	AY044436	Class A
blaOXA-1	100.0	831/831	1..831	JN420336.1 Klebsiella pneumoniae plasmid pNDM-MAR, complete sequence	1400..2230	amoxicillin, amoxicillin+clavulanic acid, ampicillin, ampicillin+clavulanic acid, cefepime, piperacillin, piperacillin+tazobactam	10898672, 16735436	HQ170510	Class D; OXA-1-like; Alternative name blaOXA-30;

ResFinder: AMR genotype results (genes and chromosomal mutations)

Aminoglycoside									
Resistance gene	Identity	Alignment Length/Gene Length	Position in reference	Contig or Depth	Position in contig	Phenotype	PMID	Accession no.	Notes
				JN420336.1 <i>Klebsiella pneumoniae</i>					MIC of ciprofloxacin does not always
Amphenicol									
Resistance gene	Identity	Alignment Length/Gene Length	Position in reference	Contig or Depth	Position in contig	Phenotype	PMID	Accession no.	Notes
catA1	99.8484848485	660/660	1..660	JN420336.1 <i>Klebsiella pneumoniae</i> plasmid pNDM-MAR, complete sequence	139127..139786	chloramphenicol	390403	V00622	Chloramphenicol acetyltransferase
catB3	100.0	442/633	1..442	JN420336.1 <i>Klebsiella pneumoniae</i> plasmid pNDM-MAR, complete sequence	821..1262	chloramphenicol	1662753	AJ009818	Chloramphenicol acetyltransferase
catB3	100.0	442/633	1..442	JN420336.1 <i>Klebsiella pneumoniae</i> plasmid pNDM-MAR, complete sequence	821..1262	chloramphenicol	7793874	U13880	Chloramphenicol acetyltransferase
blaCTX-M-15	100.0	876/876	1..876	<i>pneumoniae</i> plasmid pNDM-MAR, complete sequence	263730..264605	efepime,cefotaxime,ceftazidime,ceftriaxone,piperacillin,ticarcillin	11470367,26169409	AY044436	Class A
blaOXA-1	100.0	831/831	1..831	JN420336.1 <i>Klebsiella pneumoniae</i> plasmid pNDM-MAR, complete sequence	1400..2230	amoxicillin,amoxicillin+clavulanic acid,ampicillin,ampicillin+clavulanic acid,cefepime,piperacillin,piperacillin+tazobactam	10898672,16735436	HQ170510	Class D;OXA-1-like;;Alternative name blaOXA-30;

ResFinder: AMR genotype results (genes and chromosomal mutations)

Aminoglycoside									
Resistance gene	Identity	Alignment Length/Gene Length	Position in reference	Contig or Depth	Position in contig	Phenotype	PMID	Accession no.	Notes
				JN420336.1 Klebsiella pneumoniae					MIC of ciprofloxacin does not always
Amphenicol									
Resistance gene	Detection PointFinder Genes								Notes
catA1				acrR		No gene found			phenicol transferase
				parC		No gene found			
				gyrA		No gene found			
catB3				ramR		No gene found			phenicol transferase
				ompK35		No gene found			
				ompK36		No gene found			
catB3				ompK37		No gene found			phenicol transferase
				plasmid pNDM-MAR, complete sequence					acetyltransferase
blaCTX-M-15	100.0	876/876	1..876	pneumoniae plasmid pNDM-MAR, complete sequence	263730..264605	cefepime,cefotaxime,ceftazidime,ceftriaxone,piperacillin,ticarcillin	11470367, 26169409	AY044436	Class A
blaOXA-1	100.0	831/831	1..831	JN420336.1 Klebsiella pneumoniae plasmid pNDM-MAR, complete sequence	1400..2230	amoxicillin,amoxicillin+clavulanic acid,ampicillin,ampicillin+clavulanic acid,cefepime,piperacillin,piperacillin+tazobactam	10898672, 16735436	HQ170510	Class D;OXA-1-like;;Alternative name blaOXA-30;

Comprehensive Antibiotic Resistance Database (CARD)



The Comprehensive Antibiotic Resistance Database

A bioinformatic database of resistance genes, their products and associated phenotypes.

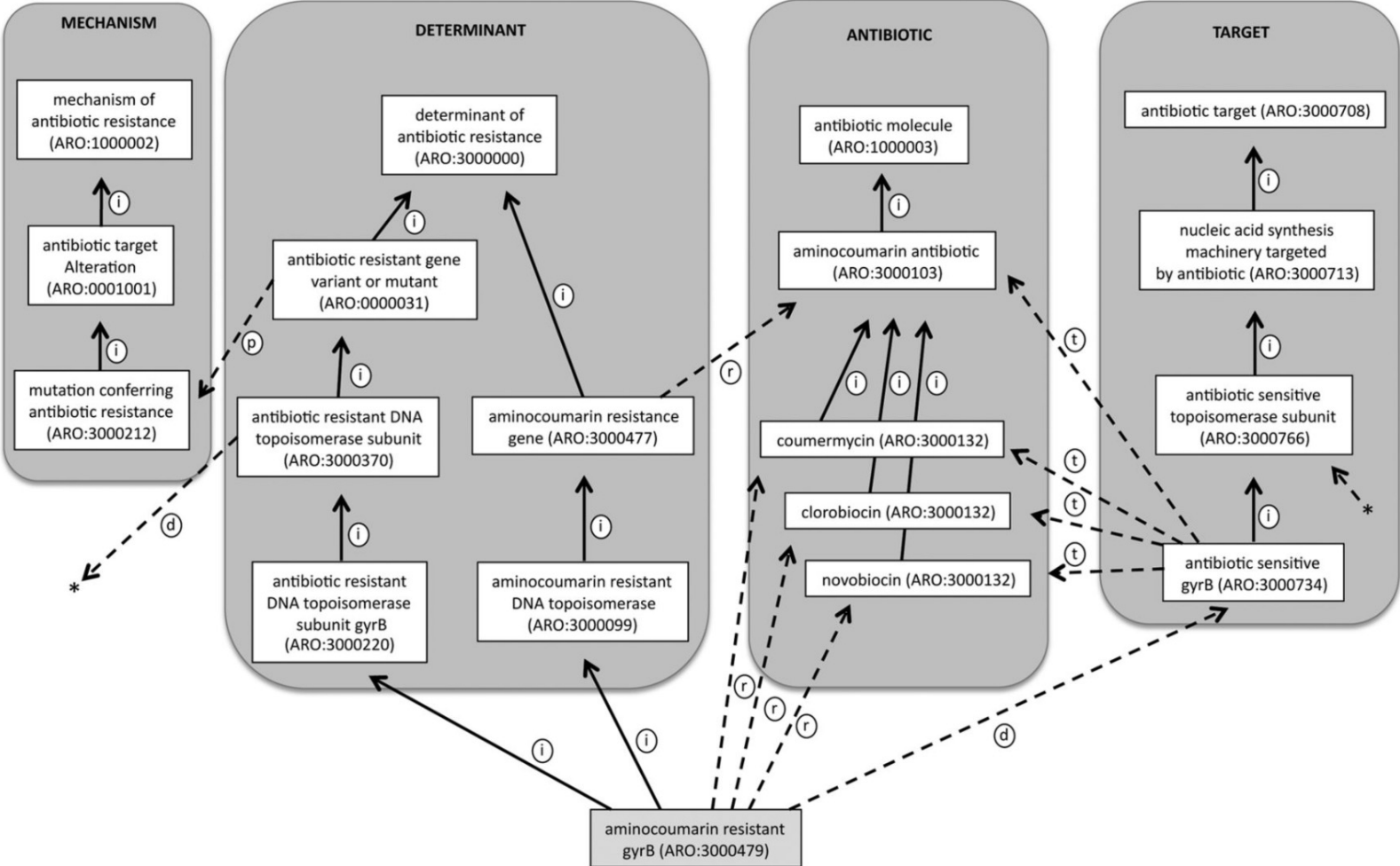
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Resistome predictions: 263 pathogens, 14795 chromosomes, 2675 genomic islands, 30591 plasmids, 105556 WGS assemblies, 231629 alleles

[CARD Bait Capture Platform 1.0.0](#) | [State of the CARD 2021 Presentations & Demonstrations](#)

- ResFinder
- ARG-ANNOT
- NCBI National Database of Antibiotic Resistant Organisms (NDARO)
- Antibiotic Resistance Genes Database (ARDB)
- Beta-lactamase Database..and more
- Literature & domain knowledge experts

Antibiotic Resistance Ontology (ARO)



Antibiotic Resistance Ontology (ARO)

CARD

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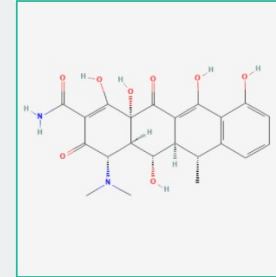
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doxycycline [Antibiotic]

[Download Sequences](#)



Accession	ARO:0000069
Synonym(s)	<i>Vibramycine Doxytetracycline Vibramycin Azodoxat Deoxyomykoin Doxycyclinum Doxiciclina Doxitard Vibravenos</i>
Definition	Doxycycline is second generation semi-synthetic derivative of the tetracycline group of antibiotics. It inhibits bacterial protein synthesis by binding to the 30S subunit of the bacterial ribosome and preventing the aminotransferase-tRNA from associating with the ribosome.
Drug Class	tetracycline antibiotic
Classification	2 ontology terms Show
Parent Term(s)	1 ontology terms Hide + tetracycline antibiotic [Drug Class]
Sub-Term(s)	13 ontology terms Hide + antibiotic sensitive 16S rRNA targeted_by_antibiotic + tetX confers_resistance_to_antibiotic + tet32 confers_resistance_to_antibiotic + tet36 confers_resistance_to_antibiotic + tetB(P) confers_resistance_to_antibiotic

Predicting AMR determinants using Resistance Gene Identifier (RGI)

Comprehensive Antibiotic Resistance Database (CARD)

CARD
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The Comprehensive Antibiotic Resistance Database
A bioinformatic database of resistance genes, their products and associated phenotypes.
4498 Ontology Terms, 2984 Reference Sequences, 1337 SNPs, 2685 Publications, 3030 AMR Detection Models
Resistome predictions: 85 pathogens, 8046 chromosomes, 18337 plasmids, 90531 WGS assemblies, 182532 alleles
CARD is Updated Monthly | CARD Bait Capture Platform Released

Browse
The CARD is a rigorously curated collection of characterized, peer-reviewed resistance determinants and associated antibiotics, organized by the Antibiotic Resistance Ontology (ARO) and AMR gene detection models.

Analyze
The CARD includes tools for analysis of molecular sequences, including BLAST and the Resistance Gene Identifier (RGI) software for prediction of resistome based on homology and SNP models.

Download
CARD data and ontologies can be downloaded in a number of formats. RGI software is available as a command-line tool. CARD Bait Capture Platform sequences and protocol available for download.

Resistomes, Variants, & Prevalence
Computer-generated resistome predictions for 85 important pathogens. Includes sequence variants beyond those reported in the scientific literature, as well as prevalence statistics for AMR genes among pathogens, genomes, and plasmids.

CARD-Live
The CARD-Live project collects pathogen identification, MLST, AMR gene list, date, and geographical region for genome sequences submitted to RGI online, providing a dynamic view of antibiotic resistant isolates being analyzed around the world.

Timeline
CARD Developers
The CARD-Live pilot project has built CARD-Live codes pathogen and resistome data for RGI online, providing a dynamic view of antibiotic resistant isolates being analyzed around the world. card.mcmaster.ca/live

Apr 14, 2020

Bioinformatics model

Legend:
■ discovered in clinical, agricultural, or environmental isolates
■ discovered via laboratory selection experiments
Bit-score Cut-off: 1400

PMID: 25631675 | S801 | E84G

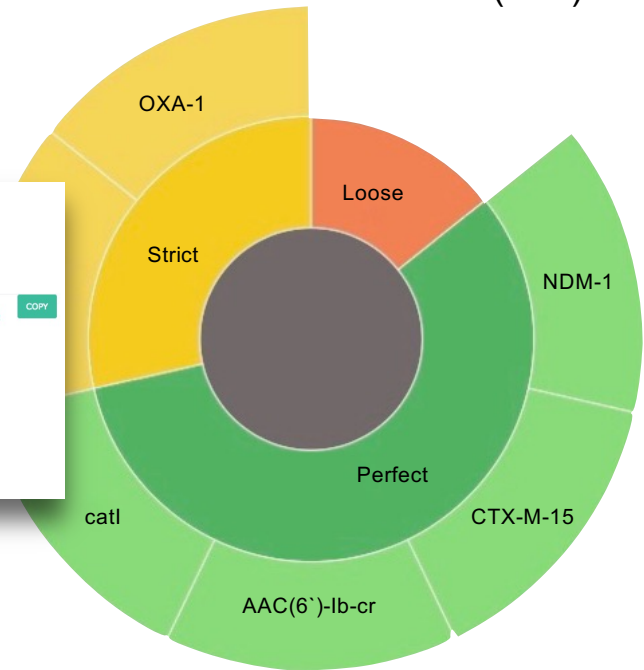
Protein DNA

>gi|AAC76055.1|-|Escherichia coli parC conferring resistance to fluoroquinolone [Escherichia coli str. K-12 substr. MG1655]
MENNARLALRETEMAYLNYSHTYVNDKALFYIGDGLKPVQRITVYANSELGLNASAF
KSEARVDDVLKYEFEQDQACREANVLAQPTSTVYVYVQDQDQMGAFDQFSTAAAMY
TESRLKATSELLLELGGQADNVVFNFDGTFQFKHLPARLFWILLNGTCTIAGVHATDI
PPIHLEVAQAALIDQPKTTLQLLDDVQDFPYPAEITTEBAEIKIYERGRGVR
RRAVWKEGAVYIALPFGVDGAVLGLIAQHWKELPVDGLADEIDENPRLIV
PNSVYDQVQVNHLEFATDLEKYEYINLNLGLDGRFAVKELELISEMVFYRDTYR
RLVRLKLVKELKELILEGLLVAFLNDEVETIIRNDEKPKALMSRFLGTLTQASALEL
KLHILAKLEPKIIEQSELEKEDQLQGLASERKNNHLKKEIQADAQAQVGDORSEFL
QEREEAASREHGLFSPYTVLQDQWRAQRHIDAPCLNFKGDSFPAAVRQGN
QVYFVYDTRVADIDFTFPAQDQSEFLQKLELPPALVQVHLEMDQKLLMADA
GYCFVCTFLVANSAGKALITLPENAVHFPVYIDASIMLAIITQAGRELMPYDGL
PGLSKGKNNKINIPSEAAAGEDGLAQLVYLPQSTLTIHVORRKLKARFELQVYGE
RKRRTLARGLQRIQWVEIDFPRASGDDEE

card.mcmaster.ca

Genomics reference sequence database

Resistance Gene Identifier (RGI)



Uses bioinformatics models to predict resistance determinants within clinical isolates

CARD: Download


CARD

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Exception: Ontologies at the Comprehensive Antibiotic Resistance Database are freely available under the [Creative Commons CC-BY license version 4.0](#) 

Exception: The CARD Bait Capture Platform is freely available under the [Creative Commons CC-BY license version 4.0](#) 

The Antibiotic Resistance Ontology (ARO), draft Mobilome Ontology (MOBIO), draft Virulence Ontology (VIRO), and Resistance Gene Identifier (RGI) are also available at [GitHub](#). The ARO is registered at the [OBO Foundry](#).

Download Ontology Files (freely available, see README), use <https://card.mcmaster.ca/latest/ontology> for automated downloads

NAME	INFO	VERSION	FILE FORMAT	DATE	ACTION
Ontology	October 2021 release - 1599 new beta-lactamases, including 72 new beta-lactamase families; separation of ADC beta-lactamases with or without carbapenemase activity; addition of diazabicyclooctane beta-lactamase inhibitors	3.1.4	OBO, OWL, TSV, JSON	2021-10-05 10:22:43.154337	DOWNLOAD

[More ontology downloads...](#)

Download CARD Data (see README), use <https://card.mcmaster.ca/latest/data> for automated downloads

NAME	INFO	VERSION	FILE FORMAT	DATE	ACTION
Data	October 2021 release - 1599 new beta-lactamases, including 72 new beta-lactamase families; separation of ADC beta-lactamases with or without carbapenemase activity; addition of diazabicyclooctane beta-lactamase inhibitors; improvements to trimethoprim-resistant dihydrofolate reductase (Dfr) detection models	3.1.4	JSON, TAB, FASTA	2021-10-05 10:24:15.645117	DOWNLOAD

[More data downloads...](#)

Track CARD Data Changes

OLD	NEW	DATE	JSON	TAB
3.1.3	3.1.4	2021-10-05 10:26:49.757985	DOWNLOAD	DOWNLOAD

[More changesets downloads...](#)

Download CARD Prevalence, Resistomes, & Variants data (see README), use <https://card.mcmaster.ca/latest/variants> for automated downloads

NAME	INFO	VERSION	FILE FORMAT	DATE	ACTION
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CARD:Live – Summary of user-submitted genome sequences

CARD:Live

Welcome to the [CARD:Live](#) dashboard. This provides summaries of detected antimicrobial resistance for user-submitted genomic samples to the online [RGI tool](#).

8376 samples

Most recent: Oct 11, 2021

[Download results](#)

Selection criteria

Please select from the options below to examine subsets of the samples.

Showing 8376/8376 samples

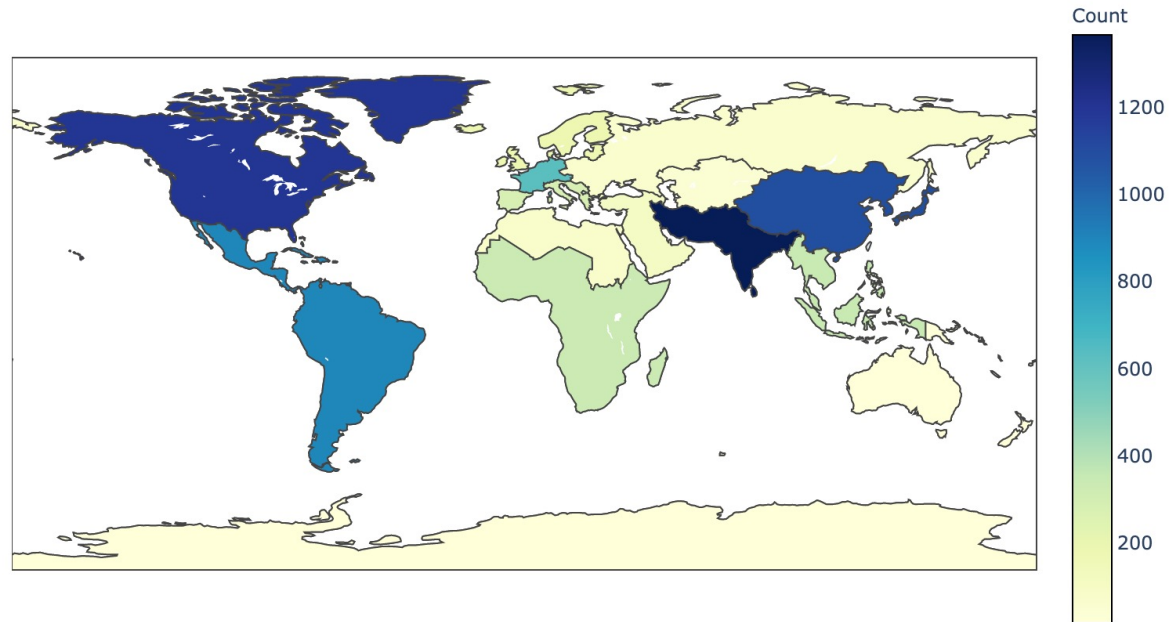
RGI *Filter by RGI results*

RGI results cutoff:

All Perfect Strict

Map *Geographic distribution of the submitted genomic samples.*

Samples by geographic region



CARD:Live – Summary of user-submitted genome sequences

Drug class resistances

CARD:Live

Welcome to the [CARD:Live](#) dashboard. This provides summaries of detected antimicrobial resistance for user-submitted genomic samples to the online [RGI tool](#).

8376 samples

Most recent: Oct 11, 2021

[Download results](#)

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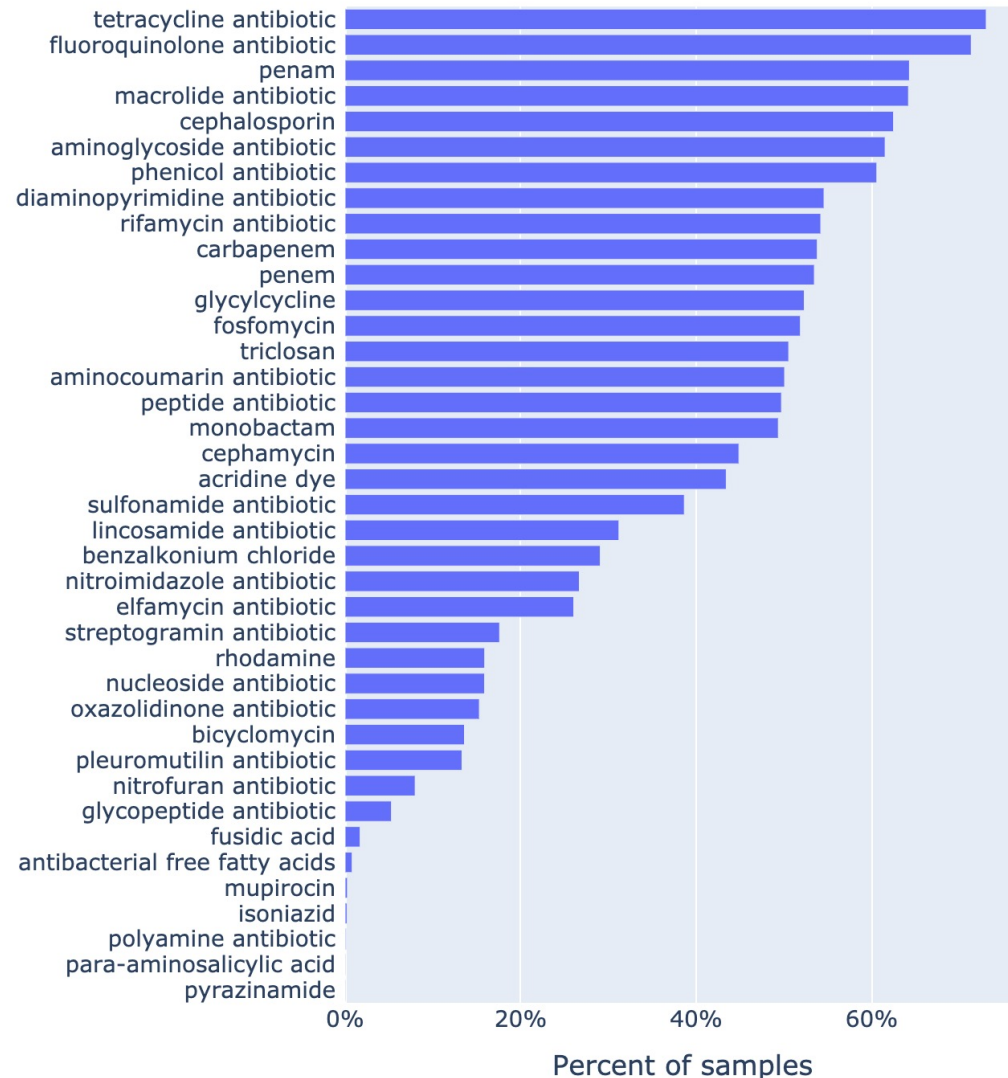
Please select from the options below to examine subsets of the samples.

Showing 8376/8376 samples

RGI *Filter by RGI results*

RGI results cutoff:

All Perfect Strict



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CARD:Live

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8376 samples

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[Download results](#)

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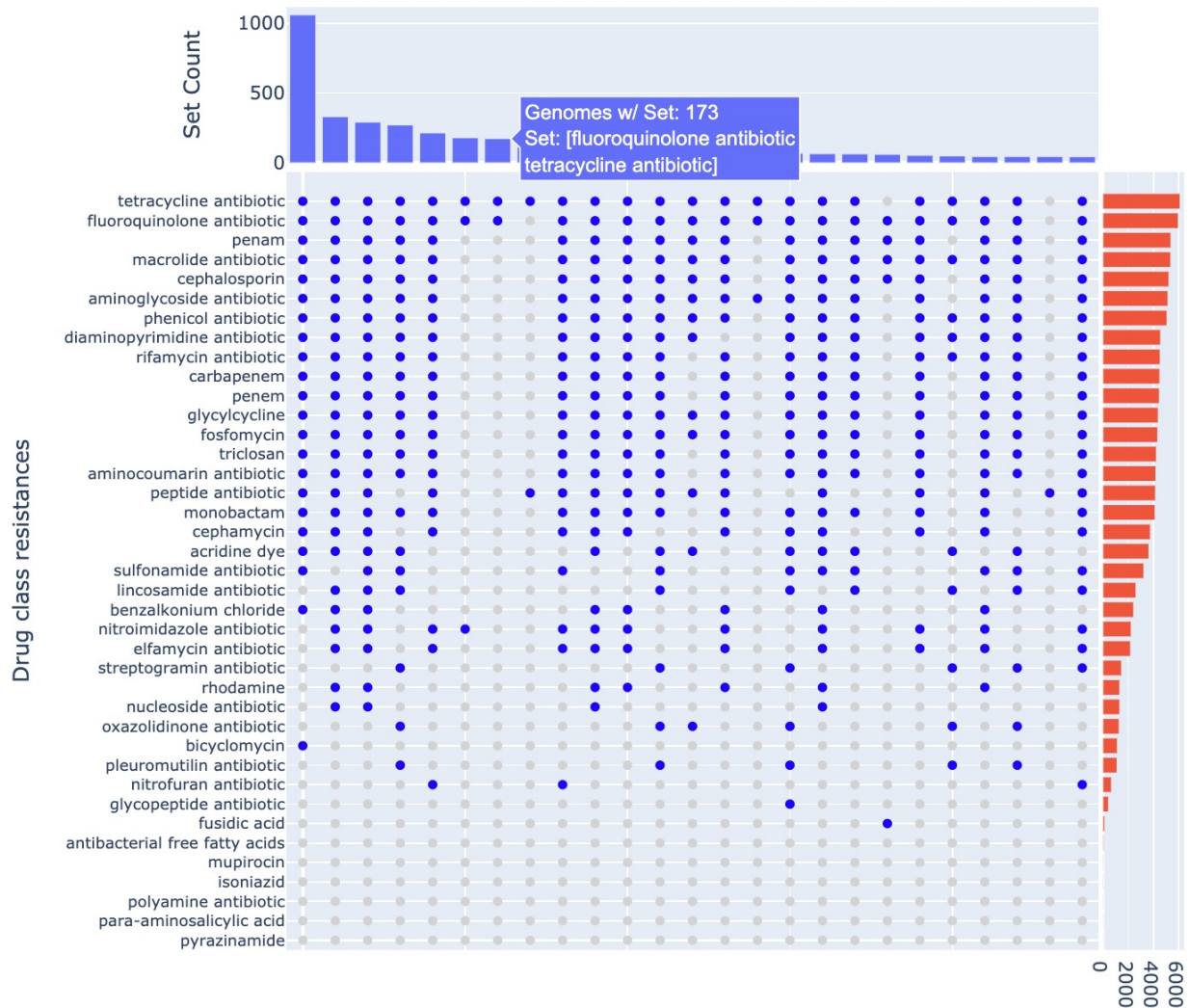
Showing 8376/8376 samples

RGI Filter by RGI results

RGI results cutoff:

All
 Perfect
 Strict

Drug class resistances UpSet Plot
(Truncated to 25 Most Common Intersections)



CARD: Prevalence – Summary of NCBI genomes

CARD

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Search

Phenotype

Prevalence of AMR genes and variants organized by Antibiotic Resistance Ontology phenotypic classification. Values reflect percentage of completely sequenced genomes, completely sequenced plasmids, whole-genome shotgun assemblies, or genomic islands that have at least one AMR determinant associated with the phenotypic class. Default view includes percentages calculated based on Perfect plus Strict RGI hits. Select the checkbox to view percentages based on only Perfect matches to AMR reference sequences curated in CARD (note: this excludes resistance via mutation as references in protein variant models are often wild-type, sensitive sequences).

Species	acridine dye	aminocoumarin antibiotic	aminoglycoside antibiotic	antibacterial free fatty acids	benzalkonium chloride	bicyclomycin
<i>Achromobacter insolitus</i>	0%	0%	85.71%	0%	0%	0%
<i>Achromobacter xylosoxidans</i>	4.4%	0%	86.81%	0%	0%	0%
<i>Acinetobacter baumannii</i>	75.53%	74.72%	76.43%	0%	0.02%	0%
<i>Acinetobacter defluvi</i>	10%	0%	10%	0%	0%	0%
<i>Acinetobacter haemolyticus</i>	35.87%	0%	58.7%	0%	0%	0%
<i>Acinetobacter indicus</i>	5%	1%	40%	0%	0%	0%
<i>Acinetobacter johnsonii</i>	4.49%	0%	13.48%	0%	0%	0%
<i>Acinetobacter junii</i>	23.44%	0%	26.56%	0%	0%	0%
<i>Acinetobacter lwoffii</i>	2.08%	0%	10.42%	0%	0%	0%
<i>Acinetobacter nosocomialis</i>	66.48%	66.48%	13.19%	0%	0%	0%
<i>Acinetobacter pittii</i>	62.04%	61.8%	47.45%	0%	0%	0.24%
<i>Acinetobacter towneri</i>	12.5%	0%	58.33%	0%	0%	0%
<i>Acinetobacter wuhouensis</i>	7.69%	0%	19.23%	0%	0%	0%
<i>Actinobacillus indolicus</i>	0%	0%	100%	0%	0%	0%
<i>Actinobacillus pleuropneumoniae</i>	0%	0%	17.65%	0%	0%	0%
<i>Actinobacillus porciconsillarum</i>	0%	0%	0%	0%	0%	0%
<i>Aeromonas caviae</i>	22.09%	0%	36.05%	0%	0%	0%
<i>Aeromonas hydrophila</i>	5.59%	0%	12.59%	0%	0%	0%

CARD: Prevalence – Summary of NCBI genomes

CARD

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Search

Genotype

Prevalence of AMR genes and variants organized by CARD detection model. Values reflect percentage of completely sequenced genomes, completely sequenced plasmids, whole-genome shotgun assemblies, or genomic islands that have at least one hit to the AMR detection model. The search box can be used to filter results by gene family names (e.g. TEM-), pathogens (e.g. Pseudomonas), or the ARO categories used in the Phenotype table above (e.g. macrolide). Multiple search terms will search for entries containing all given terms. For more complex queries, please [Download](#) the full data set.

Search:

Gene [▲]	Species [⬇]	NCBI Chromosome [⬇]	NCBI Plasmid [⬇]	NCBI WGS [⬇]	NCBI GI [⬇]
AAC(3)-Ib	<i>Serratia marcescens</i>	0%	0%	0.18%	0%
AAC(3)-Ib	<i>Enterobacter cloacae</i>	0%	0.84%	0.59%	0%
AAC(3)-Ib	<i>Enterobacter hormaechei</i>	0%	0.62%	0.76%	0%
AAC(3)-Ib	<i>Klebsiella quasipneumoniae</i>	0%	0%	0.24%	0%
AAC(3)-Ic	<i>Escherichia coli</i>	0%	0%	0.01%	0%
AAC(3)-Ic	<i>Pseudomonas aeruginosa</i>	0%	0%	0.71%	0%
AAC(3)-Ic	<i>Serratia marcescens</i>	0%	0%	0.18%	0%
AAC(3)-Id	<i>Salmonella enterica</i>	0.33%	0%	0.37%	0.33%
AAC(3)-Id	<i>Pseudomonas aeruginosa</i>	0%	0%	1%	6.94%
AAC(3)-Id	<i>Pseudomonas stutzeri</i>	0%	0%	2.25%	0%
AAC(3)-IIa	<i>Salmonella enterica</i>	0%	0%	0%	0.99%
AAC(3)-IIa	<i>Escherichia coli</i>	0%	0%	0%	0.77%
AAC(3)-IIa	<i>Klebsiella pneumoniae</i>	0%	0%	0%	6.67%

CARD: Resistomes & Variants – Details of NCBI genomes

CARD

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Search

Resistomes

Antimicrobial resistance (AMR) genome annotation and variants data were generated using the [Resistance Gene Identifier \(RGI\)](#), a tool for putative AMR gene detection from submitted sequence data using the AMR detection models available in CARD. To generate these data, RGI was used to analyze molecular sequence data available in [NCBI Genomes](#) for 263 pathogens of interest (see [Sampling](#)), plus genomic islands available in Islandviewer. For each of these pathogens, complete chromosome sequences, predicted genomic islands, complete plasmid sequences, and whole genome shotgun (WGS) assemblies were analyzed individually by RGI.

Genome and variants data is available under both the Perfect and Strict paradigms of RGI, the former tracking perfect matches to the curated reference sequences and mutations in the CARD, while the latter detects previously unknown variants of known AMR genes, including secondary screen for key mutations, using detection models with curated similarity cut-offs to ensure the detected variant is likely a functional AMR gene. For more information, see the [Resistance Gene Identifier](#).

The reported results are entirely dependant upon the curated AMR detection models in CARD, the algorithms available in RGI (recently expanded to include rRNA mutations and efflux over-expression models, see the [Resistance Gene Identifier](#)), and the sequence data available at NCBI. These data will change over time as CARD curation, RGI software, and NCBI data evolve.

CARD Resistomes & Variants 3.0.9 is based on sequence data acquired from NCBI on June 1, 2021 and [Islandviewer 4](#), analyzed using RGI 5.2.0 (DIAMOND homolog detection) and CARD 3.1.2.

CARD Resistomes & Variants

Pathogen, NCBI accession, data type, percent identity between the sequence(s) detected and the CARD reference sequence, and RGI detection criteria.

The search box can be used to filter results by gene names (e.g. TEM-), pathogens (e.g. Pseudomonas), or drug class (e.g. macrolide). Multiple search terms will search for entries containing all given terms. For more complex queries, please Download the full data set.

Clicking on the Accession will provide pre-compiled RGI results, while clicking on the Data Type will link to the original data at NCBI or IslandViewer.

Show entries

Search:

Accession	Pathogen	Data Type	Perfect Hits	Strict Hits	Drug Classes
NC_002774.1	<i>Staphylococcus aureus</i>	ncbi_plasmid	AAC(6')-Ie-APH(2'')-Ia	qacA	aminoglycoside antibiotic, fluoroquinolone antibiotic
NC_003140.1	<i>Staphylococcus aureus</i>	ncbi_plasmid		PC1 beta-lactamase (blaZ)	penam
NC_003384.1	<i>Salmonella enterica</i>	ncbi_plasmid	TEM-1, catI, dfrA14	tetR, tet(B), sul2, APH(6)-Id, APH(3'')-Ib	aminoglycoside antibiotic, cephalosporin, diaminopyrimidine antibiotic, monobactam, penam, penem, phenicol

CARD: Resistomes & Variants – Details of NCBI genomes

CARD

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NDM-4

[Download Sequences](#)

Accession	ARO:3002355
Definition	NDM-4 is a beta-lactamase found in Escherichia coli
AMR Gene Family	NDM beta-lactamase
Drug Class	cephalosporin , penem , penam , carbapenem , cephamycin
Resistance Mechanism	antibiotic inactivation
Resistomes with Perfect Matches	Enterobacter hormaechei ^{WGS} , Escherichia coli ^{p+WGS} , Klebsiella pneumoniae ^{D+WGS}
Resistomes with Sequence Variants	Enterobacter hormaechei ^{WGS} , Escherichia coli ^{p+WGS} , Klebsiella pneumoniae ^{D+WGS}
Classification	18 ontology terms Show
Parent Term(s)	2 ontology terms Show
Publications	Nordmann P, et al. 2012. Antimicrob Agents Chemother 56(4): 2184-2186. NDM-4 metallo-beta-lactamase with increased carbapenemase activity from Escherichia coli. (PMID 22252797)

Resistomes

Prevalence of **NDM-4** among the sequenced genomes, plasmids, and whole-genome shotgun assemblies available at NCBI or IslandViewer for 263 important pathogens (see [methodological details and complete list of analyzed pathogens](#)). Values reflect percentage of genomes, plasmids, genome islands, or whole-genome shotgun assemblies that have at least one hit to the AMR detection model. Default view includes percentages calculated based on Perfect plus Strict RGI hits. Select the checkbox to view percentages based on only Perfect matches to AMR reference sequences curated in CARD (note: this excludes resistance via mutation as references in protein variant models are often wild-type, sensitive sequences).

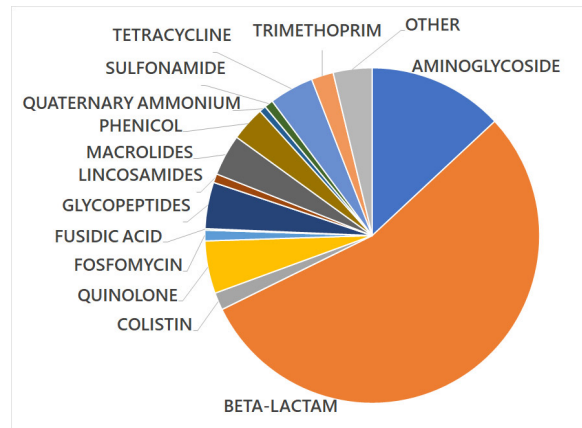
Prevalence: protein homolog model ([view sequences](#))

Species	NCBI Chromosome	NCBI Plasmid	NCBI WGS	NCBI GI
<i>Enterobacter hormaechei</i>	0%	0%	0.08%	0%
<i>Escherichia coli</i>	0%	0.02%	0.02%	0%
<i>Klebsiella pneumoniae</i>	0%	0.05%	0.07%	0%

Show Perfect Only



National Database of Antibiotic Resistant Organisms (NDARO)



AMRFinderPlus

NCBI: AMRFinderPlus database (Reference Gene Catalog)

Database sources

- Lahey Clinic compilation of beta-lactamase sequences (<http://www.lahey.org/studies/> and personal communications from Dr. George Jacoby and Karen Bush)
- Pasteur Institute collection of beta-lactamase sequences
- ResFinder
- Comprehensive Antibiotic Resistance Database (CARD)
- RAC and Integrrall collections of AMR proteins found in integrons
- Center for Veterinary Medicine
- Marilyn Roberts personal communications
- "Oxford" - Derrick Crook personal communications

NCBI: AMRFinderPlus database (Reference Gene Catalog)



National Library of Medicine
National Center for Biotechnology Information

Log in

[Health](#) > [Pathogen Detection](#) > Reference Gene Catalog

[Help](#)

Search

db version: 2021-09-30.1 [Changelog](#)

Bacterial Antimicrobial Resistance Reference Gene Database

Filters

Page 88 of 392 Records per Page 20 Choose columns Download

Displaying 1741 - 1760 of 7828

#	Allele	Gene fa...	Product name	Scope	Type	Subtype	Class	Subclass	Refseq ...	Refseq ...	Genban...	Genban...	Curated...
1741	blaFAR-1	blaFAR	class A extended-spectrum beta-lactamase FAR-1	core	AMR	AMR	BETA-L...	BETA-L...	WP_07...	NG_049...		AF0246...	Yes
1742	blaFEZ-1	blaFEZ	subclass B3 metallo-beta-lactamase FEZ-1	core	AMR	AMR	BETA-L...	CARBAP...	WP_05...	NG_049...	CAB969...	Y17896.1	No
1743	blaFIA-1	blaFIA	subclass B1 metallo-beta-lactamase FIA-1	core	AMR	AMR	BETA-L...	CARBAP...	WP_04...	NG_057...		HE7966...	Yes
1744	blaFIM-1	blaFIM	subclass B1 metallo-beta-lactamase FIM-1	core	AMR	AMR	BETA-L...	CARBAP...	WP_05...	NG_049...	AFV915...	JX5707...	No
1745	blaFONA-1	blaFONA	class A beta-lactamase FONA-1	core	AMR	AMR	BETA-L...	BETA-L...	WP_04...	NG_049...	CAB616...	AJ2512...	No
1746	blaFONA-2	blaFONA	class A beta-lactamase FONA-2	core	AMR	AMR	BETA-L...	BETA-L...	WP_06...	NG_049...	CAB616...	AJ2512...	No
1747	blaFONA-3	blaFONA	class A beta-lactamase FONA-3	core	AMR	AMR	BETA-L...	BETA-L...	WP_06...	NG_049...	CAB616...	AJ2512...	No
1748	blaFONA-4	blaFONA	class A beta-lactamase FONA-4	core	AMR	AMR	BETA-L...	BETA-L...	WP_06...	NG_049...	CAB616...	AJ2512...	No

NCBI: AMRFinderPlus

Element type	Element subtype	Description
AMR	AMR	Antimicrobial resistance gene
AMR	POINT	Known point mutation associated with antimicrobial resistance
VIRULENCE	VIRULENCE	Virulence gene
VIRULENCE	ANTIGEN	Gene codes for a known antigen; this will be a future expansion of functionality
STRESS	ACID	Acid resistance gene
STRESS	BIOCIDE	Biocide resistance gene
STRESS	HEAT	Heat resistance gene
STRESS	METAL	Metal resistance gene

Organism option	Point mutation screening	Are certain plus genes excluded?	Taxa
Campylobacter	Yes	No	<i>Campylobacter coli</i> and <i>C. jejuni</i>
Enterococcus_faecalis	Yes	No	<i>Enterococcus faecalis</i>
Enterococcus_faecium	Yes	No	<i>Enterococcus faecium</i>
Escherichia	Yes	Yes	<i>Escherichia</i> sp. including <i>Shigella</i> , <i>E. albertii</i> , <i>E. fergusonii</i>
Klebsiella	No	Yes	<i>Klebsiella pneumoniae</i> , <i>K. oxytoca</i>
Salmonella	Yes	Yes	<i>Salmonella</i> sp.
Staphylococcus_aureus	Yes	No	<i>Staphylococcus aureus</i>
Staphylococcus_pseudintermedius	No	Yes	<i>Staphylococcus pseudintermedius</i>
Vibrio_cholerae	No	Yes	<i>Vibrio cholerae</i>

NCBI: Other AMR resources

- Isolate browser

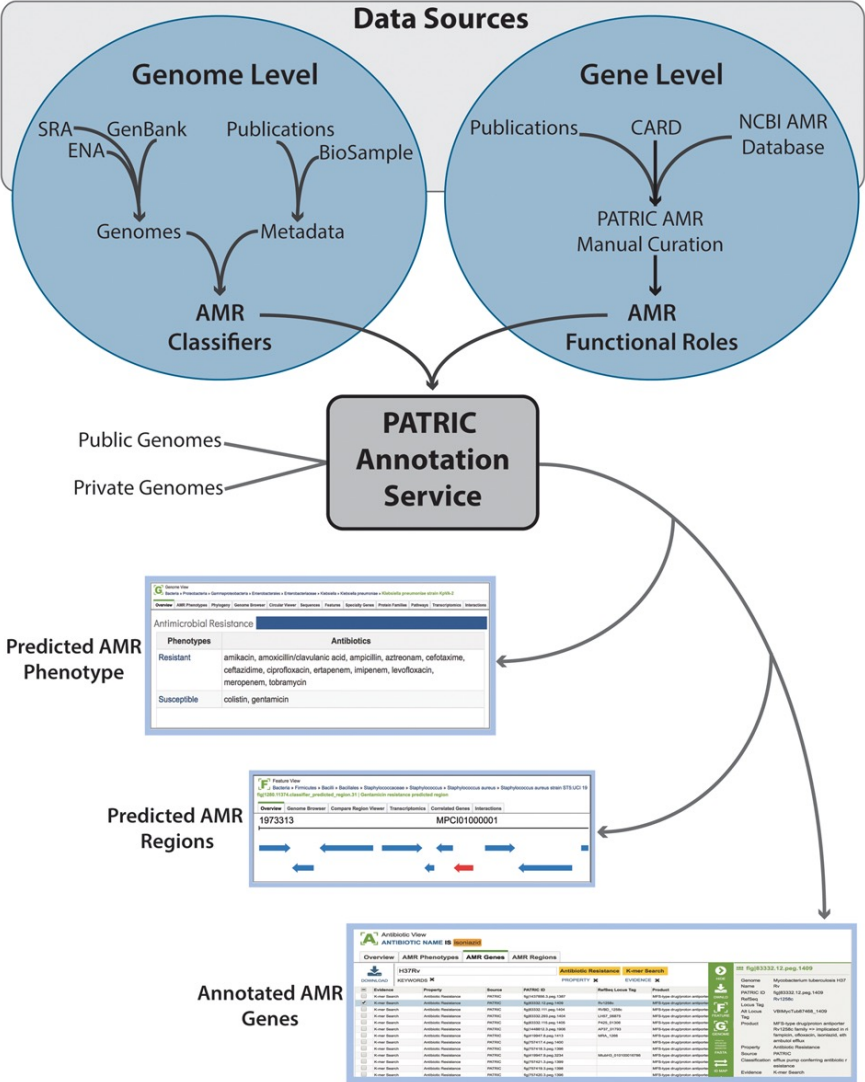
Matched Isolates												
Page 4761 of 47604 Records per Page 20 Choose columns Download Hide plus AMR genotypes Expand all Cross-browser selection Display												
#	Organism group	Strain	Isolate identifiers	Create date	Locat...	Isolation source	Isolation ...	AST phenotypes	BioSample	Assembly	AMR genotypes	
952061	Providencia alcalifaciens	CCUG 70746	A4_Pmi CCUG 70746 CCUG:70746 SRS2514200	2018-06-06	Swed...	feces	clinical	Resistant (33) Intermediate (1) Susceptible (1) Other (1) Expand All	SAMN07602702	GCA_003194305.1	Complete (19) aadA2 aph(3'')-Ib aph(3')-VI Mistranslation (1) aadA1 Show all 20 gene	
952062	Klebsiella pneumoniae	CCUG 70747	A6_Kpn CCUG 70747 SRS2514203	2018-06-06	Swed...	wound	clinical	Resistant (31) Intermediate (0) Susceptible (3) Other (2) Expand All	SAMN07602916	GCA_003194325.1	Complete (15) aac(6)-Ib3 aac(6)-II aadA1 Mistranslation (1) blaOXA Point (2) gyrA_D87G gyrA_S83Y Show all 18 gene	

- Pathogen Detection Reference Hidden Markov Model (HMM) Catalog
- Microbial Browser for Identification of Genetic and Genomic Elements (MicroBIGG-E)

#	Scientific name	Protein	BioSample	Isolate	Contig	Start	Stop	Strand	Element sy...	Element name	Type	Scope	Subtype	Class
1000...	Streptococcus pneu...		SAMEA2298260	PDT000527789.2	CAAQNF010000014.1	13578	15617	+	pbp2b	Streptococcus p...	AMR	core	AMR	BETA-LAC...
1000...	Acinetobacter baum...	HAV6107621.1	SAMD00034432	PDT000173791.3	DADBKE010000097.1	4283	5122	-	sul1	sulfonamide-res...	AMR	core	AMR	SULFONA...
1000...	Streptococcus pneu...		SAMEA2298261	PDT000527790.2	CAAQOJ010000017.1	45164	47080	+	tet(M)	tetracycline resi...	AMR	core	AMR	TETRACY...
1000...	Acinetobacter baum...	HAV6107623.1	SAMD00034432	PDT000173791.3	DADBKE010000097.1	5680	6546	-	blaCARB-2	PSE family carb...	AMR	core	AMR	BETA-LAC...
1000...	Acinetobacter baum...	HAV6107666.1	SAMD00034432	PDT000173791.3	DADBKE010000104.1	4721	5254	-	ant(2'')-Ia	aminoglycoside ...	AMR	core	AMR	AMINOGL...

- Submit sequence and phenotype data

PathoSystems Resource Integration Center (PATRIC)



PATRIC: AMR database

- PATRIC (in-house)
- CARD
- NCBI National Database of Antibiotic Resistant Organisms (NDARO)
- ARDB

PATRIC 3.6.12 ORGANISMS DATA WORKSPACES SERVICES HELP All Data Types Find a gene, genome, microbe All terms Register Login

Taxon View
Bacteria (452132 Genomes)

Overview Phylogeny Taxonomy Genomes AMR Phenotypes Sequences Features **Specialty Genes** Protein Families Pathways Subsystems Transcriptomics Interactions

This tab has been filtered to view data limited to Reference and Representative Genomes in your view.

DOWNLOAD KEYWORDS Antibiotic Resistance PROPERTY x HIDE

Public	Property	Source	Evidence	Classification	Antibiotics Class
true (235800)	Antibiotic Resistance (235800) Essential Gene (1328123) Human Homolog (256161) Transporter (127971) Virulence Factor (127543) Drug Target (87764)	PATRIC (214999) CARD (17553) NDARO (3138) ARDB (110)	K-mer Search (214999) BLAT (20344) BLASTP (454) Literature (3)	efflux pump conferring antibiotic resistance (23631) protein altering cell wall charge conferring antibiotic resistance (23631) regulator modulating expression of antibiotic resistance gene (8914) antibiotic resistant gene variant or mutant (8029) gene conferring resistance via absence (6499)	undefined (20344) peptide antibiotics (19676) aminoglycosides (16195) cycloserine (14737) fusidic acid (14007) fluoroquinolones quinolones quinoline

<input type="checkbox"/> Evidence	Property	Source	PATRIC ID	RefSeq Locus Tag	Source ID	Gene	Product	Pubmed	Identity	E-value
<input type="checkbox"/> Literature	Antibiotic Res	CARD	fig 1562701.3.peg.112		CP002695.1		DNA topoisomerase IV subunit A (EC 5.99.1.3)		87	4e-23
<input type="checkbox"/> Literature	Antibiotic Res	CARD	fig 1562701.3.peg.137		CP002695.1		DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)		80	0.0
<input type="checkbox"/> Literature	Antibiotic Res	CARD	fig 1562701.3.peg.137		CP002695.1		Translation elongation factor Tu		87	0
<input type="checkbox"/> K-mer Search	Antibiotic Res	PATRIC	fig 1380600.3.peg.229				Translation elongation factor G	17980694;192895		
<input type="checkbox"/> K-mer Search	Antibiotic Res	PATRIC	fig 1069631.3.peg.438	C660_22169			DNA gyrase subunit A (EC 5.99.1.3)	9293187		
<input type="checkbox"/> K-mer Search	Antibiotic Res	PATRIC	fig 1185766.4.peg.299	DL1_08120			16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.42)	17238915		
<input type="checkbox"/> K-mer Search	Antibiotic Res	PATRIC	fig 1348973.3.peg.343	M670_03560			Dihydrofolate reductase (EC 1.5.1.3)	20169085;252880		
<input type="checkbox"/> K-mer Search	Antibiotic Res	PATRIC	fig 1173021.3.peg.122				Translation elongation factor G	17980694;192895		

PATRIC: AMR phenotypes

Taxon View
Bacteria (452132 Genomes)

Overview Phylogeny Taxonomy Genomes **AMR Phenotypes** Sequences Features Specialty Genes Protein Families Pathways



KEYWORDS



<input type="checkbox"/>	Genome Name	Antibiotic	Resistant Phenotype	Measurement Sign	Measurement Value	Measurement Units	Lab typing Method	Computation Method	Evidence	Pubmed
<input type="checkbox"/>	Escherichia coli BIDMC 20B	meropenem	Susceptible		32		MIC		Laboratory Met	28096418
<input type="checkbox"/>	Escherichia coli BIDMC 6	meropenem	Resistant		32		MIC		Laboratory Met	28096418
<input type="checkbox"/>	Escherichia coli strain 150721	colistin		<=	1	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli strain 15-AB01509	colistin		<=	1	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli strain 15F001211	colistin			4	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli strain 16-AB00129	colistin		<=	1	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli strain 15-AB01312	colistin		<=	1	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli strain 15051805CO	colistin			8	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli strain 11-14155	colistin		>	4	mg/L	MIC		Laboratory Met	31440216
<input type="checkbox"/>	Escherichia coli strain 150542127AF	colistin			4	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli BIDMC 2B	meropenem			32				Laboratory Met	28096418
<input type="checkbox"/>	Escherichia coli strain 15-AB01045	colistin		<=	1	mg/L	MIC		Laboratory Met	29439754
<input type="checkbox"/>	Escherichia coli BIDMC 20A	cefepime			2	mg/L	MIC		Laboratory Met	28096418
<input type="checkbox"/>	Escherichia coli BIDMC 20A	meropenem	Resistant		8		MIC		Laboratory Met	28096418
<input type="checkbox"/>	Serratia marcescens strain C080	ertapenem	Resistant	>	1	mg/L	MIC			

PATRIC: Genomes

Genome View
 Bacteria » Proteobacteria » Gammaproteobacteria » Enterobacterales » Enterobacteriaceae » Escherichia » Escherichia coli » **Escherichia coli strain 1501**

Overview AMR Phenotypes Phylogeny Genome Browser Circular Viewer Sequences Features Specialty Genes Protein Families Pathway

Interactions

Escherichia coli strain 15051805

Length: 5115630bp, Contigs: 110

Organism Info

Genome ID 562.58732
Genome Name Escherichia coli strain 15051805
NCBI Taxon ID 562
Genome Status WGS
Serovar H28
MLST ST-4096
Antimicrobial Resistance AMR Phenotypes

Genome Quality

Genome Quality Good
Coarse Consistency 97
Fine Consistency 96

Sharing

None available

Isolate Info

Isolation Source Slaughterhouse
Collection Year 2015

Antimicrobial Resistance

Phenotypes	Antibiotics
Resistant	ampicillin, cefotaxime, ceftazidime, chloramphenicol, ciprofloxacin, colistin, gentamicin, nalidixic acid, sulfamethoxazole, tetracycline, trimethoprim
Susceptible	meropenem, tigecycline

Genomic Features

	PATRIC	RefSeq
CDS	5149	0
tRNA	84	0
crispr_repeat	14	0
crispr_spacer	12	0
rRNA	8	0
crispr_array	2	0

Protein Features

FIGfam assigned

PATRIC: Genomes

Genome View
Bacteria » Proteobacteria » Gammaproteobacteria » Enterobacteriales » Enterobacteriaceae » Escherichia » Escherichia coli » **Escherichia coli strain 150!**

Overview AMR Phenotypes Phylogeny Genome Browser Circular Viewer Sequences Features Specialty Genes Protein Families Pathway

Interactions

Isolation Source Slaughterhouse
Collection Year 2015
Collection Date 2015-06-30
Isolation Country Italy

Host Info

Host Name Cow, Bos taurus
Body Sample Site caecum

Sequence Info

Contigs 110
Genome Length 5115630
GC Content 50.386013
PATRIC CDS 5149

Phenotype Info

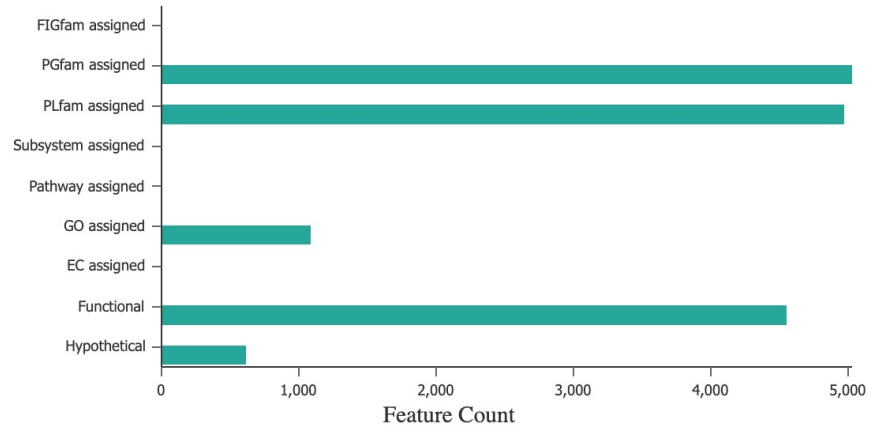
None available

Project Info

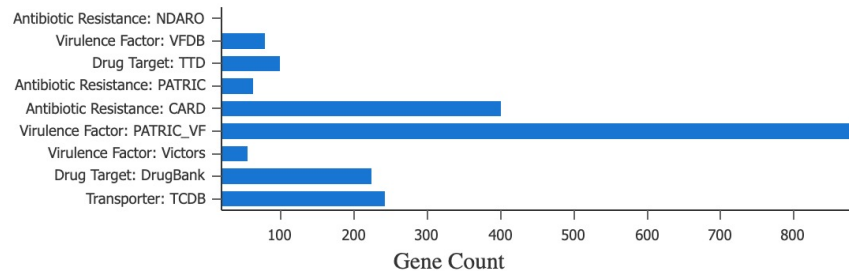
Publication 29951045
BioSample SAMEA104412500
Accession
SRA Accession ERS2030442

Other

Additional Metadata • id number:15051805
Insert Date 4/1/2020
Last Modified 4/1/2020



Specialty Genes



PATRIC: Regions

- Computationally predicted small genomic regions associated with AMR

PATRIC 3.6.12 ORGANISMS DATA WORKSPACES SERVICES HELP All Data Types Find a gene, genome, microarray, etc

Feature List View (3123774 Genomic Features)

Feature List Overview **Features**

DOWNLOAD KEYWORDS PATRIC ANNOTATION x FILTERS

<input type="checkbox"/>	Genome Name	Genome ID	PATRIC ID ▲	RefSeq Locus Tag	Gene Symbol	Feature Type	Start	End	Strand	Product
<input type="checkbox"/>	Pseudomonas aeruginosa PAK	1009714.25	fig 1009714.25.cl			classifier_prec	1573744	1573758	+	Levofloxacin resistance predicted region
<input type="checkbox"/>	Pseudomonas aeruginosa PAK	1009714.25	fig 1009714.25.cl			classifier_prec	4203159	4203175	+	Levofloxacin resistance predicted region
<input type="checkbox"/>	Pseudomonas aeruginosa PAK	1009714.25	fig 1009714.25.cl			classifier_prec	4741881	4741895	+	Levofloxacin resistance predicted region
<input type="checkbox"/>	Pseudomonas aeruginosa PAK	1009714.25	fig 1009714.25.cl			classifier_prec	4794465	4794479	+	Levofloxacin resistance predicted region
<input type="checkbox"/>	Pseudomonas aeruginosa PAK	1009714.25	fig 1009714.25.cl			classifier_prec	5398216	5398241	+	Levofloxacin resistance predicted region
<input type="checkbox"/>	Pseudomonas aeruginosa PAK	1009714.25	fig 1009714.25.cl			classifier_prec	6395377	6395391	+	Levofloxacin resistance predicted region
<input type="checkbox"/>	Klebsiella pneumoniae KCTC 2242	1049565.29	fig 1049565.29.cl			classifier_prec	70440	70456	+	Trimethoprim_Sulfamethoxazole resistance p
<input type="checkbox"/>	Klebsiella pneumoniae KCTC 2242	1049565.29	fig 1049565.29.cl			classifier_prec	115327	115342	+	Meropenem resistance predicted region
<input type="checkbox"/>	Klebsiella pneumoniae KCTC 2242	1049565.29	fig 1049565.29.cl			classifier_prec	125942	125957	+	Piperacillin_Tazobactam resistance predicted
<input type="checkbox"/>	Klebsiella pneumoniae KCTC 2242	1049565.29	fig 1049565.29.cl			classifier_prec	165053	165067	+	Tetracycline resistance predicted region
<input type="checkbox"/>	Staphylococcus aureus subsp. aureu	1074919.15	fig 1074919.15.cl			classifier_prec	152	170	+	Penicillin resistance predicted region
<input type="checkbox"/>	Staphylococcus aureus subsp. aureu	1074919.15	fig 1074919.15.cl			classifier_prec	23911	23929	+	Penicillin resistance predicted region
<input type="checkbox"/>	Staphylococcus aureus subsp. aureu	1074919.15	fig 1074919.15.cl			classifier_prec	30792	30806	+	Erythromycin resistance predicted region
<input type="checkbox"/>	Staphylococcus aureus subsp. aureu	1074919.15	fig 1074919.15.cl			classifier_prec	30795	30809	+	Methicillin resistance predicted region
<input type="checkbox"/>	Staphylococcus aureus subsp. aureu	1074919.15	fig 1074919.15.cl			classifier_prec	4584	4603	+	Penicillin resistance predicted region

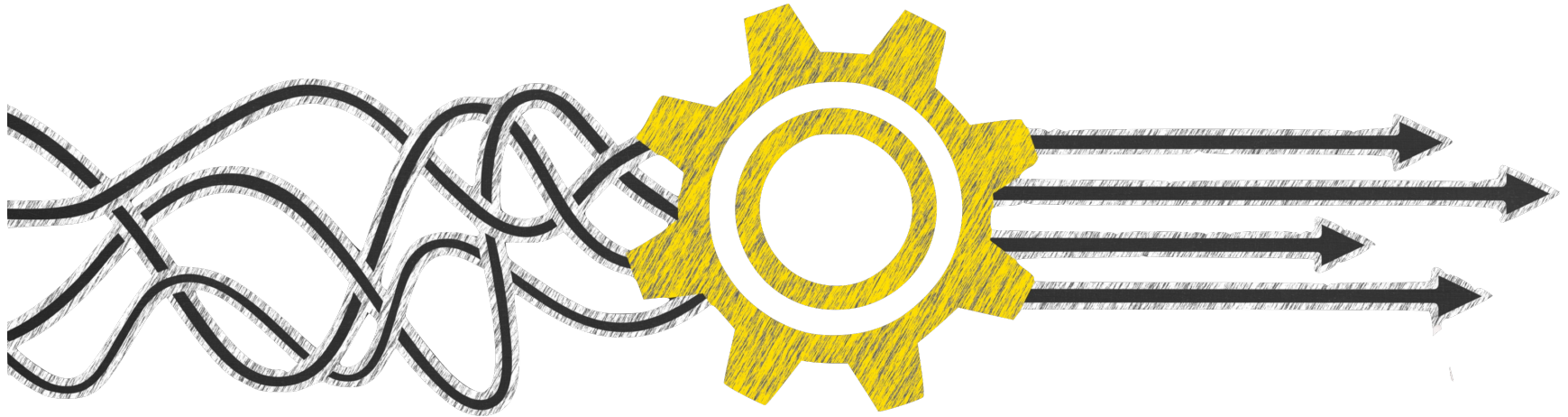
Davis, et al. *Nucleic Acids Res*, 2020.

[https://www.patricbrc.org/view/FeatureList/?eq\(feature_type,classifier_predicted_region\)#view_tab=features&filter=or\(eq\(annotation,%22PATRIC%22\)\)](https://www.patricbrc.org/view/FeatureList/?eq(feature_type,classifier_predicted_region)#view_tab=features&filter=or(eq(annotation,%22PATRIC%22)))

Summary of AMR databases and resources

	ResFinder	CARD/RGI	NCBI AMRFinderPlus	PATRIC
AMR context	Acquired resistance, chromosomal mutations	<ul style="list-style-type: none"> Website Command-line 	All (can include additional classes of genes)	All
Annotation Usage	<ul style="list-style-type: none"> Website Command-line 	<ul style="list-style-type: none"> Website Command-line 	<ul style="list-style-type: none"> Command-line 	<ul style="list-style-type: none"> Website Command-line
Matched genotype-phenotype isolates	No	No	Yes	Yes
Other resources	<ul style="list-style-type: none"> PointFinder 	<ul style="list-style-type: none"> Antibiotic Resistance Ontology CARD:Live CARD:Prevalence CARD:Resistomes&Variants 	<ul style="list-style-type: none"> Isolate Browser Hidden Markov Model (HMM) Catalog MicroBIGG-E 	<ul style="list-style-type: none"> PATRIC:Antibiotics PATRIC:Phenotypes PATRIC:Regions

Future directions



- Standardization of AMR databases
- Inclusion of metadata in AMR databases
- Specialized databases and tools for species (e.g., *Mycobacterium tuberculosis*)
- Harmonization of AMR resources