



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

<http://card.mcmaster.ca>

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Inventors

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Available Online

<https://card.mcmaster.ca/>

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Overview

The CARD is an ontology- and model-based framework for detection of antibiotic resistance genes. It contains an expert-curated collection of characterized, peer-reviewed resistance determinants and associated antibiotics, organized by the Antibiotic Resistance Ontology (ARO) and AMR gene detection models. The software utilizes these detection models for predicting AMR from genome sequences.

Other associated tools include the Resistance Gene Identifier (RGI) which is a novel genome analysis tool for resistome prediction. It annotates DNA and protein sequences and detects matches to CARD reference sequences, variants of known AMR genes and emergent threats.

Resistomes is a computer-generated data set including genome annotation and variants data using RGI for 85 pathogens of interest. For each of these pathogens, complete chromosome sequences, plasmid sequences, and whole genome shotgun assemblies were analyzed individually by RGI to generate prevalence data. Results are further categorized using the ARO.

Benefits

- Expert-curated database that is updated monthly
As of November 29, 2019:
 - 4358 Ontology Terms, 2909 Reference Sequences, 1318 SNPs, 2663 Publications, 2943 AMR Detection Models
 - Resistome predictions: 85 pathogens, 8046 chromosomes, 18337 plasmids, 90531 WGS assemblies, 182532 alleles
- Software for prediction of resistance genes from isolates or metagenomic samples from clinical, environmental, or agricultural samples

Applications

- Predict antimicrobial resistance (AMR) from genome sequences
- Metagenomic analysis
- Pathogen of origin prediction
- Prevalence of AMR determinants
- Regulatory submissions and product registration for agricultural products
- Commercial services to analyze genomes
- Understanding molecular mechanisms of drug resistance, particularly drug development