

# AMRProfiler: A Comprehensive Tool for Identifying Antimicrobial Resistance Genes and Mutations Across Species

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## Introduction

Antimicrobial resistance (AMR) poses a significant global health challenge. Rapid advances in whole genome sequencing (WGS) have enabled in silico tools to identify AMR genes and explore resistance mechanisms. Despite progress, existing tools like ResFinder, CARD, and AMRFinder have limitations, such as redundancy in databases, limited mutation detection, and lack of rRNA analysis.

**AMRProfiler** (<https://dianalab.e-ce.uth.gr/amrprofiler>) addresses these challenges by providing:

- A curated, non-redundant database of 7,600 AMR gene entries.
- Comprehensive point mutation analysis across 266 core genes.
- The first systematic approach to rRNA mutation detection in ~18,000 species.

## Data collection and curation process

AMRProfiler integrates data from ResFinder, the Reference Gene Catalog, and CARD to curate a comprehensive, non-redundant database of 7,600 AMR gene alleles and 4,380 mutations across 266 core genes. Data from CARD (4,805 alleles), the Reference Gene Catalog (6,637 alleles), and ResFinder (3,106 alleles) were merged and deduplicated. RefSeq genomes were analyzed to identify core genes and rRNA genes (5S, 16S, 23S), enabling the detection of mutations across ~18,000 bacterial species. This curated database forms the foundation for AMRProfiler's robust analysis capabilities.

## Algorithm

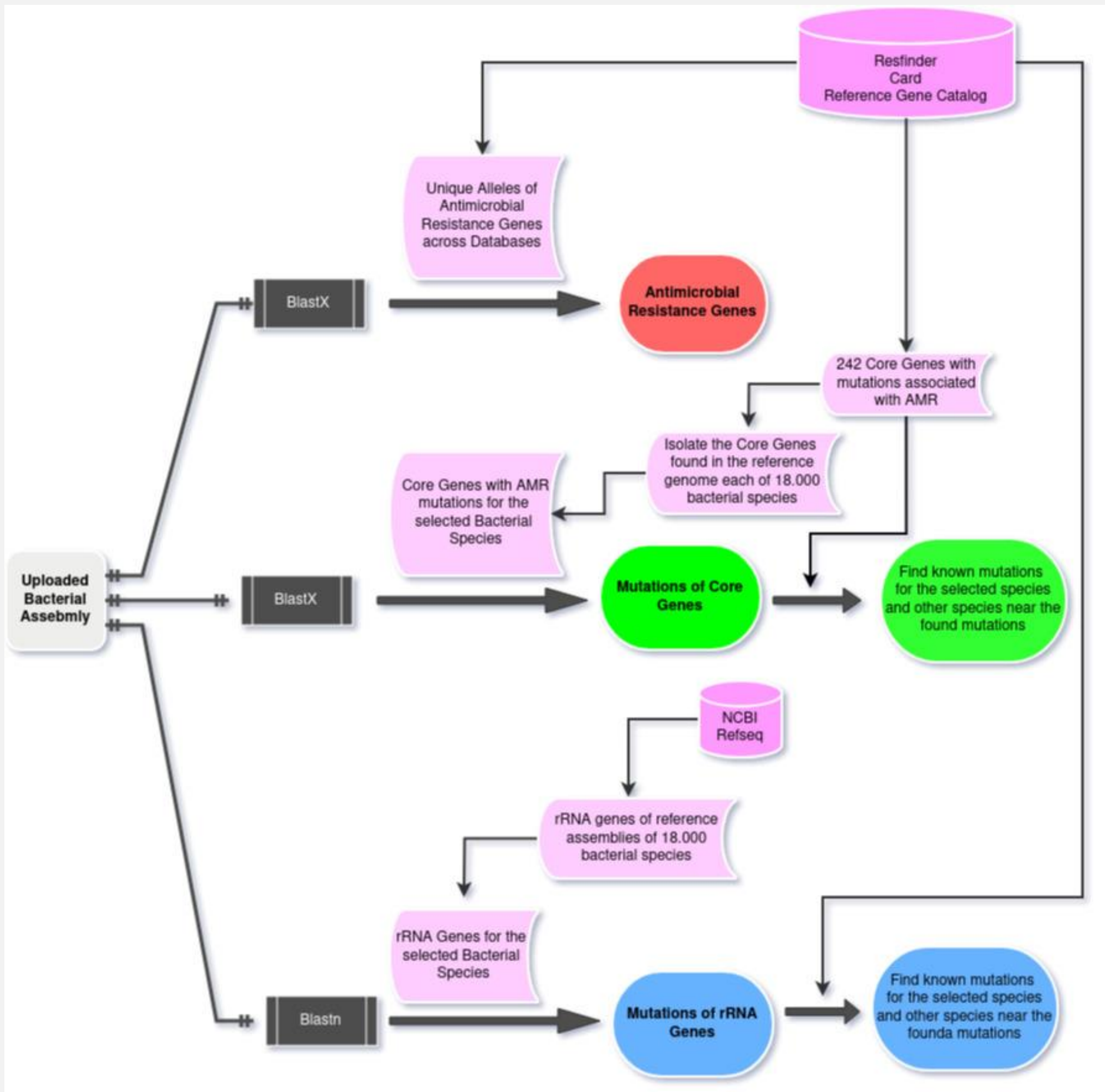


Figure 1: Overview of the AMRProfiler workflow.

## Interface

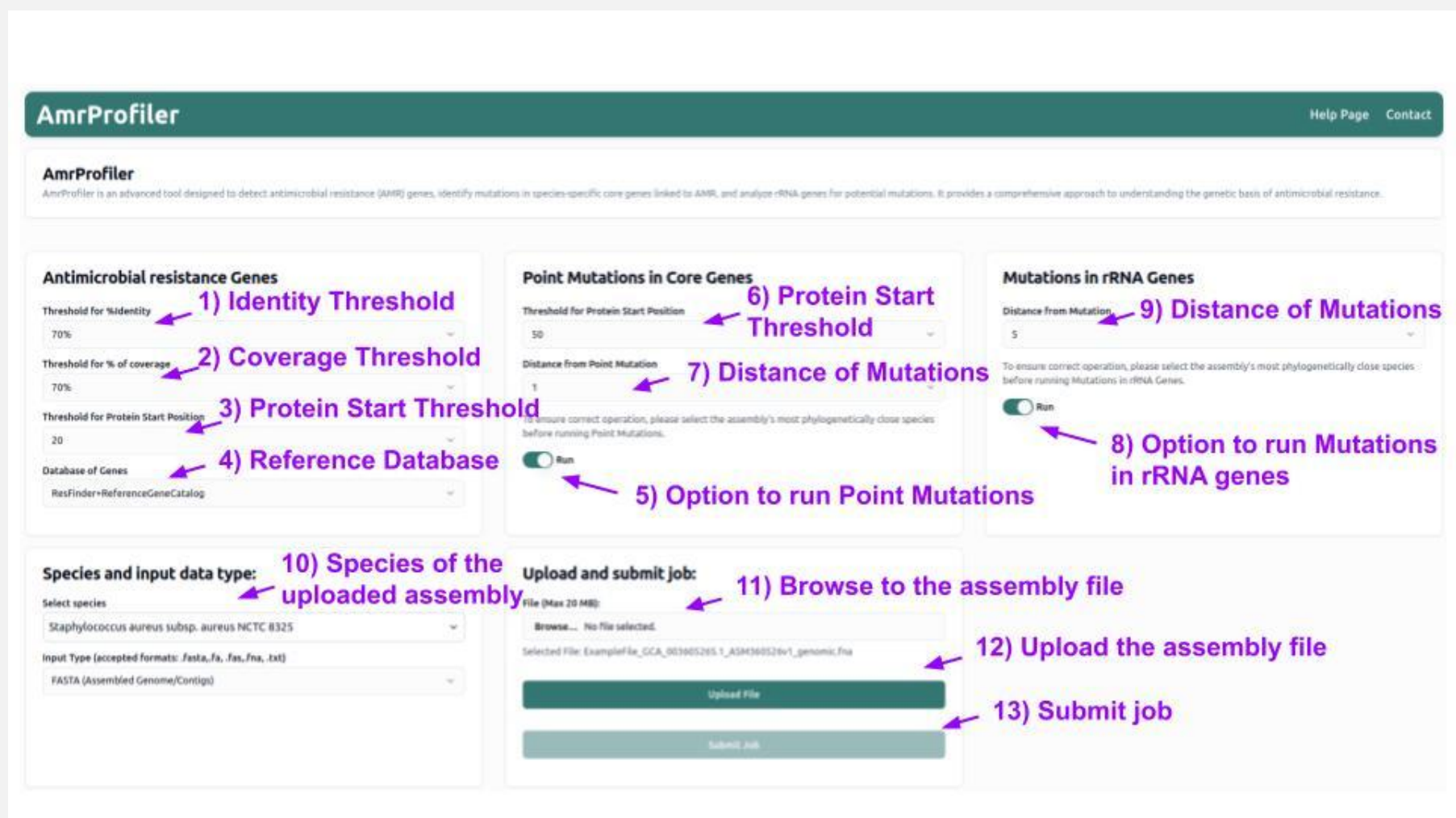


Figure 2: User interface of AMRProfiler

## Results



Figure 3: Interface of the results of AMRProfiler

## Evaluation

AMRProfiler was validated using *Acinetobacter baumannii* assembly GCF\_033142795.1 alongside AMRFinder, ResFinder, and CARD. For AMR genes, AMRProfiler detected all genes identified by the other tools and uniquely identified the genes *adeC*, *amvA*, *dfrA40*, and *abaF*. For point mutations, AMRFinder detected only one point mutation in *gyrA*, whereas AMRProfiler identified multiple point mutations in 27 genes, including experimentally validated mutations in *gyrA*, *gyrB*, *parC*, and *parE*. Additionally, AMRProfiler identified all rRNA gene copies and their mutations

## Conclusion

AMRProfiler enhances precision in identifying AMR genes, linking AMR genotypes and phenotypes. Its robust and user-friendly design supports comprehensive AMR gene, core gene mutation, and rRNA mutation analysis across multiple species. An online web server for AMRProfiler will be launched in the coming months.

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