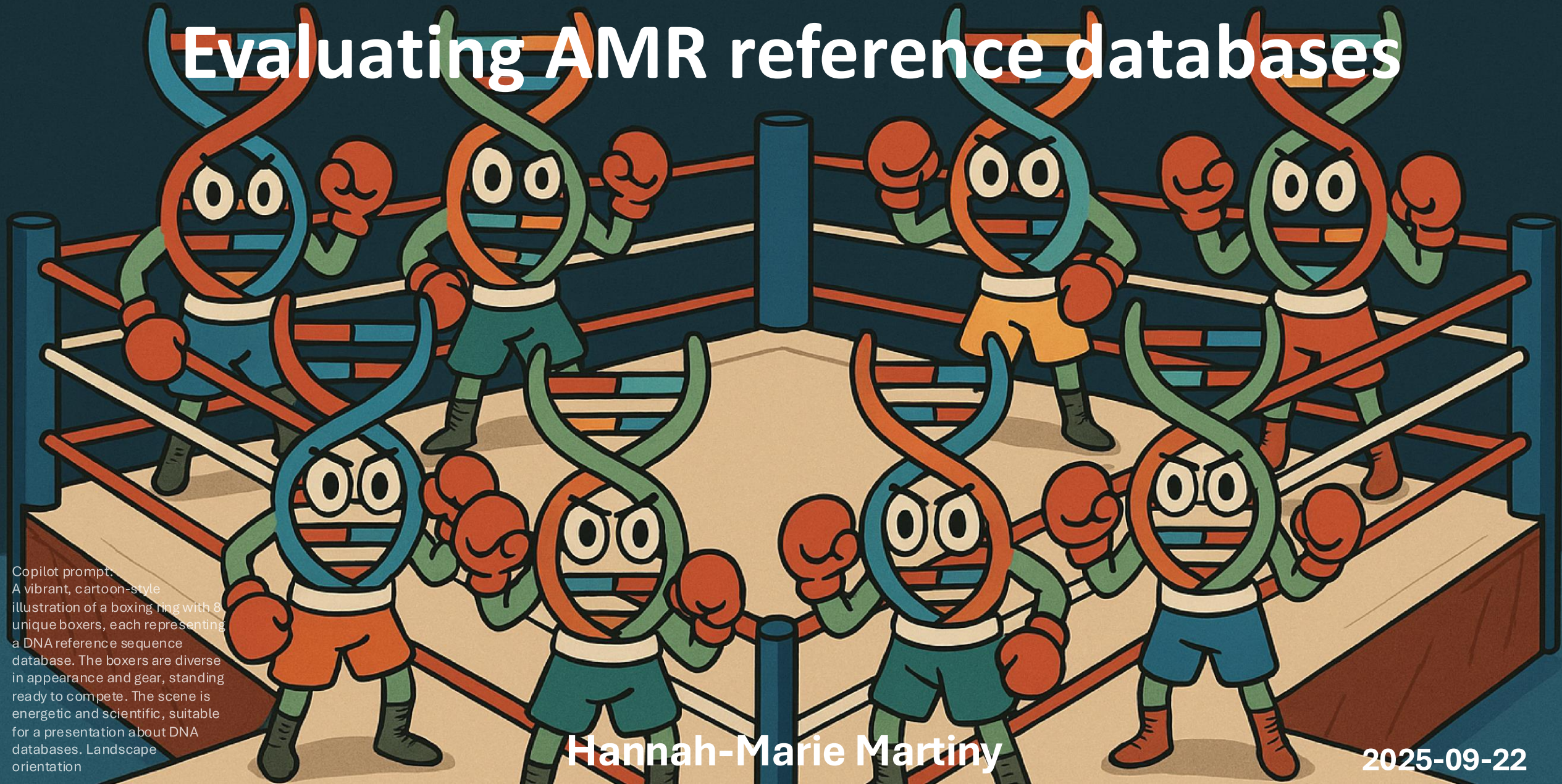


DATABASE SHOWDOWN

Evaluating AMR reference databases



Copilot prompt:
A vibrant, cartoon-style
illustration of a boxing ring with 8
unique boxers, each representing
a DNA reference sequence
database. The boxers are diverse
in appearance and gear, standing
ready to compete. The scene is
energetic and scientific, suitable
for a presentation about DNA
databases. Landscape
orientation

Hannah-Marie Martiny

2025-09-22

2023-11-06

A build up

2024-09-30

2025-03-10



Non-cultivable ARGs appear to be more widespread geographically in urban sewage samples

Hannah-Marie Martiny^{1*}, Alessandro Fuschi², Nikiforos Pyrounakis¹, Christian Brinch¹, Global Sewage Consortium, Frank M. Aarestrup¹

* Authors contributed equally to this work

¹ Genomic Epidemiology, Technical University of Denmark, Kgs. Lyngby, Denmark
² Department of Physics and Astronomy (DIFA), University of Bologna, Bologna, Italy
³ Department of Physics of Complex Systems, ELTE Eötvös Loránd University, Budapest, Hungary

PanRes

A COMBINED COLLECTION OF
CURRENT ARG DATABASES

2025-09-04

PanRes 2

A resource for antimicrobial resistance research

Martynas Baltusis, Nikiforos Pyrounakis, Hannah-Marie Martiny, Attila Beleon, Rolf Sommer Kaas, Frank M Aarestrup, Thomas N. Petersen, Patrick Munk



2025- ?

PanRes 2 - An antimicrobial resistance resource with 3D based protein homology search

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Geographics and bacterial networks differently shape the acquired and latent global sewage resistomes

*Hannah-Marie Martiny¹, *Patrick Munk¹, Alessandro Fuschi², Agnes Becsei³, Nikiforos Pyrounakis¹, Christian Brinch¹, Global Sewage Consortium#, D G Joakim Larsson⁴, Marion Koopmans⁵, Daniel Remondini², Istvan Csabai³, Frank M. Aarestrup¹

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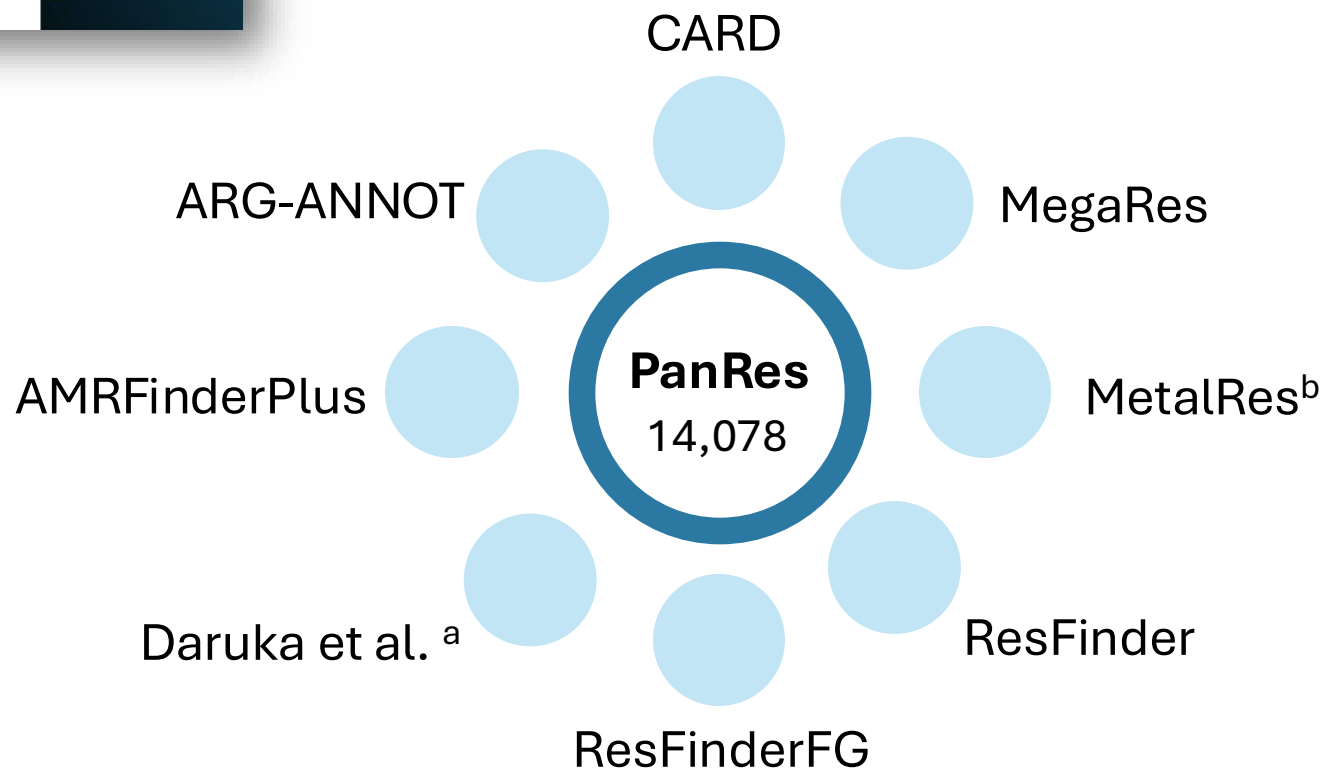
³ Department of Physics of Complex Systems, ELTE Eötvös Loránd University, Budapest, Hungary

⁴ Department of Infectious Diseases, Institute of Biomedicine, University of Gothenburg, and Centre for Antibiotic Resistance Research in Gothenburg, Sweden

⁵ Erasmus Medical Centre, Rotterdam, The Netherlands



PanRes 2.0



Martiny, H. M., Pyrounakis, N., Petersen, T. N., Lukjančenko, O., Aarestrup, F. M., Clausen, P. T., & Munk, P. (2024). ARGprofiler—a pipeline for large-scale analysis of antimicrobial resistance genes and their flanking regions in metagenomic datasets. *Bioinformatics*, 40(3), btae086.

^aDaruka, L., Czikkely, M. S., Szili, P., Farkas, Z., Balogh, D., Grézal, G., ... & Pál, C. (2025). ESKAPE pathogens rapidly develop resistance against antibiotics in development in vitro. *Nature Microbiology*, 10(2), 313-331.

^b <https://zenodo.org/records/8108201>



Expand the gene collection with new genes



Predict protein structures and build HMMs



Enhance the usability with ontology



Niki
Pyrounakis



Martynas
Baltusis



Attila
Beleon



Amulya
Baral



Rolf
Sommer
Kaas



Frank
Aarestrup



Thomas N.
Petersen



Patrick
Munk



PanRes 2.0

Harmonizing resistance annotations

Genes	ResFinder mechanism	CARD mechanism
<u>oqxA</u>	efflux pump	antibiotic efflux
<u>blaACC</u> , <u>blaACT</u> , <u>catB1</u> , <u>blaBEL</u>	enzymatic inactivation	antibiotic inactivation
<u>lnu(B)</u>	enzymatic inactivation	antibiotic target protection
<u>aad-</u> , <u>aac-</u> , <u>aph</u> , <u>blaKPC</u> , <u>blaPAU</u> , ...	enzymatic modification	antibiotic inactivation
<u>cmx</u> , <u>fexA</u> , <u>fexB</u> , <u>floR</u> , <u>tet</u> , <u>mef</u> , <u>otr(C)</u> , ...	increased efflux	antibiotic efflux
<u>cmlV.1</u>	increased efflux	antibiotic inactivation
<u>tet(57)</u> , <u>mef(A)</u>	increased efflux	antibiotic target protection
<u>dfrA-</u> , <u>dfrB-</u> , <u>sul1</u> , <u>sul2</u> , <u>sul3</u>	purine synthesis	antibiotic target replacement
<u>ARR-8.1</u>	ribosylation	antibiotic inactivation
<u>cfr</u> , <u>erm</u> , <u>mcr</u> , <u>vanA</u>	target modification	antibiotic target alteration
<u>mecA</u> , <u>mecB</u> , <u>mecC</u> , <u>mecD</u>	target modification	antibiotic target replacement
<u>armA</u> , <u>rmtA</u> , <u>rmtB</u> , <u>rmtC</u> , <u>rmtD</u> , <u>rmtE</u> , <u>rmtF</u> , <u>rmtG</u> , <u>rmtH</u> , <u>sgm</u>	target protection	antibiotic target alteration
<u>fusB</u> , <u>fusC</u> , <u>tetO</u> , <u>tetW</u> , <u>tet</u> , <u>Isa(A)</u> , <u>Isa(B)</u> , <u>Isa(C)</u> , <u>msr(E)</u> , ...	target protection	antibiotic target protection



Enhance the
usability with
ontology



Niki
Pyrounakis



Martynas
Baltusis



Attila
Beleon



Amulya
Baral



Rolf
Sommer
Kaas



Frank
Aarestrup



Thomas N.
Petersen



Patrick
Munk

PanRes 2.0 Database

PanRes (Pan Resistance) is a curated collection of genes conferring resistance to antibiotics, heavy metals, and biocides. We have aggregated unique gene sequences from multiple databases like ResFinder, CARD, MegaRes, AMRFinderPlus, ARGANNOT, BacMet, and functionally verified genes and unified the ontology.

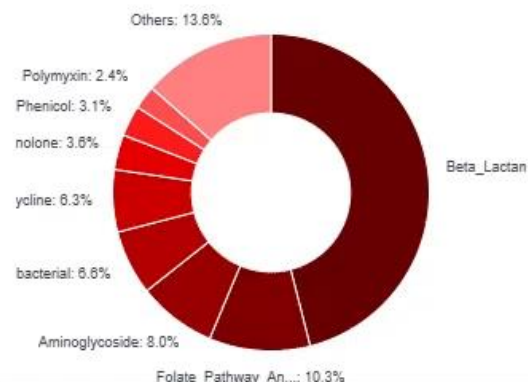


Click any button below to browse the Panres 2 ontology by antibiotic classes, predicted antibiotic resistance phenotype(s), resistance mechanisms, and by source database.

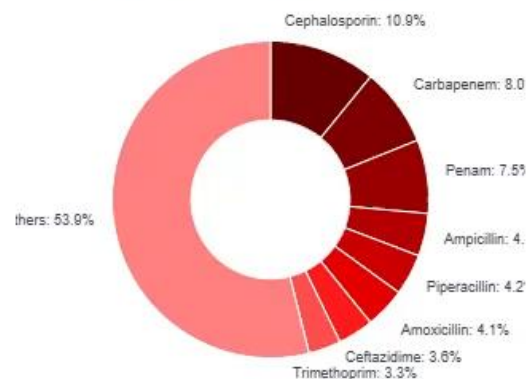
[Antibiotic Classes](#)[Source Databases](#)[Resistance Phenotypes](#)[Resistance Mechanisms](#)

PanRes in Numbers

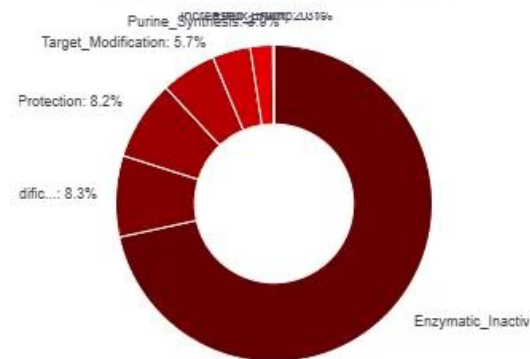
By Antibiotic Class



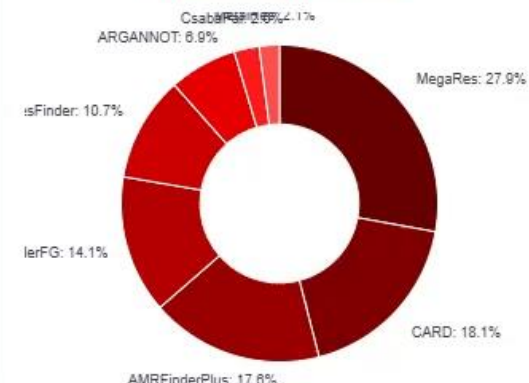
By Predicted Phenotype



By Resistance Mechanism



By Source Database



Citation

If you use the PanRes database or website, please cite:

Hannah-Marie Martiny, Nikiforos Pyrounakis, Thomas N Petersen, Oksana Lukjančenko, Frank M Aarestrup, Philip T L C Clausen, Patrick Munk, ARGprofiler—a pipeline for large-scale analysis of antimicrobial resistance genes and their flanking regions in metagenomic datasets, *Bioinformatics*, Volume 40, Issue 3, March 2024, btac086, <https://doi.org/10.1093/bioinformatics/btac086>

2023-11-06

A build up

2024-09-30

2025-03-10



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PanRes

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CURRENT ARG DATABASES

2025-09-04

PanRes 2

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2025- ?

PanRes 2 - An antimicrobial resistance resource with 3D based protein homology search

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*Corresponding author

Geographics and bacterial networks differently shape the acquired and latent global sewage resistomes

*Hannah-Marie Martiny¹, *Patrick Munk¹, Alessandro Fuschi², Agnes Becsei³, Nikiforos Pyrounakis¹, Christian Brinch¹, Global Sewage Consortium#, D G Joakim Larsson⁴, Marion Koopmans⁵, Daniel Remondini², Istvan Csabai³, Frank M. Aarestrup¹

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⁴ Department of Infectious Diseases, Institute of Biomedicine, University of Gothenburg, and Centre for Antibiotic Resistance Research in Gothenburg, Sweden

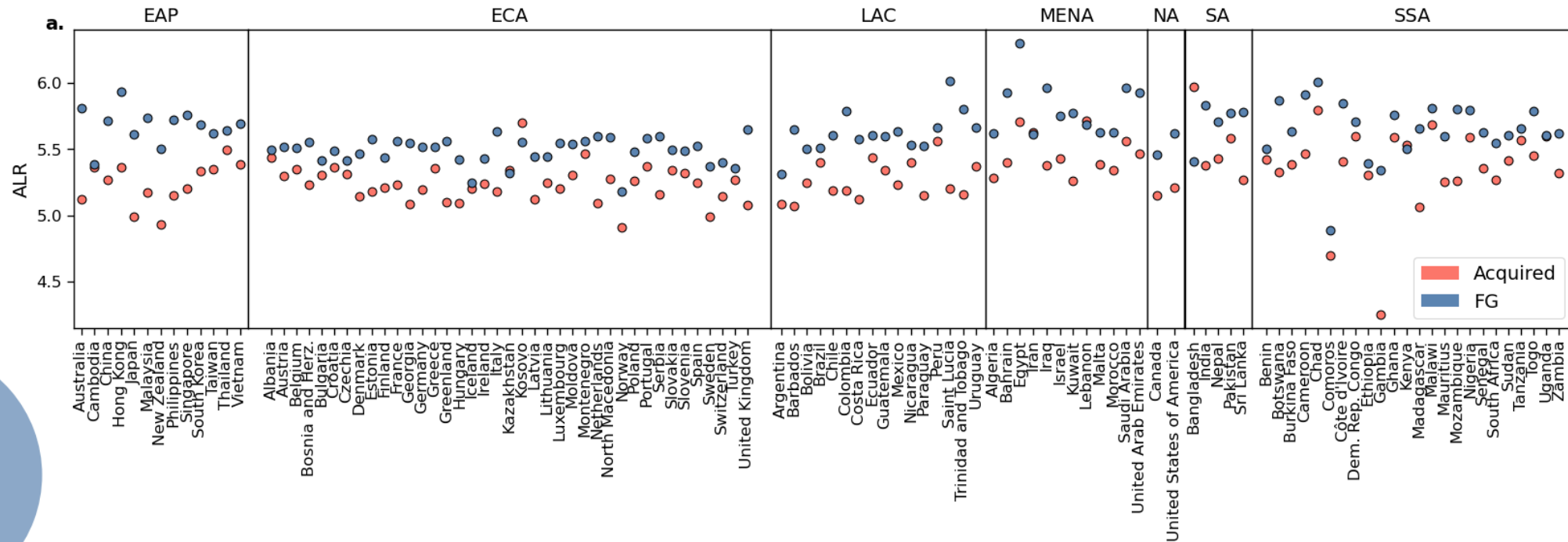
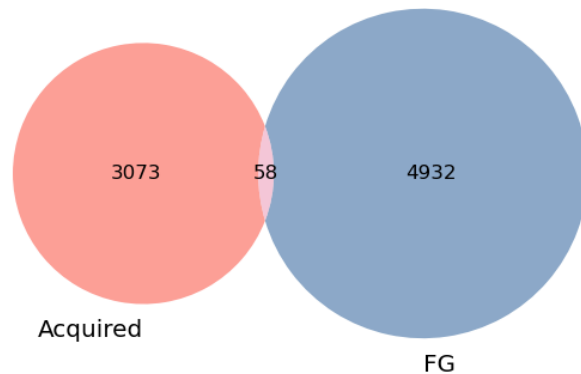
⁵ Erasmus Medical Centre, Rotterdam, The Netherlands

Geographics and bacterial networks differently shape the acquired and latent global sewage resistomes

Acquired
ResFinder

FG
ResFinderFG¹
Daruka et al. (2025)²

Allele overlap



¹ Gschwind, R., Ugarcina Perovic, S., Weiss, M., Petitjean, M., Lao, J., Coelho, L. P., & Ruppé, E. (2023). ResFinderFG v2. 0: a database of antibiotic resistance genes obtained by functional metagenomics. *Nucleic Acids Research*, 51(W1), W493-W500.

² Daruka, L., Czikkely, M. S., Szili, P., Farkas, Z., Balogh, D., Grézel, G., ... & Pál, C. (2025). ESKAPE pathogens rapidly develop resistance against antibiotics in development in vitro. *Nature Microbiology*, 10(2), 313-331.

Geographics and bacterial networks differently shape the acquired and latent global sewage resistomes



Alessandro Fuschi Ágnes Becsei Niki Pyrounakis



Patrick Munk Frank Aarestrup

Acquired
ResFinder

FG
ResFinderFG¹
Daruka et al. (2025)²

Allele overlap

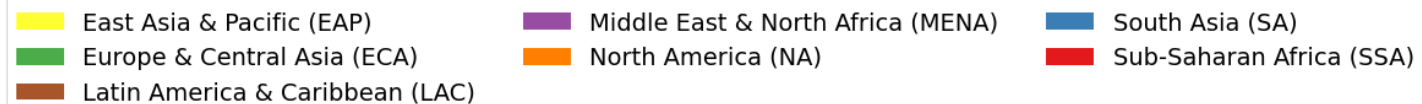
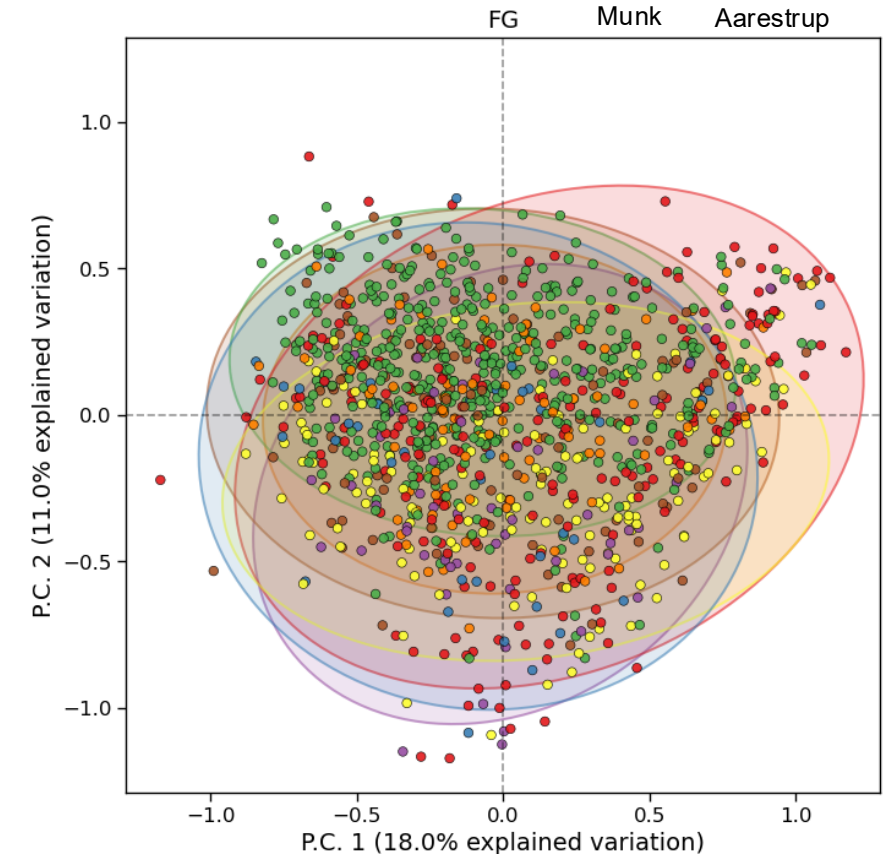
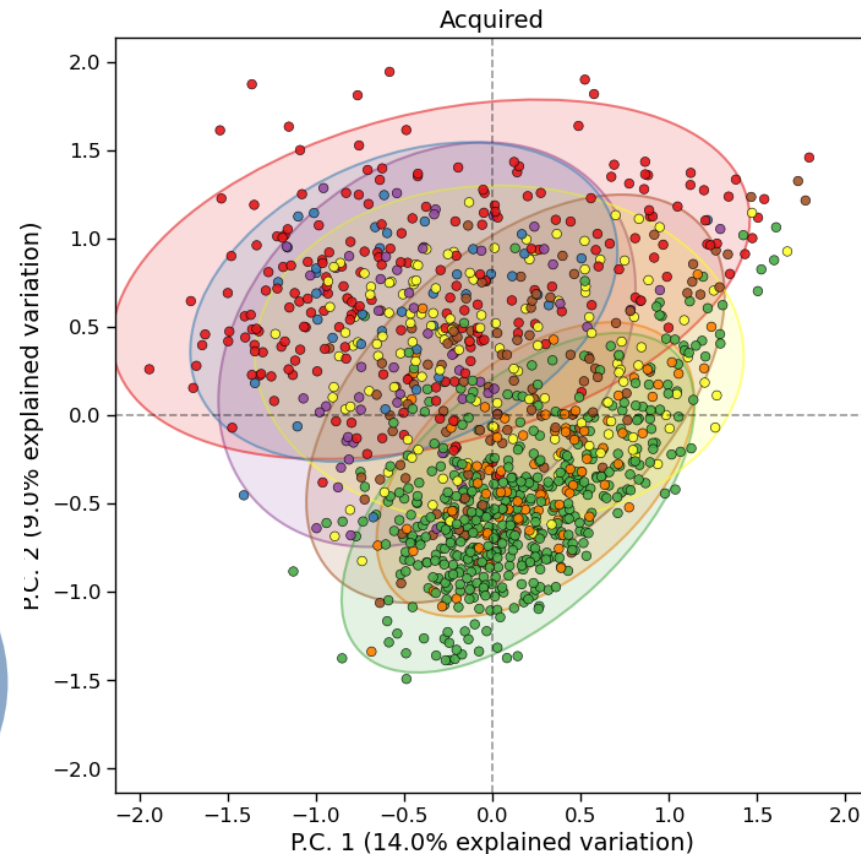
3073

58

4932

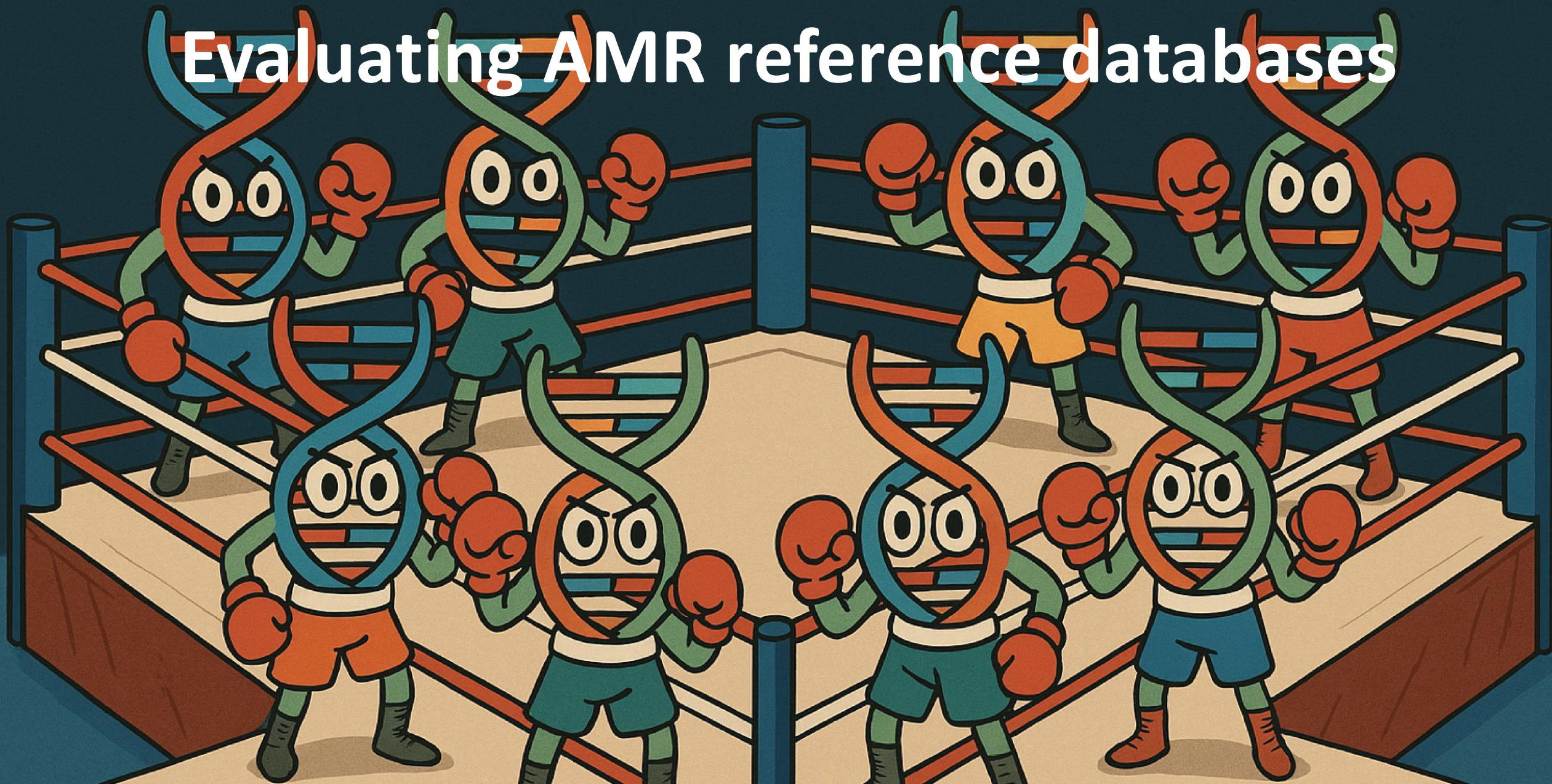
Acquired

FG

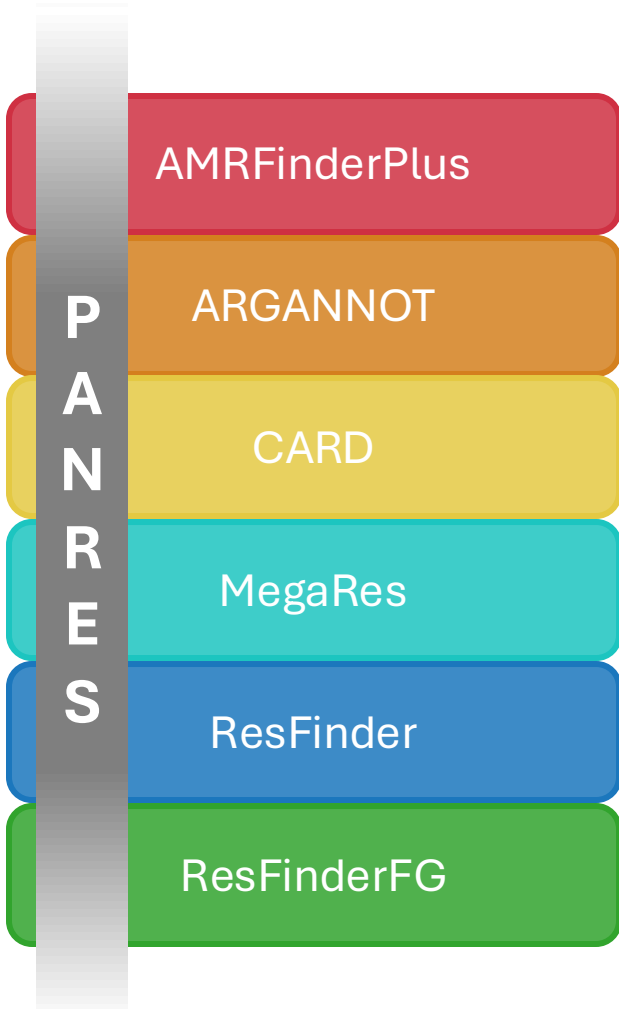


DATABASE SHOWDOWN

Evaluating AMR reference databases



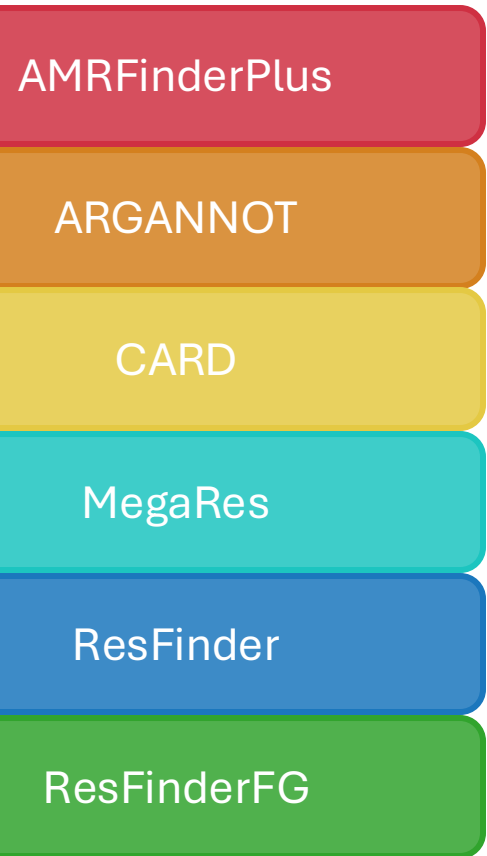
What about the other AMR databases?



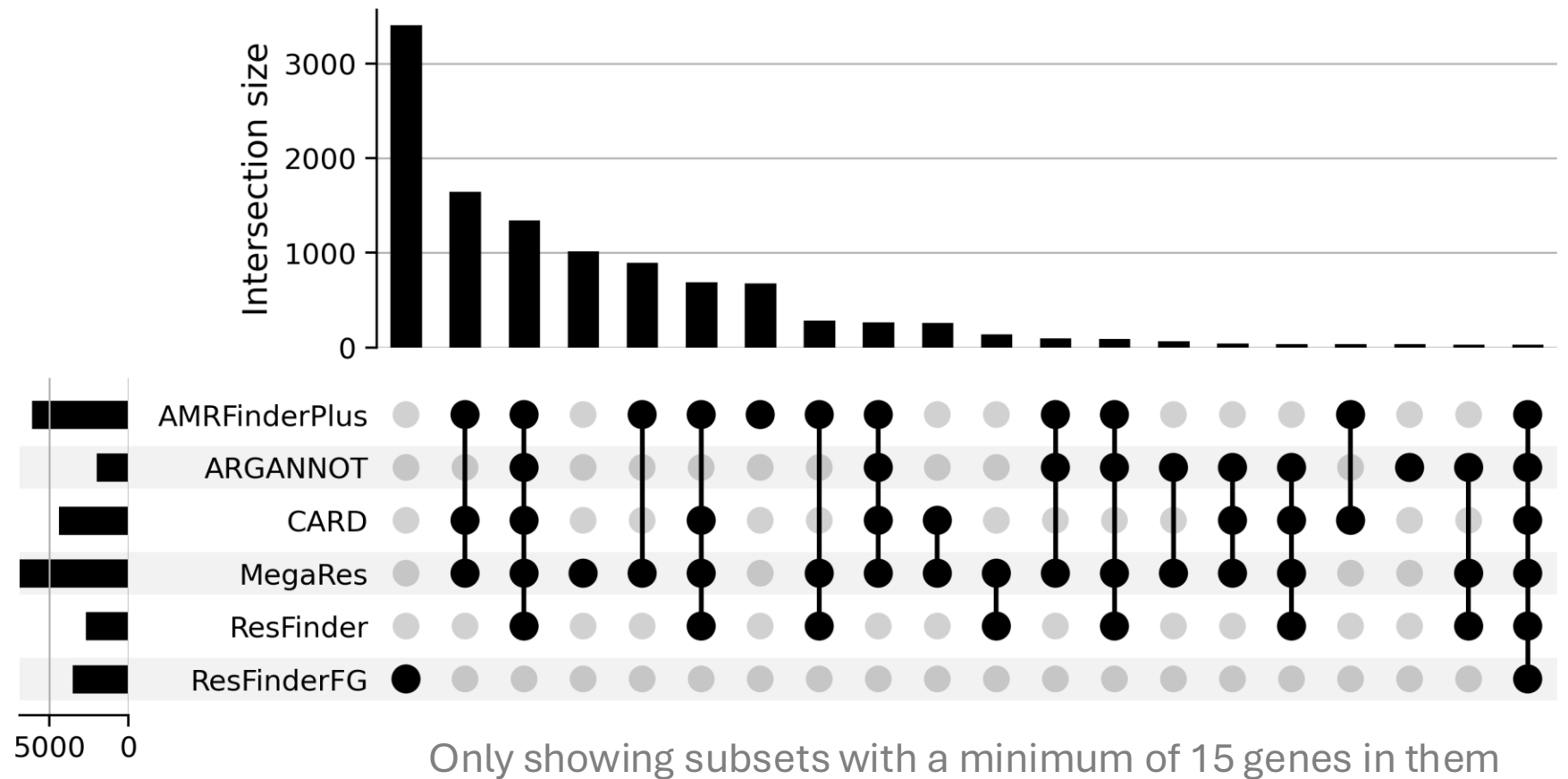
Both harmonizing the labels for PanRes and analyzing the sewage samples led us to wonder:

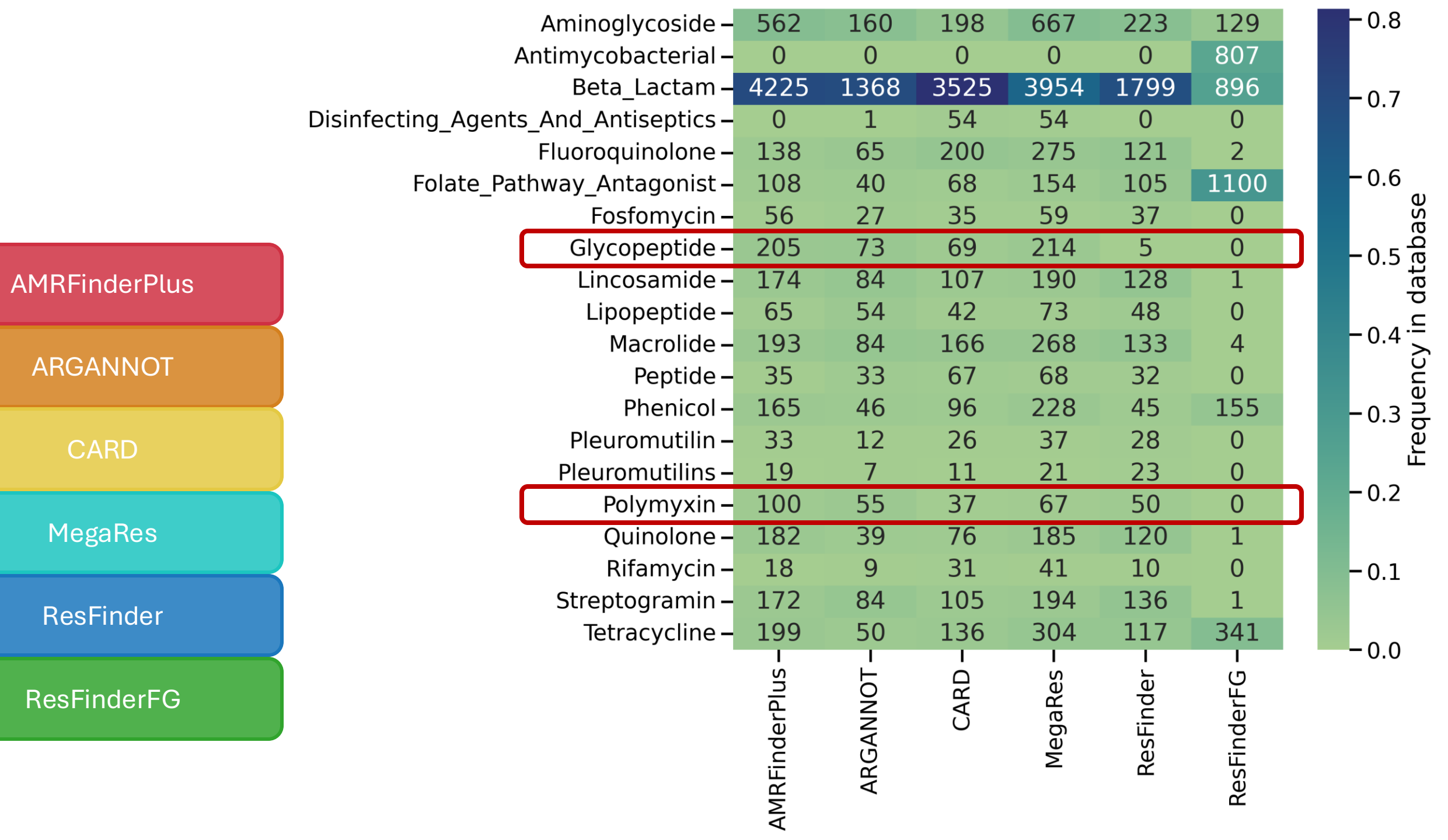
- How similar is the content of the databases?
- How are they being used in the literature?
- How does the choice of database change AMR results?

What about the other AMR databases?



Database overlaps in gene content

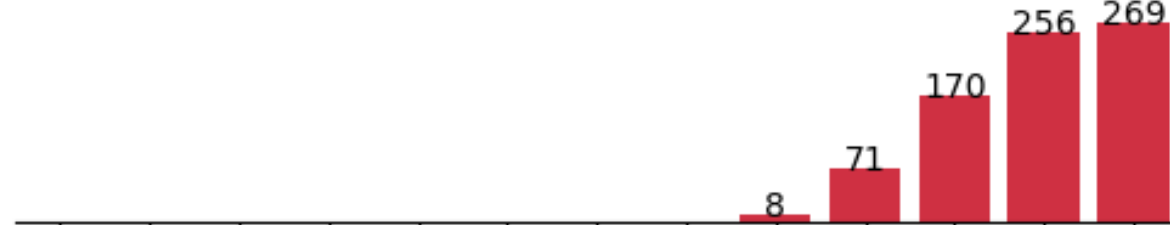




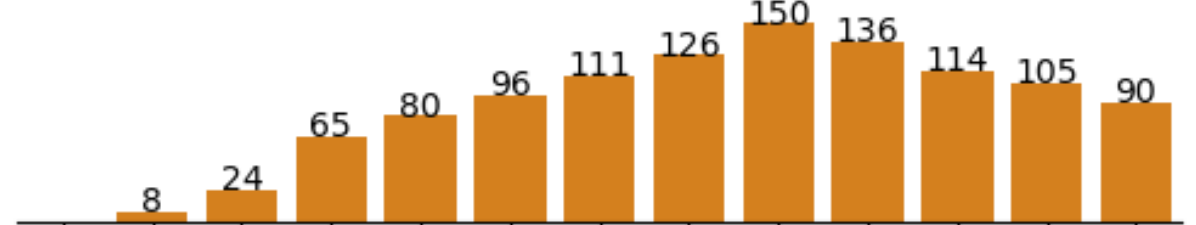
What about the other AMR databases?

Citation counts (Scopus)

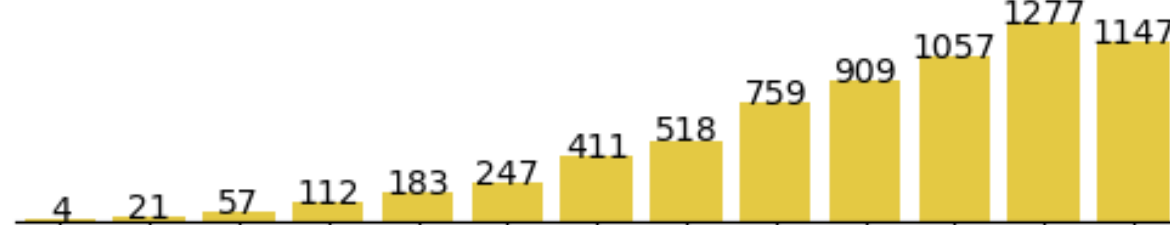
AMRFinderPlus



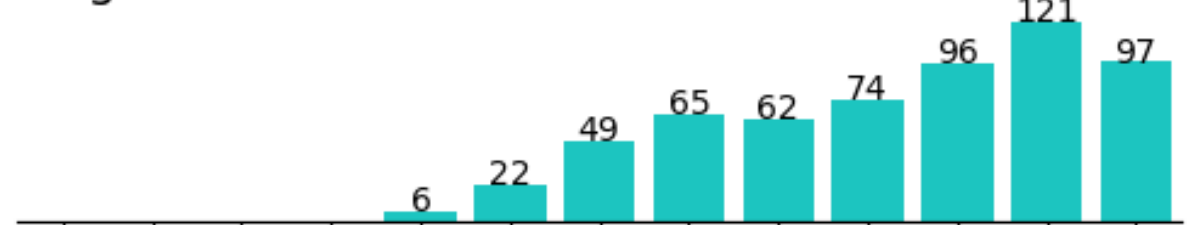
ARGANNOT



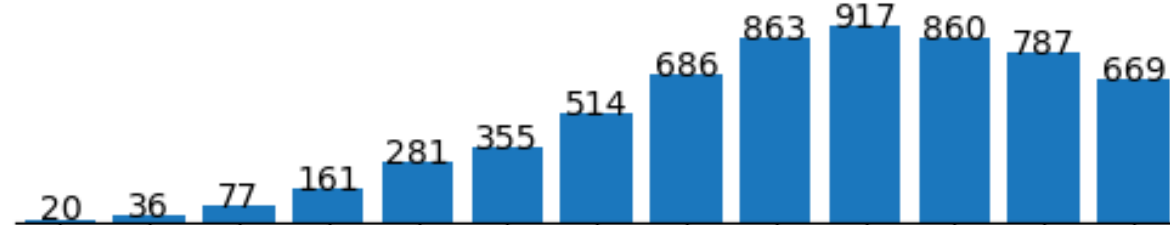
CARD



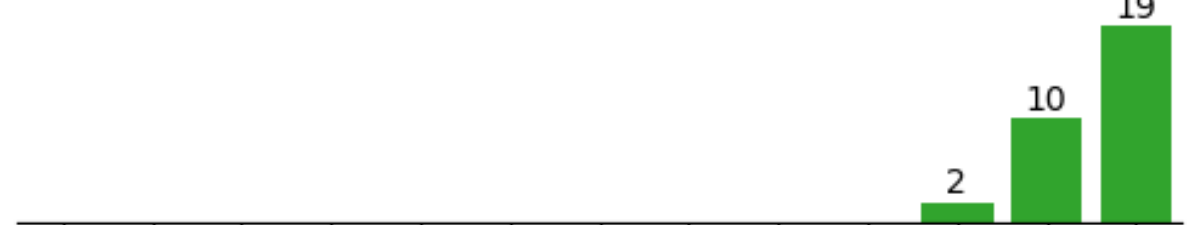
MegaRes



ResFinder



ResFinderFG

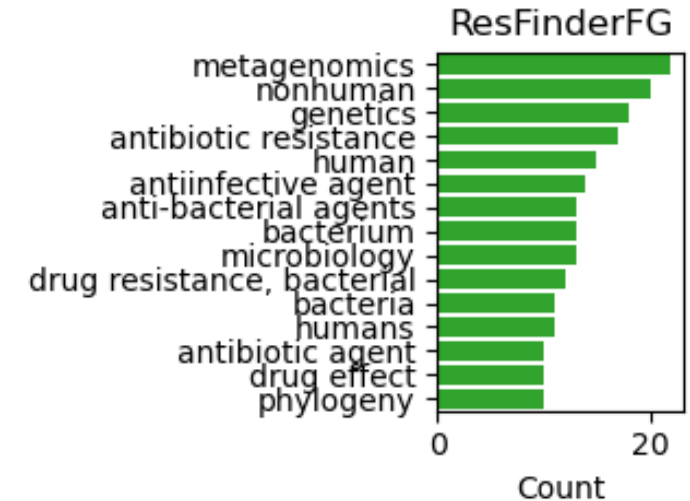
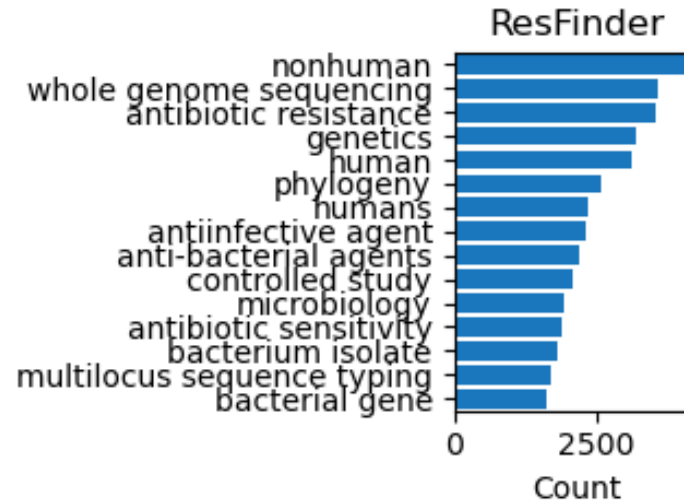
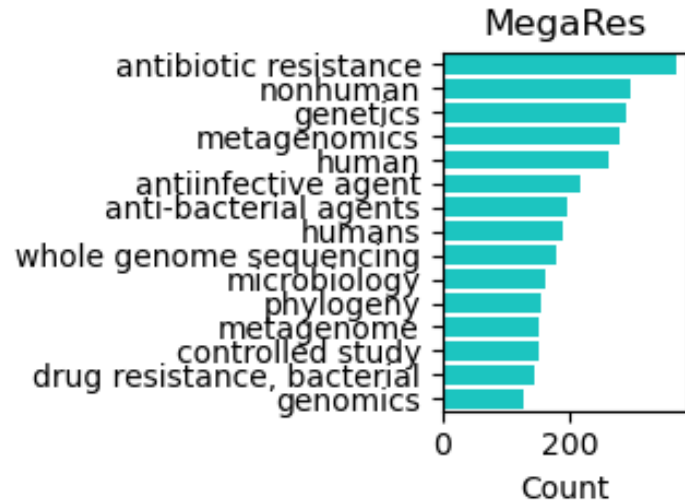
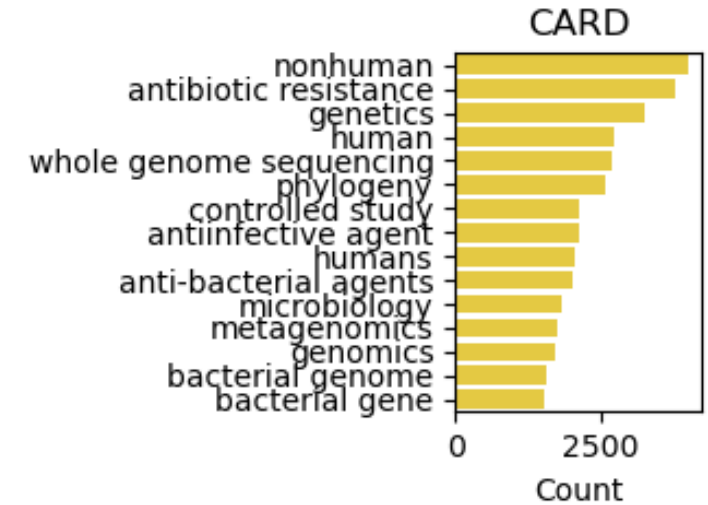
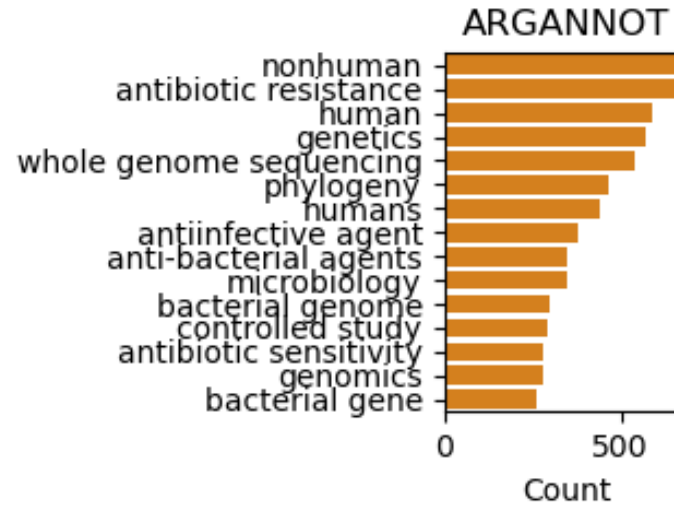
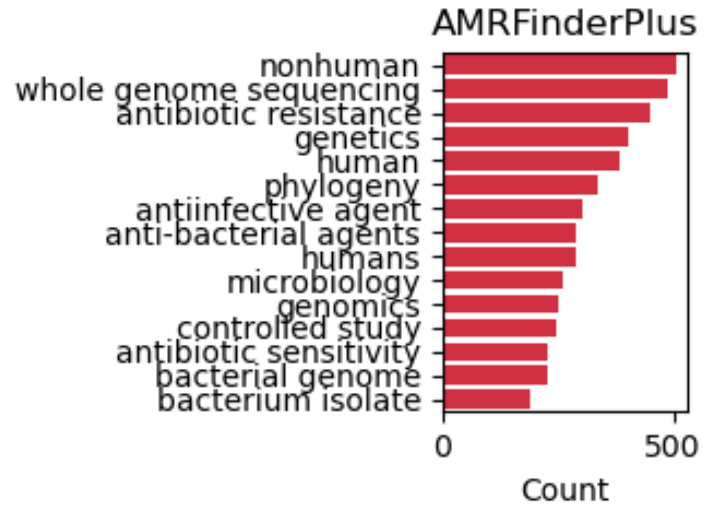


2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025

2013 2014 2015 2016 2017 2018 2019 2020 2021 2022 2023 2024 2025

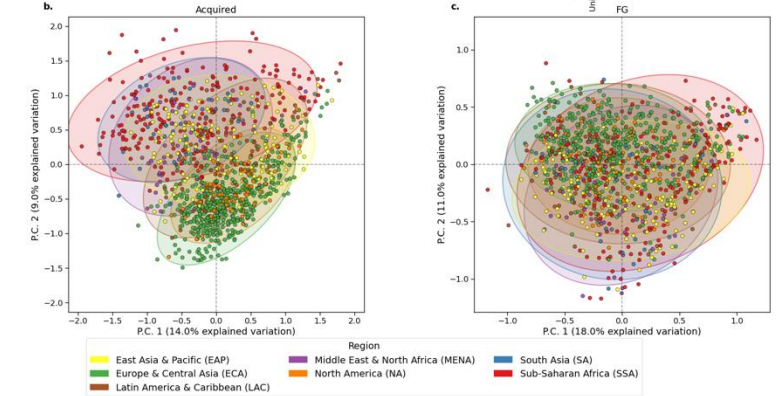
What about the other AMR databases?

Keywords counts (Scopus)

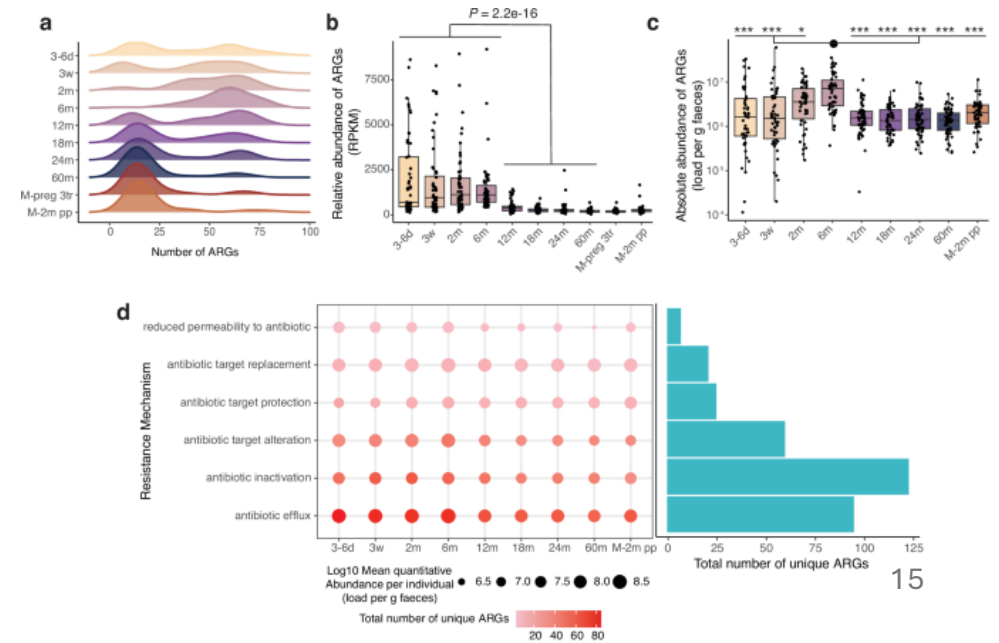
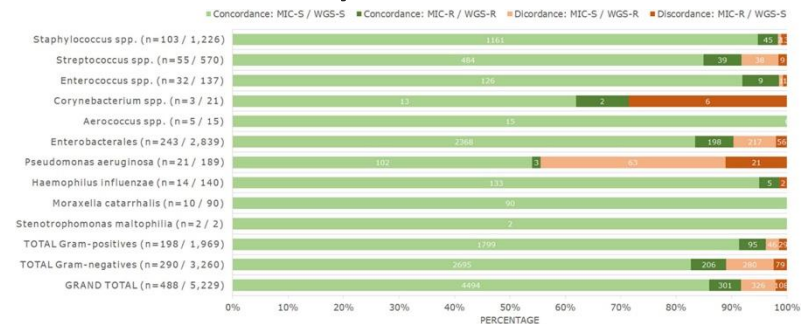


Datasets to use for evaluation

- Global Sewage samples
- One Day in Denmark¹: phenotypic vs genotypic
- Temporal dynamics and microbial interactions shaping the gut resistome in early infancy²



One Day in Denmark¹



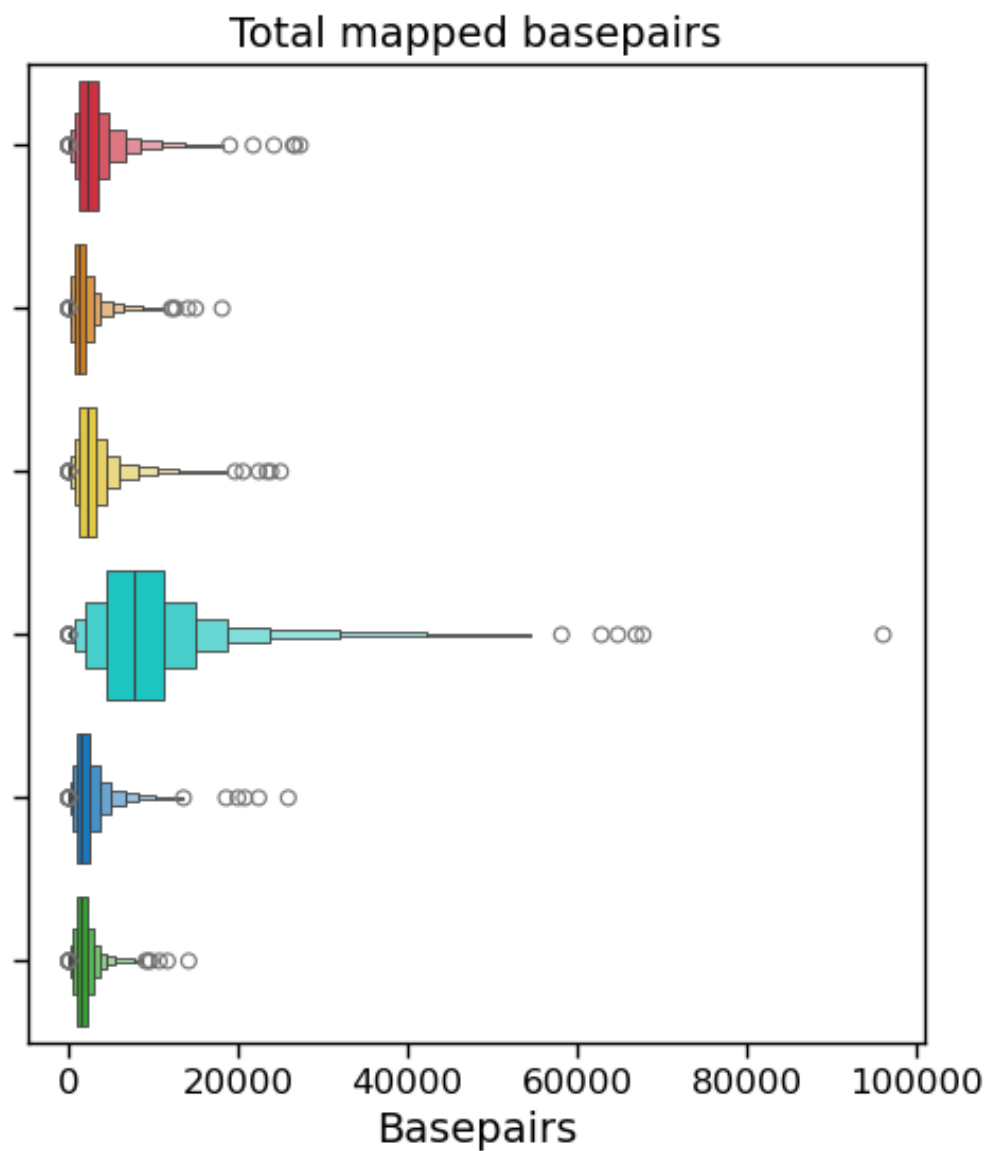
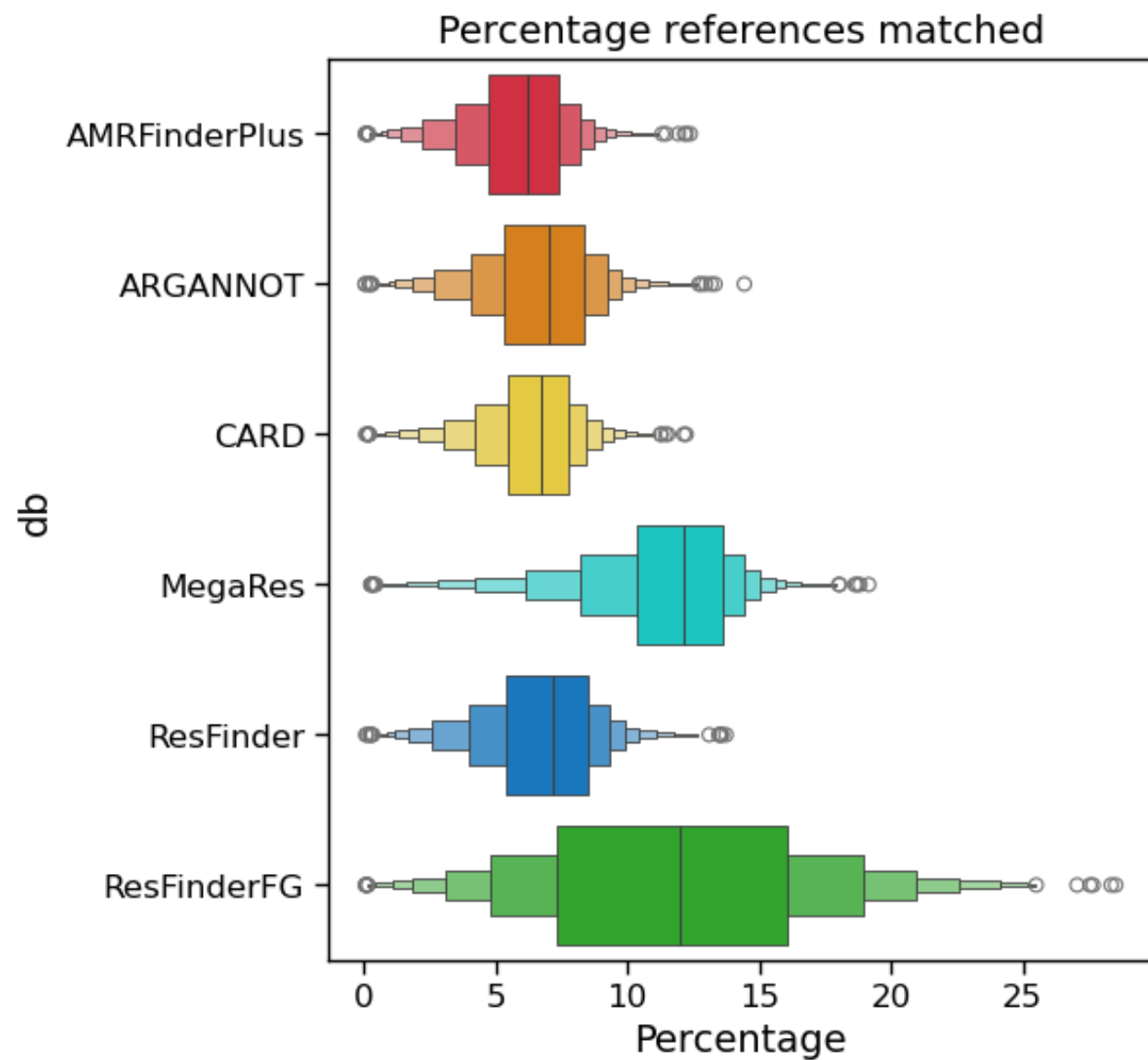
¹ Rebelo, A. R., Bortolaia, V., Leekitcharoenphon, P., ... & Aarestrup, F. M. (2022). One day in Denmark: comparison of phenotypic and genotypic antimicrobial susceptibility testing in bacterial isolates from clinical settings. *Frontiers in microbiology*, 13, 804627.

² Chatzigiannidou, I., Johansen, P. L., Dehli, R. K., Moll, J. M., Eriksen, C., Myers, P. N., ... & Brix, S. (2025). Temporal dynamics and microbial interactions shaping the gut resistome in early infancy. *Nature Communications*, 16(1), 8139.

Copilot prompt:
Follow the same style as the title
slide. A cartoon-style illustration of
a single smiling boxer standing in a
boxing ring. The boxer is wearing
boxing gloves and shorts, and there
is a large question mark above his
head, symbolizing an open question
or uncertainty. The mood is friendly
and lighthearted, and the
background is a simple boxing
arena. Landscape orientation



Comments? Want to get involved?



Abundance: bpTotal/length

