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Computational Approaches to Unveil the Hidden Diversity of Siderophores in Bacterial Genomes

Prof. Dr. Nadine Ziemert

@NadineZiemert.bsky.social

DZIF

Bacteria are Nature´s Chemists

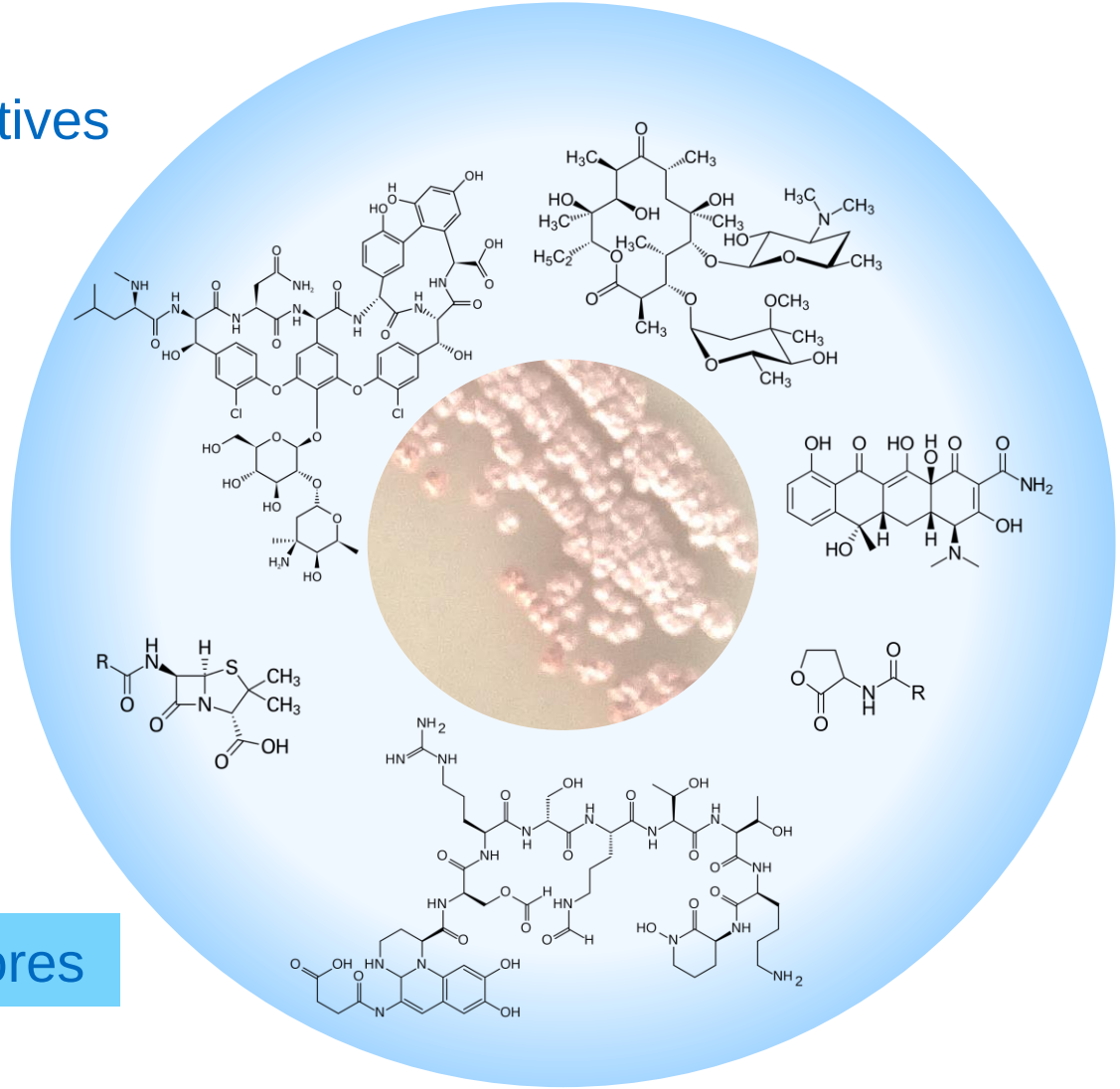
Preservatives

Medicine

Antioxidants

Biosurfactants

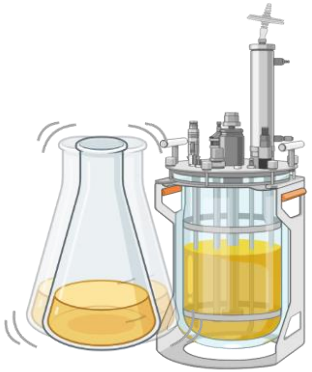
Siderophores



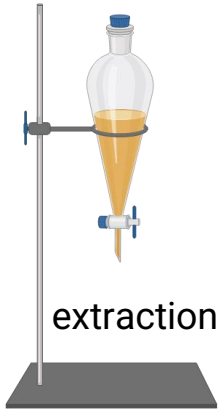
- Intra-species & inter-kingdom communication
- Warfare
- Storage
- Nutrient acquisition
- Development

Classical Discovery

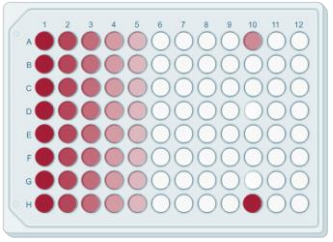
strain isolation



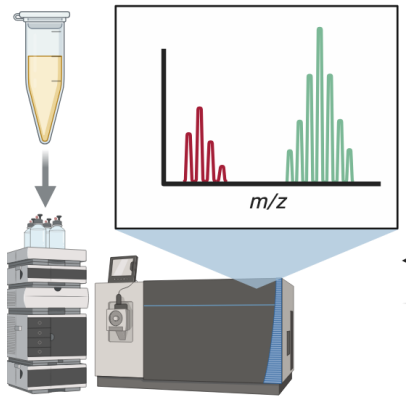
fermentation



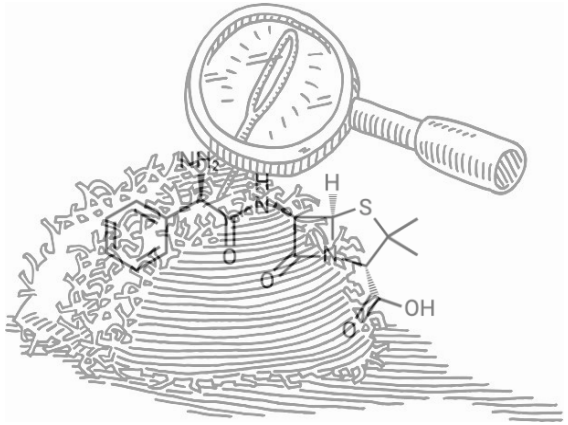
extraction



bioassay



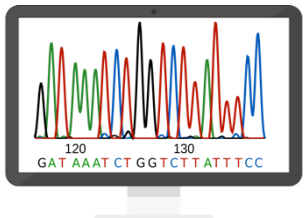
isolation



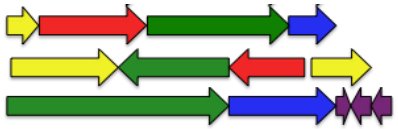
structure elucidation

Genome Mining for BGCs

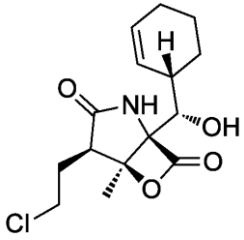
Genome Sequences



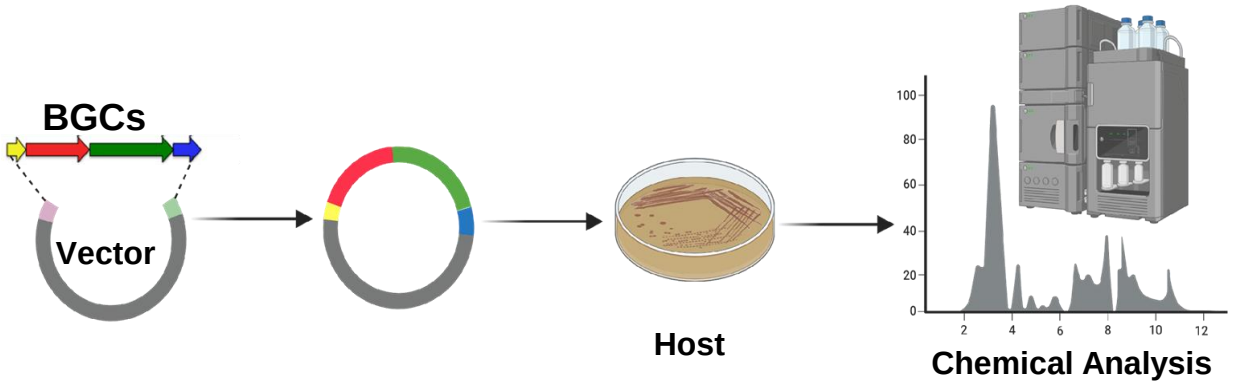
Natural Products Biosynthetic Gene Clusters

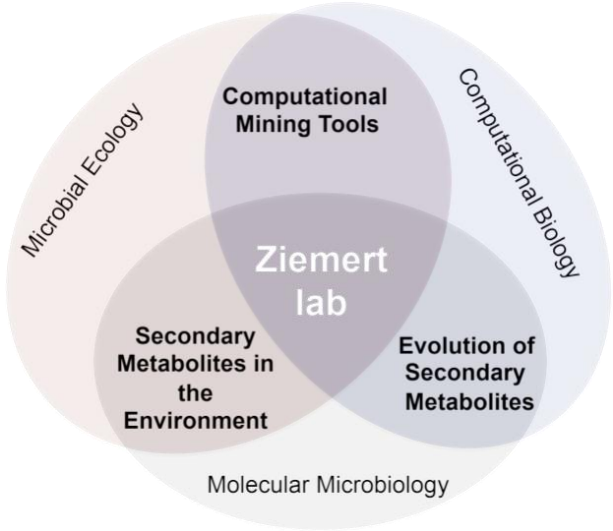


Natural Product



Heterologous Expression/ Analytical Chemistry to get compounds





(Gavriilidou *et al.,* 2022 Nat Microbiol) (Hansen *et al*., 2023 Nat Com.)

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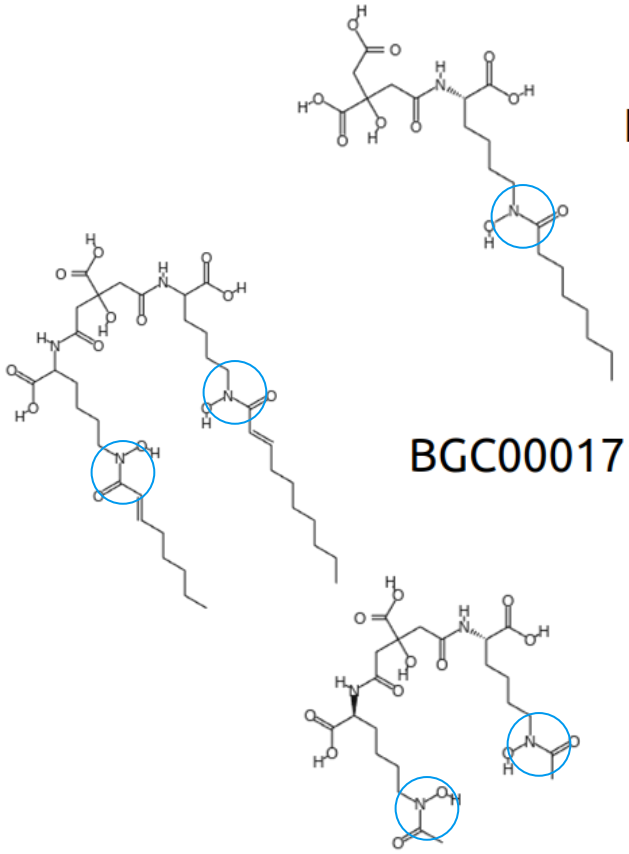
Main Questions

- **Ho much Siderophore Diversity is encoded in bacterial genomes?**
- **How are they distributed across the bacterial kingdom?**
- **Can we use high throughput methods to predict them and reprogram them?**

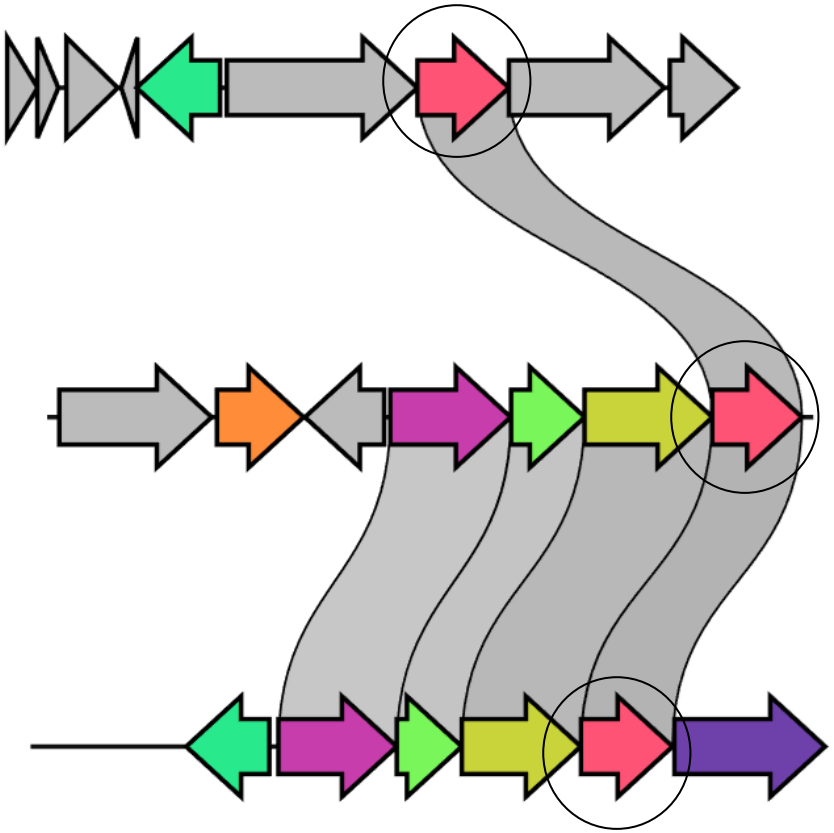
How to detect Siderophore genes



Woodybactin
NC_010506.1:1-10640

Ochrobactin
BGC0001713 (reversed):11163-1

Aerobactin
BGC0001499:1-11578



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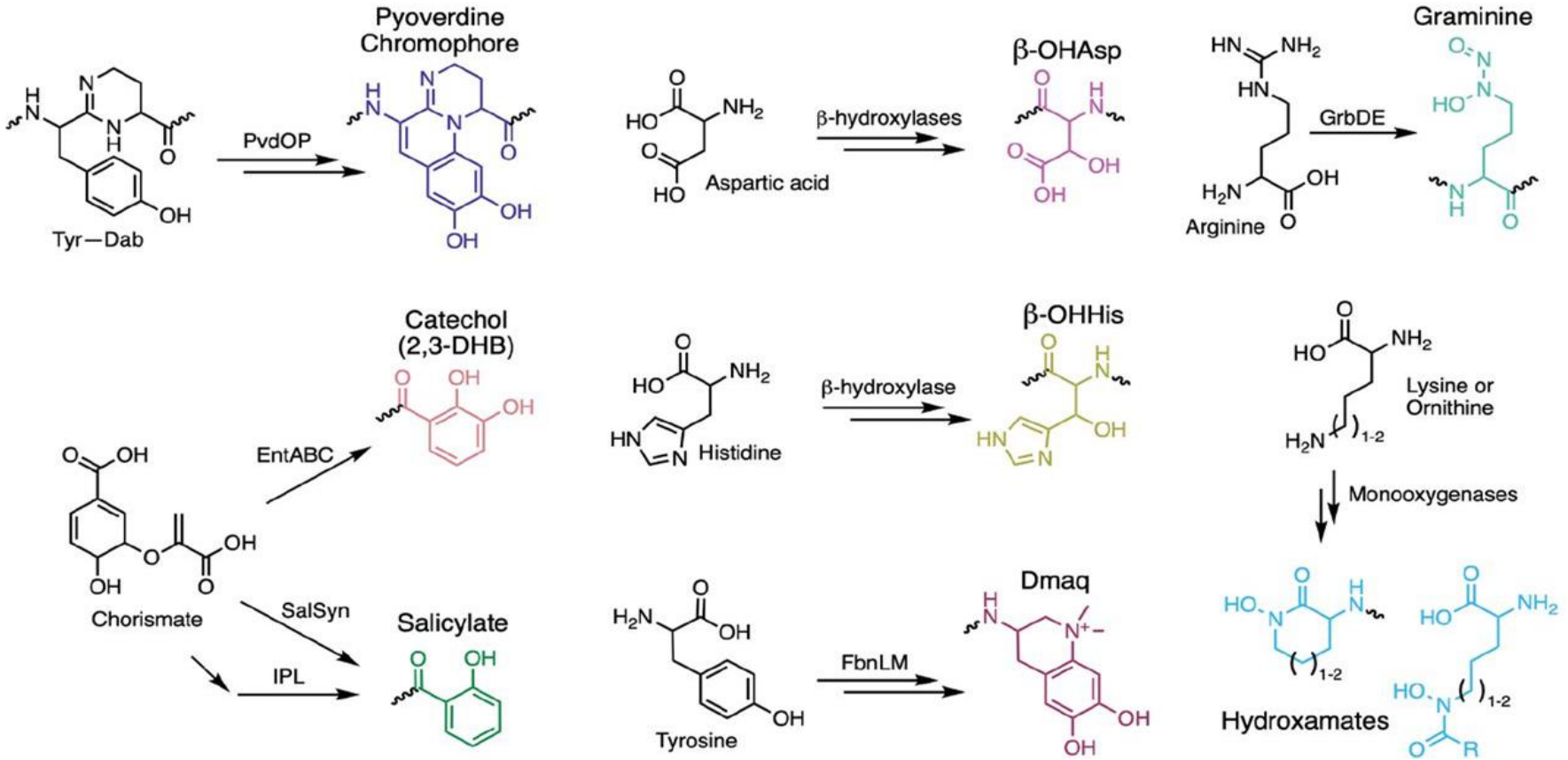
Bita
Pourmohsenin

Siderophore Diversity



Automated prediction of peptide metallophores

Reitz*, Pourmohsenin*, *et. al.* 2025, elife

Zach
Reitz

Marnix
Medema

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A Roadmap to Siderophores

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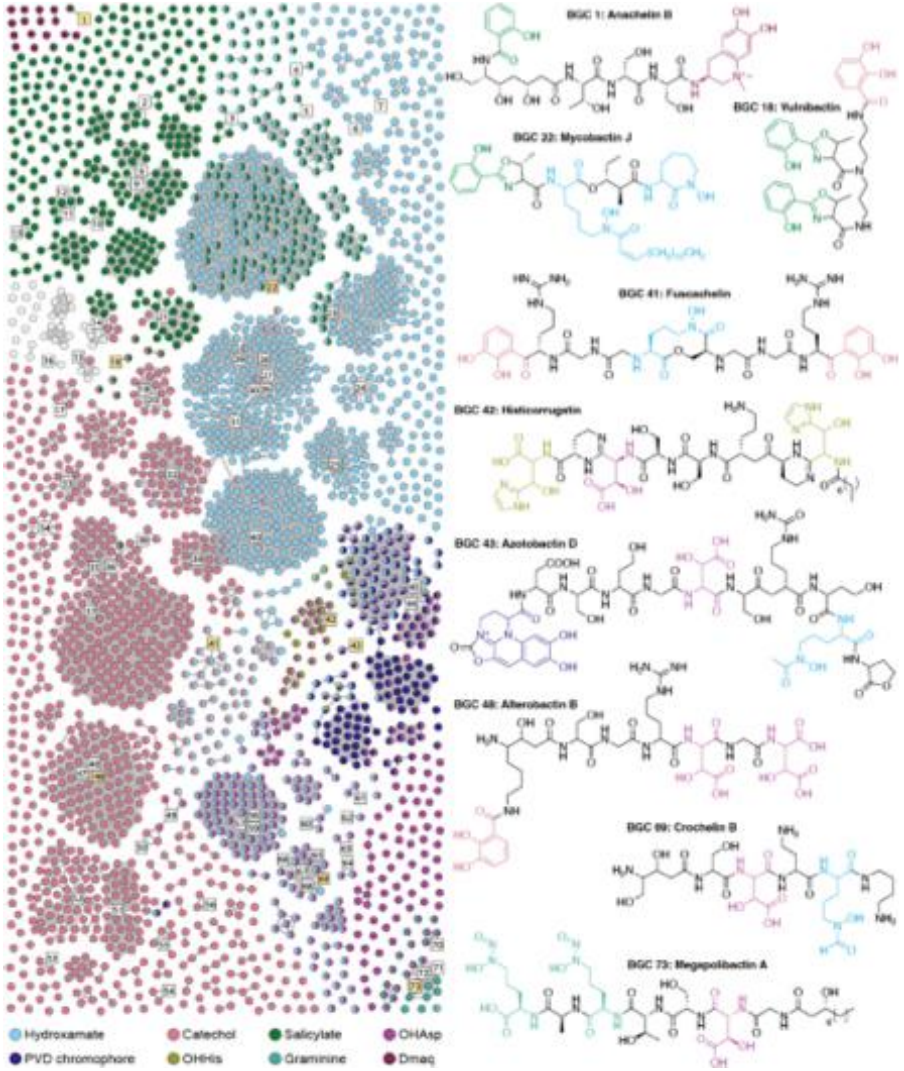
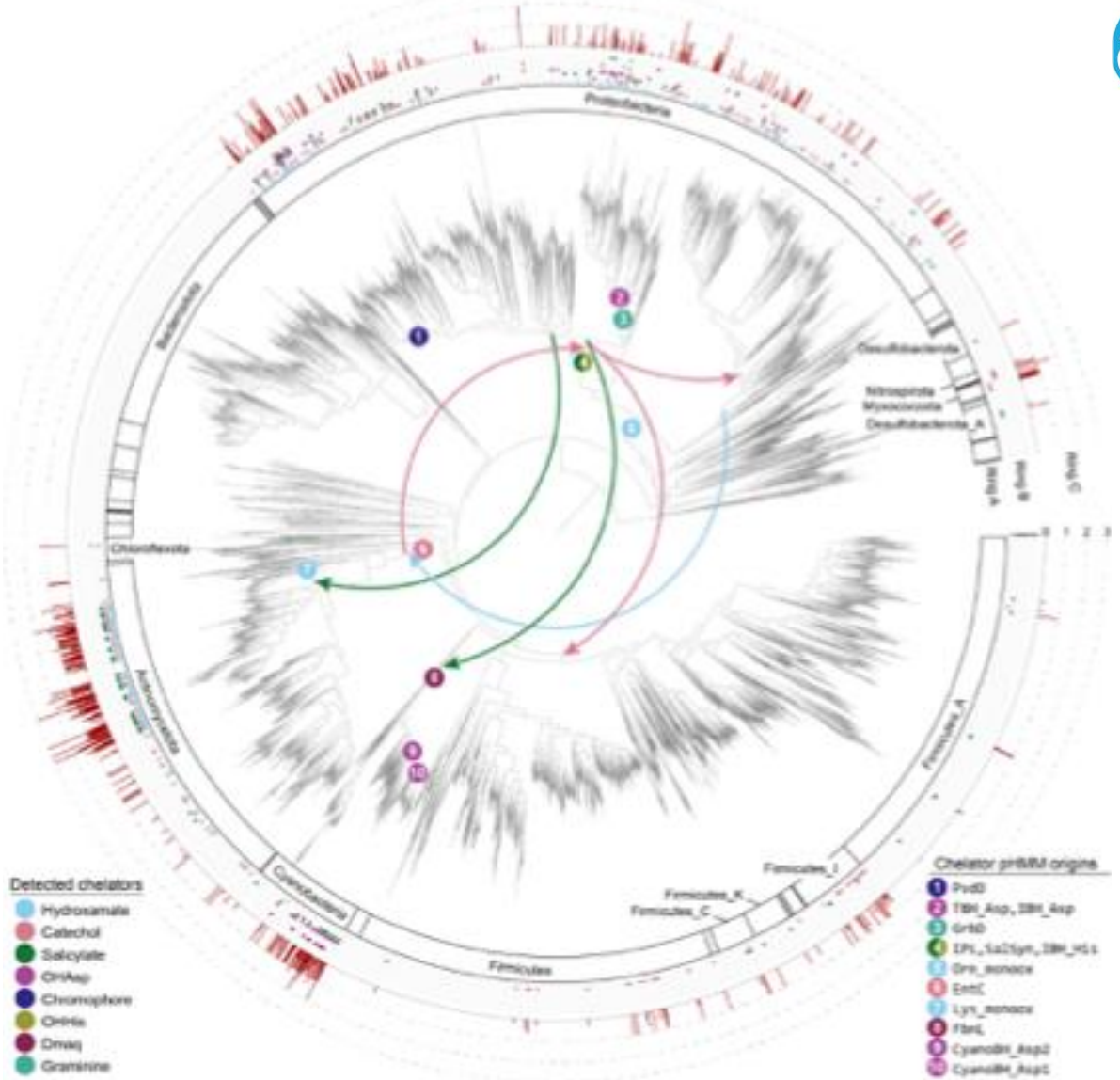
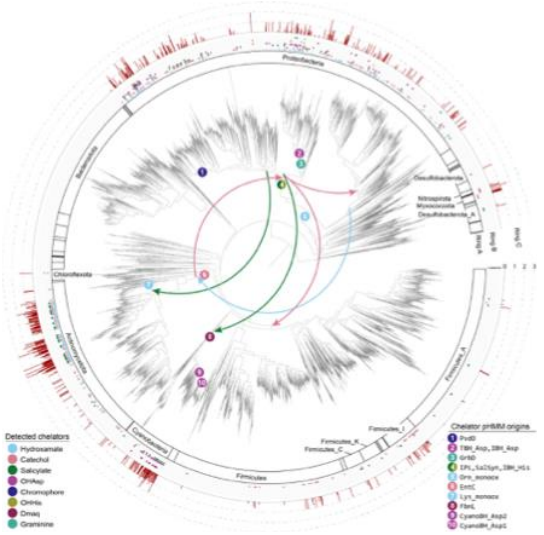




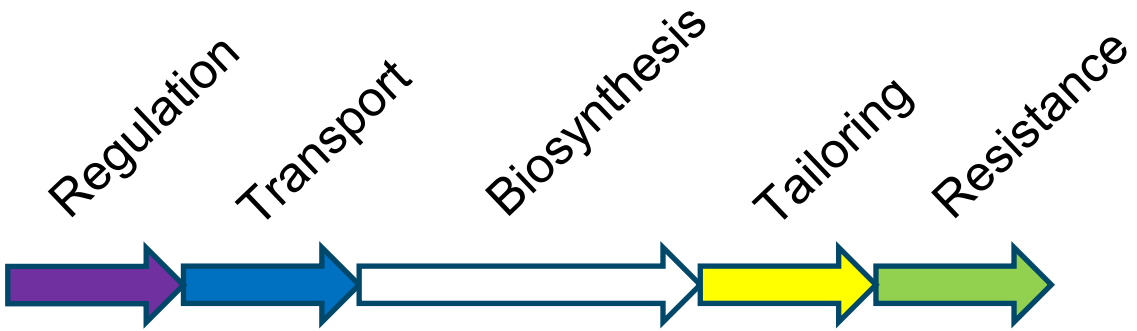
Reitz*, Pourmohsenin*, *et. al.* 2025, elife

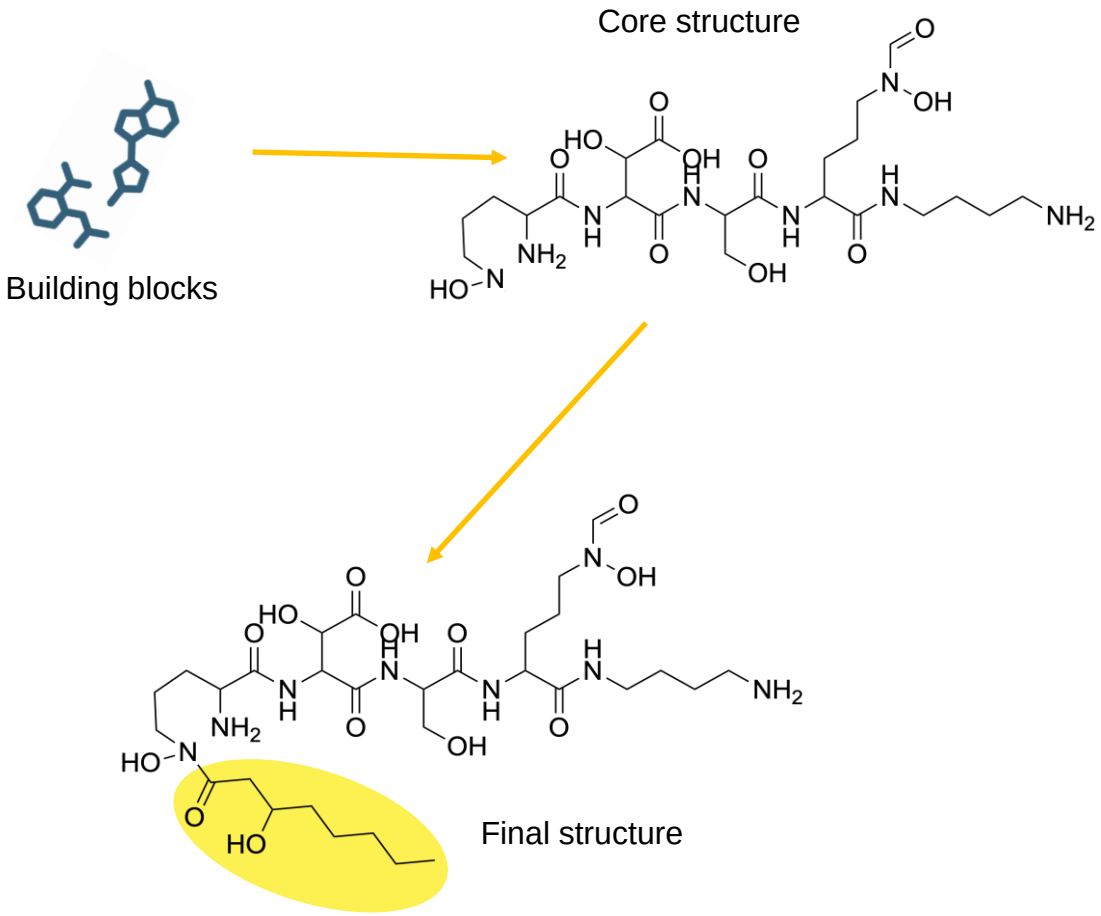
Roadmap to Siderophore Diversity

- **Automated siderophore gene detection methods allow to study the diversity of siderophore encoded in bacterial genomes**
- **Specific taxa have more potential to produce new siderophores**

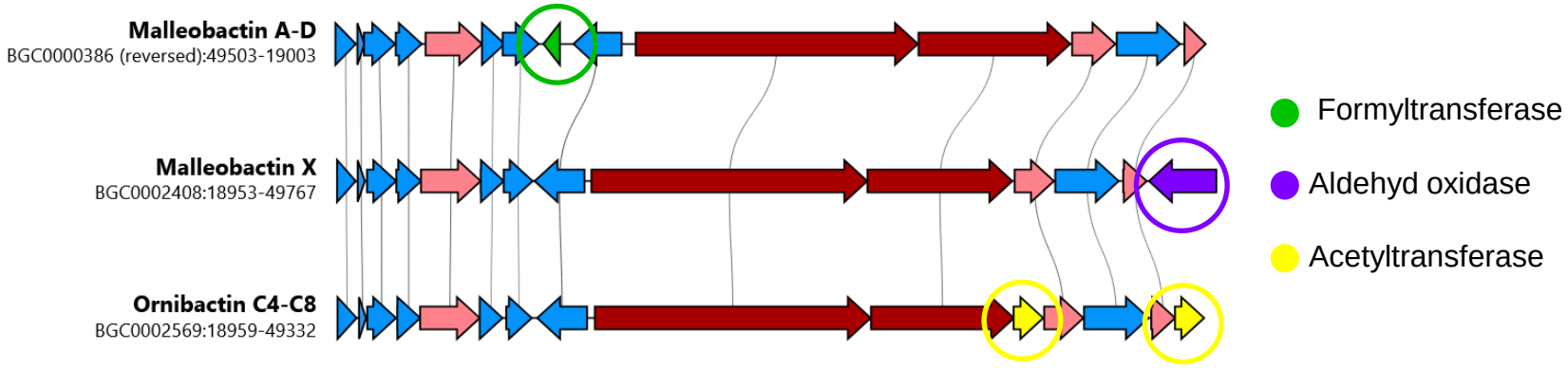


Reprogramming of Siderophores





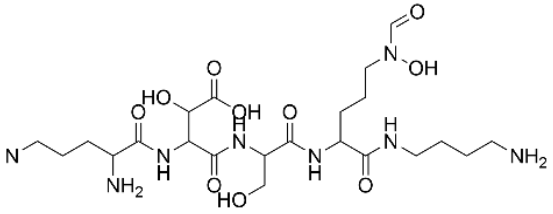
Diversity within related BGCs families

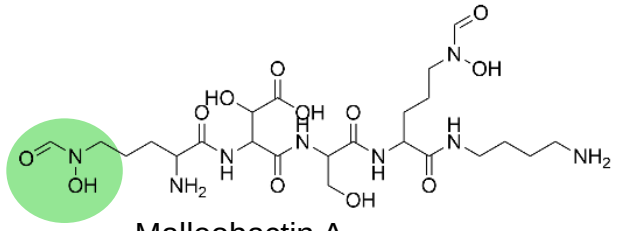


- Conserved Core Structure
- Variations introduced by tailoring enzymes

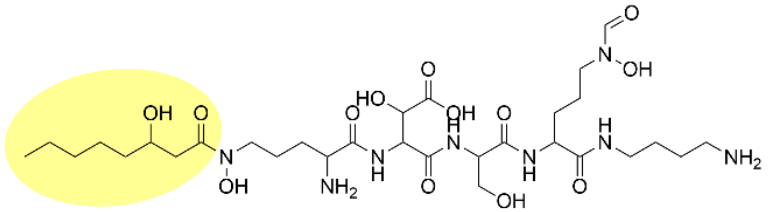
→ **Lead to altered chemical properties**

Core structure

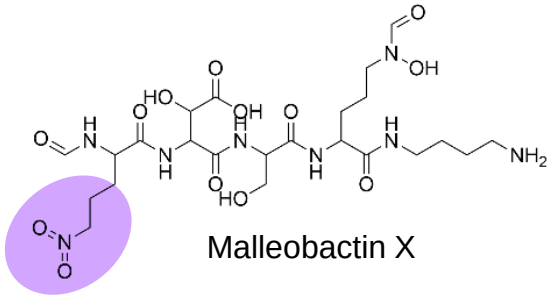




Malleobactin A

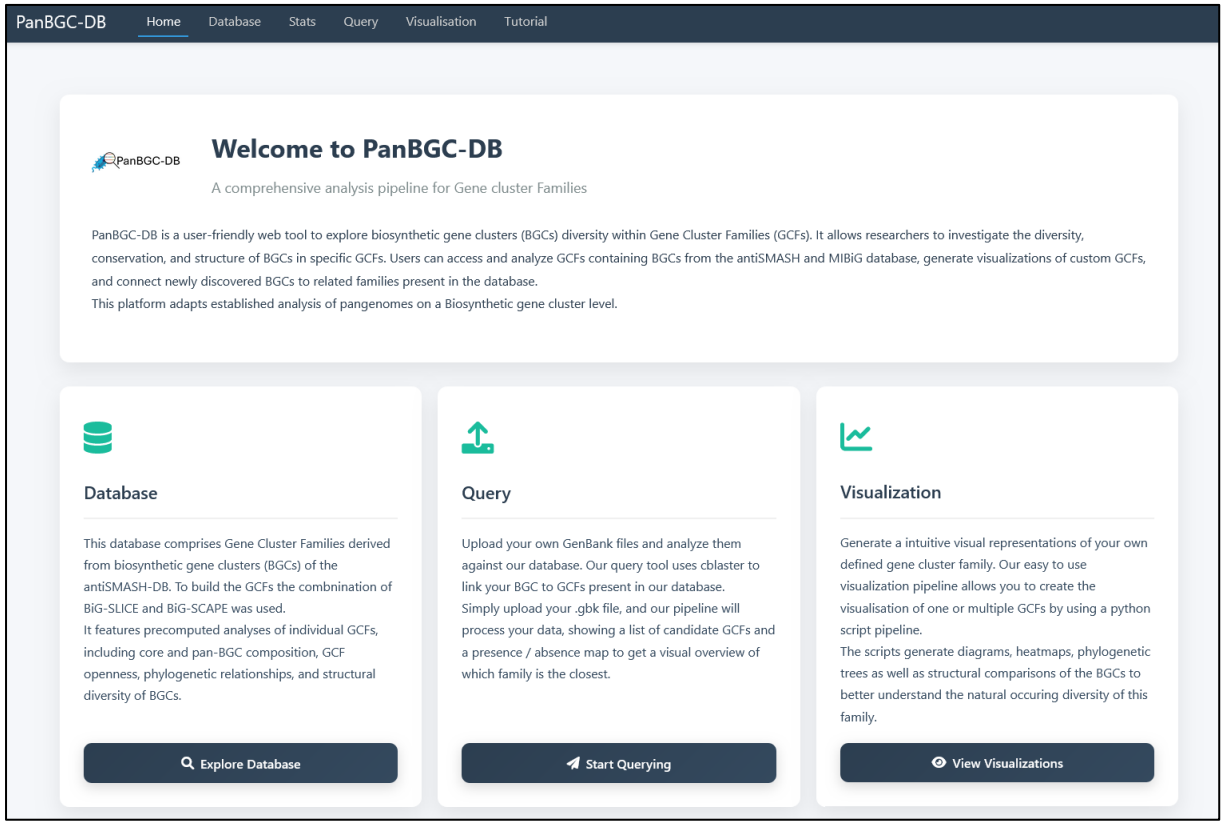


Ornibactin C8



Malleobactin X

Identify changeable Building Blocks for Siderophore Reprogramming



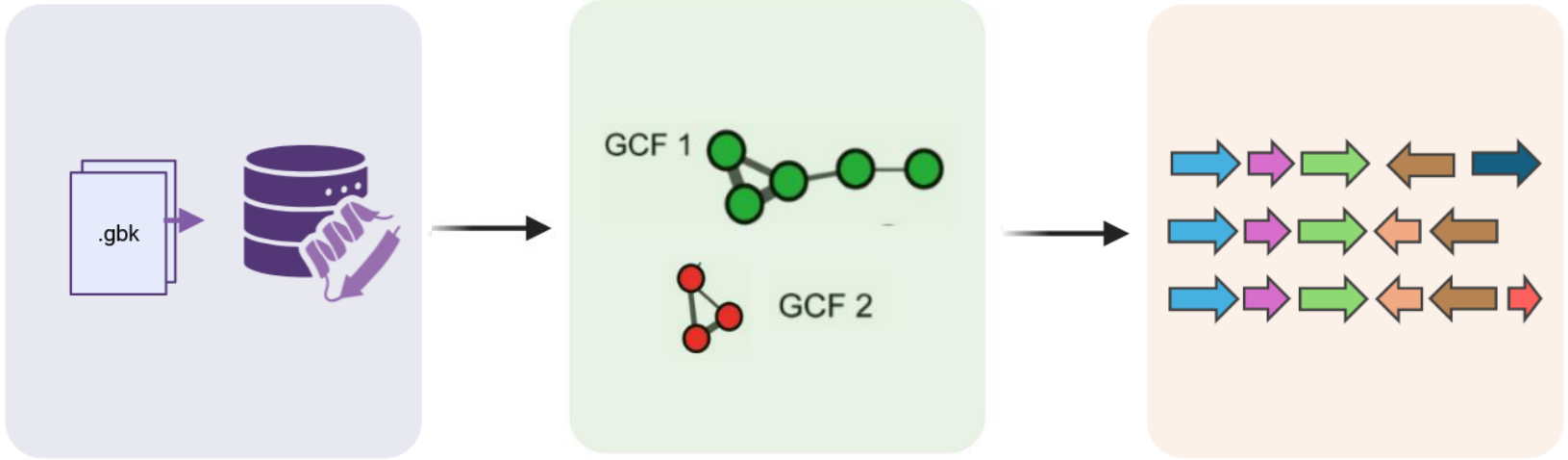
PanBGC-DB

https://panbgc-db.cs.uni-tuebingen.de/

Davide Paccagnella

Paccagnella *et al.*, 2025, ISME Communications

The PanBGC pipeline



Siderophore Biosynthetic Gene Clusters

anti SMASH DB

Group into Gene Cluster Families

BiGSCAPE

Visualize core and tailoring genes for plug´n play

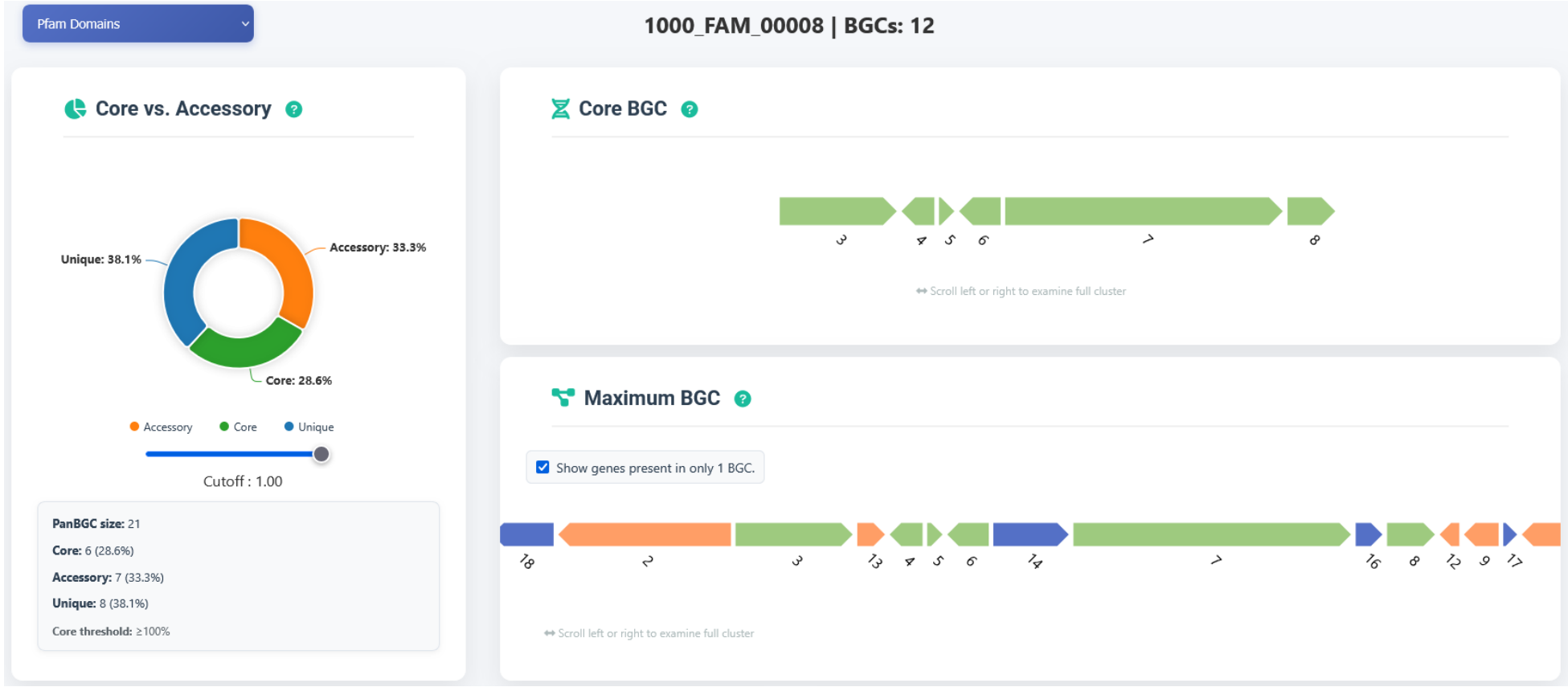
PanBGC-DB

→ **Total of 80.698 GCFs**

Paccagnella *et al.,* 2025, ISME Communications

Analytics for each GCF

- Theoretical Core and maximum BGC based on variable cut off

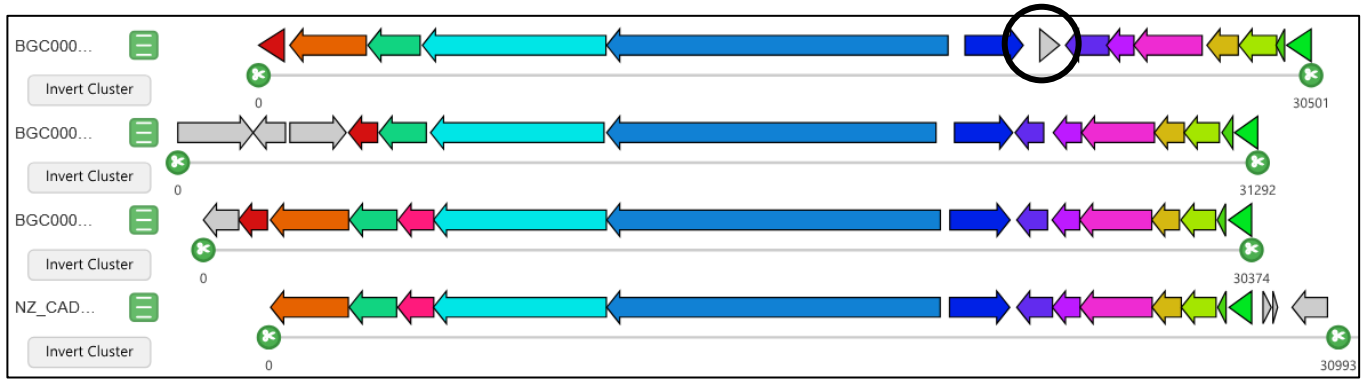


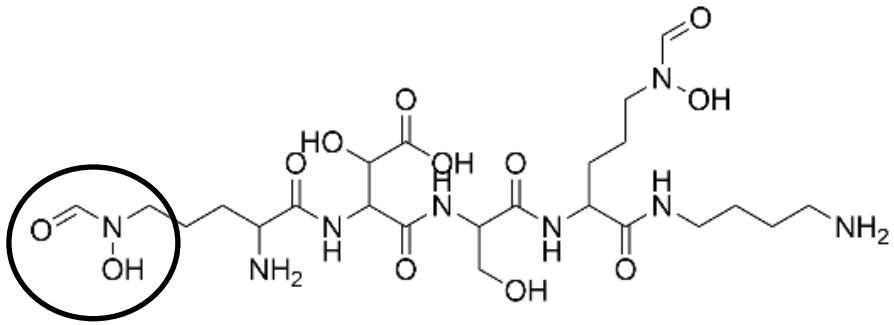
Paccagnella *et al.*, 2025, ISME Communications

GCF visualisation

Ornibactin / Malleobactin family

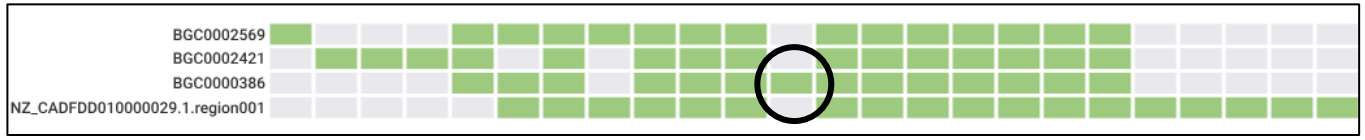
Cluster comparison





Malleobactin A

Presence / absence table

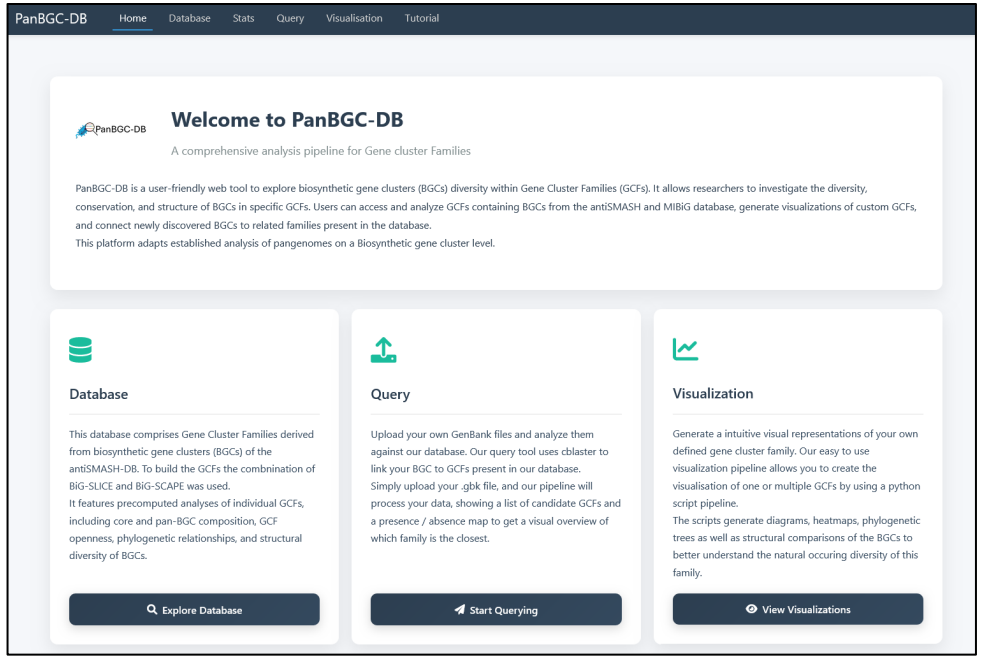


Paccagnella *et al.*, 2025, ISME Communications

Roadmap towards Siderophore Engineering

- Core genes are responsible for the main biosynthetic machinery that builds the main structure
- Accessory genes are responsible to tailor the core structure

The PanBGC-DB provides a roadmap for plug´n play reactions to reengineer Siderophores !



Ziemertlab: Fighting antibacterial resistance since 2015!

Thank you!

The SECRETed project has received funding from the European Union's Horizon 2020 research and innovation programme under the Grant Agreement No. 101000794