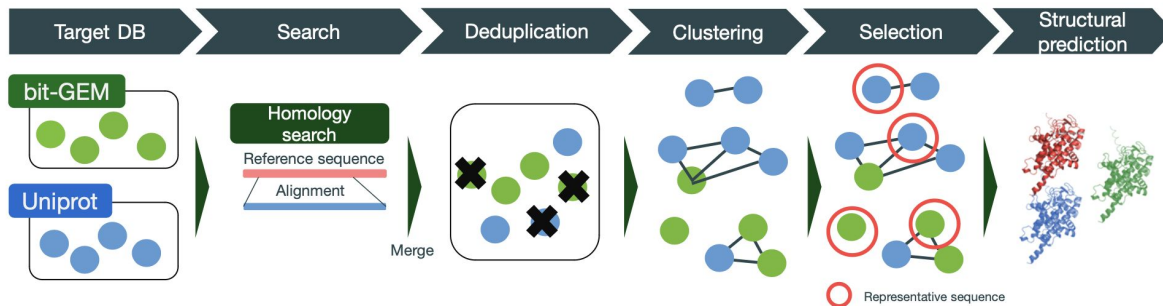


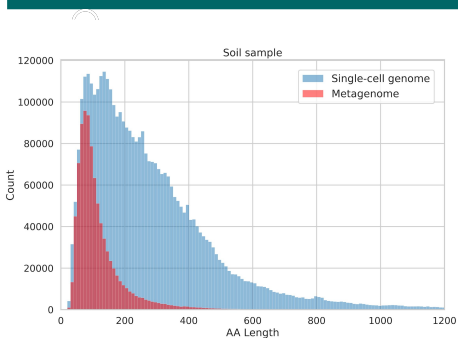
# bit-QED

## Enzyme Discovery Services

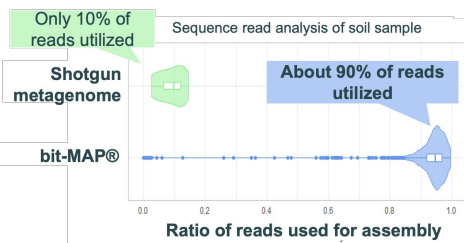
• Diverse Database • Wet/Dry Platform • High-Quality Data



Search high quality genomes from the largest database available

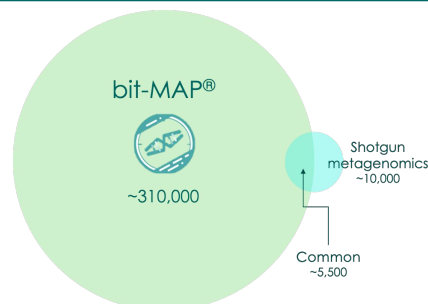


Gene size distributions:  
bit-MAP® can robustly recover long genes



Data size of NGS data

- Single-cell genome: ~240 Gbp
- Metagenome: ~80 Gbp

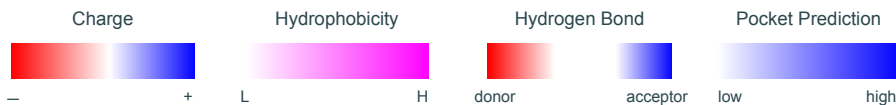
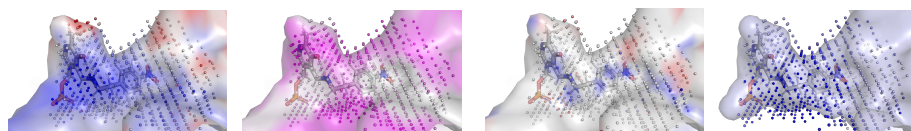


# of CDS obtained (>200 a.a. residues)

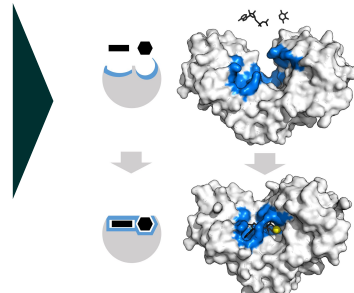
Data size: 40 Gbp (both)

bit-MAP® is >30x more efficient at discovering microbial genes

Proprietary 3D modeling and pocket predictions to shortlist candidates



Binding Energy Calculations Predict Substrate Reactivity

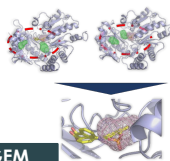




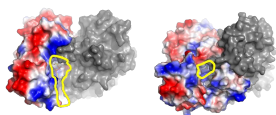
# End-to-end enzyme discovery platform

## 3D Structural modeling pipeline

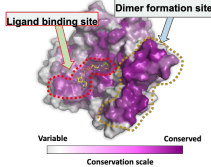
Predict substrate pocket



Predict substrate selectivity



Evolutionary sequence conservation



bit-GEM database

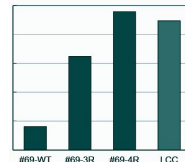


## ML-driven Activity optimization



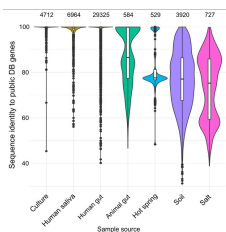
Directed Evolution

Enhancement of Activity

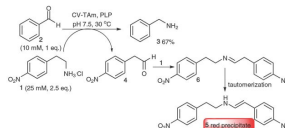
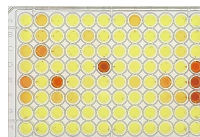


Novel enzymes or activities

## In silico enzyme screening



Enzyme mining



## Robotic wet screening platform

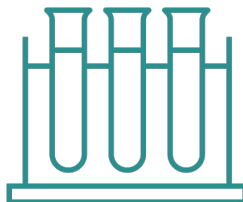
(Baud D. et al., Chem. Commun., 2015, 51, 17225)



# Let our expertise be your partner



Time Saving



Less Lab Work



More Relevant Results

→With our cutting-edge in silico analysis, laboratory work is greatly reduced, as we are able to quickly and accurately shortlist candidates for analysis.

→Our technology provides a streamlined approach to enzyme discovery, saving valuable time and resources in your R&D process. With our platform, you can expect efficient and effective results, enabling you to focus on the next stages of your project.



Contact us today:  
info@bitbiome.bio

