HARNESSING ENVIRONMENTAL MICROBIOTA FOR THE DISCOVERY OF NOVEL BIOCATALYTIC ENZYMES USING MICROBIAL SINGLE-CELL GENOME SEQUENCING

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Environmental microbiota represent a vast, untapped resource for novel biocatalytic enzymes. We have developed a proprietary microbial genome database using a microbial single-cell sequencing method named bit-MAP(R). This method efficiently recovers microbial genes from intricate environmental microbiota, such as soil microbiomes, and as a result, our database contains unique enzyme genes that are not present in public databases.

To capitalize on this resource, we devised a computational pipeline, bit-QED, to identify enzymes capable of executing specific reactions of interest. This pipeline primarily analyzes the active sites of enzymes, characterizing them based on surface features like charge, hydrophobicity, and hydrogen bond potential (Fig.1). These features are quantified for each voxel within a three-dimensional lattice and subsequently integrated and clustered by mapping into a two-dimensional space.

We demonstrated that bit-QED is effective in identifying biocatalytic enzymes, we experimentally confirmed that selected enzymes carried out the anticipated enzymatic reactions.

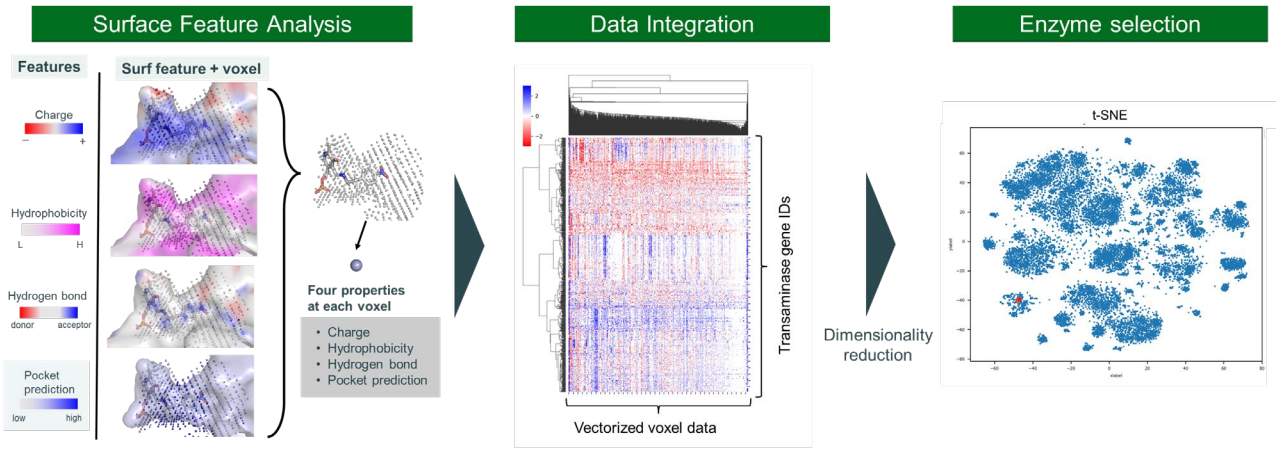

Figure 1. A schematic of bit-QED, in silico computational pipeline for enzyme discovery from a large-scale gene database.