BIOWORKS FOUNDRIES

high-throughput characterization and modification of diverse microbes

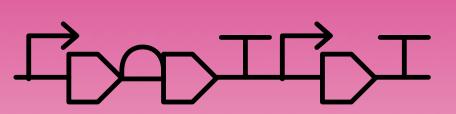




largest capacity organism foundry in the world

DESIGN

design spec

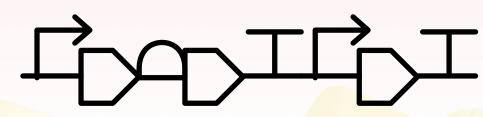


synthesis/assembly strategy

SAMPLES EXIST

SYNTHESIZE

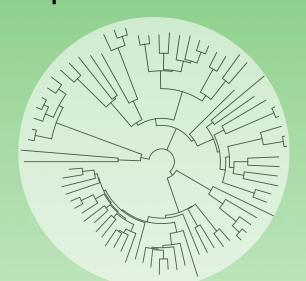
sequence-verified construct



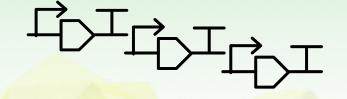
BUILD

part spec EC 1.2.1.51

bioinformatic part search



standardized designs for synthesis

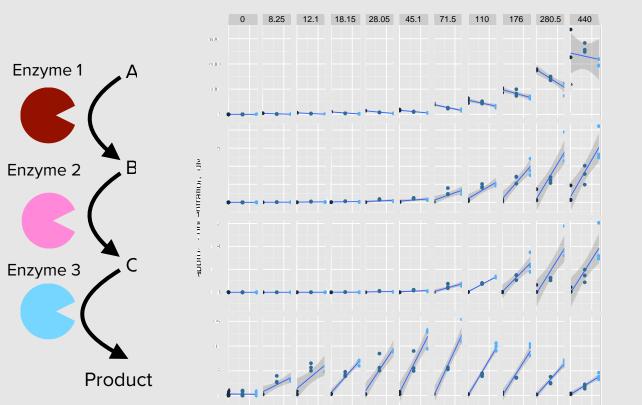


TEST AND FERMENTATION

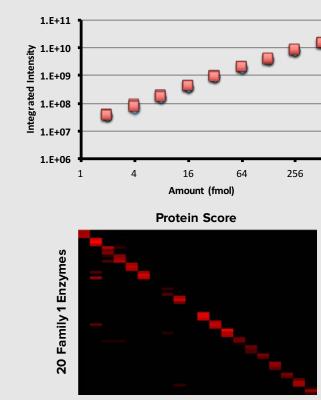
FOUNDRY CAPABILITIES

Metabolomics

- global, central, and secondary metabolism
- multiplexed LCMS, GCMS
- pathway enzyme analysis and optimization







Proteomics

- enzyme expression and solubility
- global native protein expression
- robot-mediated mixing for mux

Next-generation Sequencing

DNA and RNA sequencing with MiSeq, NextSeq

Nanoliter-scale processing

larger-scale: 384-well plates

improved precision

- strain verification and QC
- combine with bioinformatics and proteomics to identify gene clusters

With LCMS and μ PLC, we can screen thousands of enzymes/day



ACTIVE BUSINESS UNITS

- +cultured ingredients: flavors, fragrances
- +strain improvement
- + probiotics

High-density culture evaluation

- strain optimization for scale up
- medium/feed optimization
- real-time tracking of cell density, pH, temp, fluorescence and pO2





- DOE-based approaches to process
- + automated control,



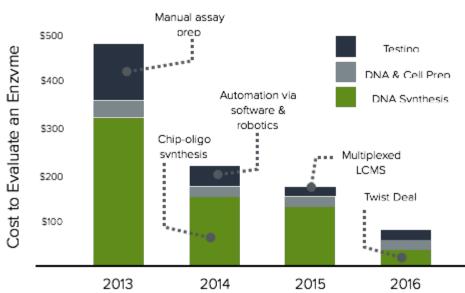
Parallel small-scale fermentation

optimization

monitoring, and sampling

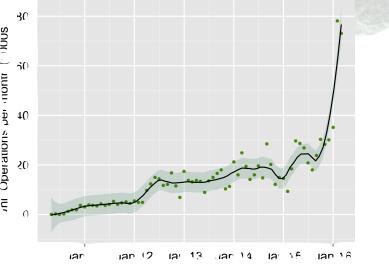


Rapid expansion



Time (hours)

exponential growth in efficiency



exponential growth in scale



next gen. foundry under way

direct-to MS preparation

Misha Wolfson

Boston, MA 02210

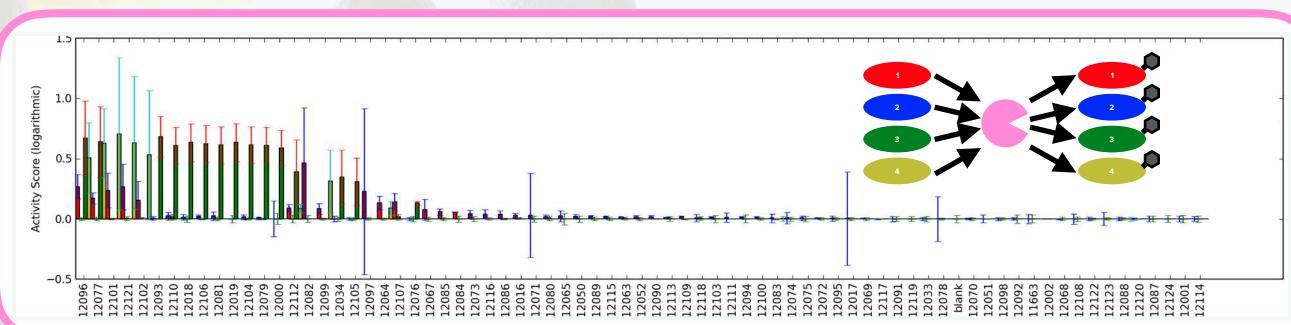
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- Enzyme specificity and activity on multiple substrates × hundreds of enzymes in a single experiment



PRESENTER RELEVANT CONTACTS

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