bitBiome

Discovery and Engineering using bitBiome's Microbial Genome Database



bitBiome's platform technologies generate the data to power innovation in biomanufacturing



SEQUENCE

bit-MAP

The **one and only single-cell sequencing** for microbes that's 100x more efficient than conventional methods



CATALOG

bit-GEM

The **world's most diverse database**—3.5 billion + sequences and growing—built on single-cell sequencing of microbes from natural samples



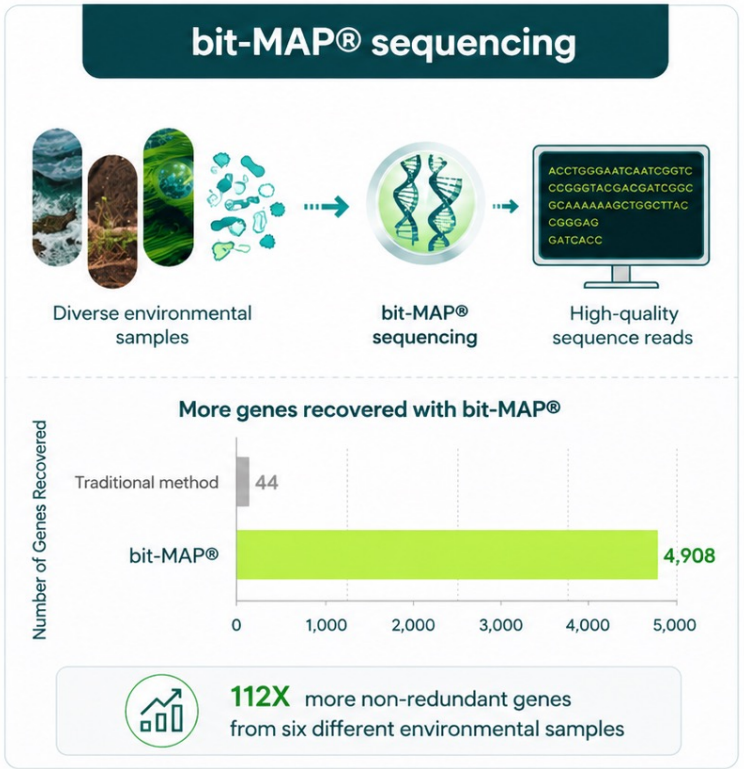
Edit

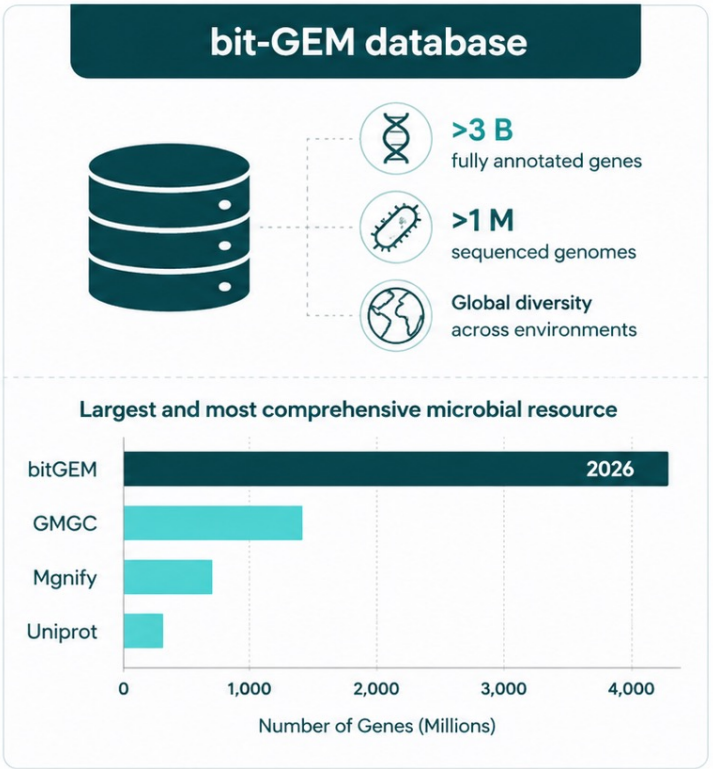
bit-EVO

Customized bio- and cheminformatics and AI-driven enzyme engineering, strain development and ingredient manufacture

bitBiome

Proprietary bit-MAP® and bit-GEM Biggest Enablers for bitBiome technology stack

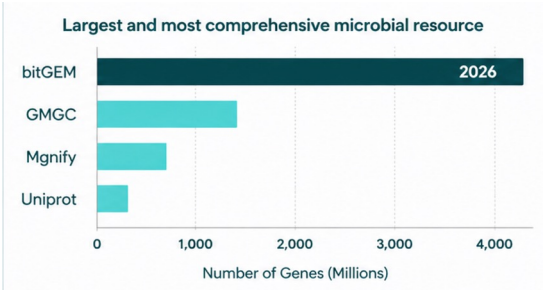




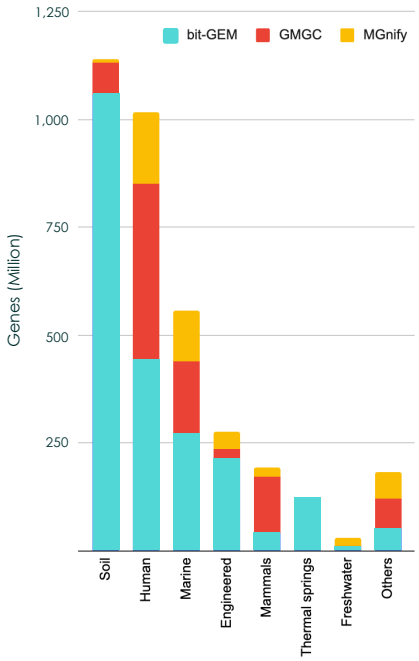
bit-GEM: World's largest single-cell genome database

>3.5+ B fully annotated genes
>1 M sequenced genomes

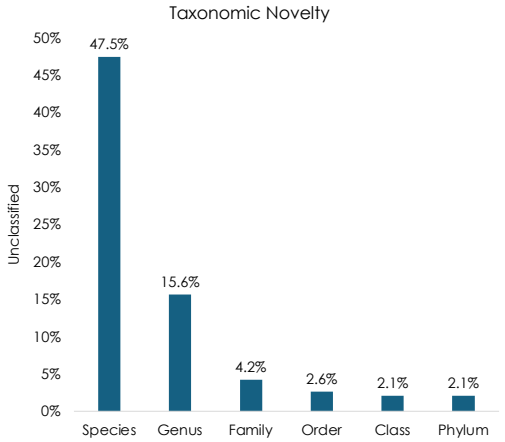




High Environmental Diversity



High Taxonomic Diversity



- Unclassified: <95% similarity to known taxa in bit-GEM or public databases

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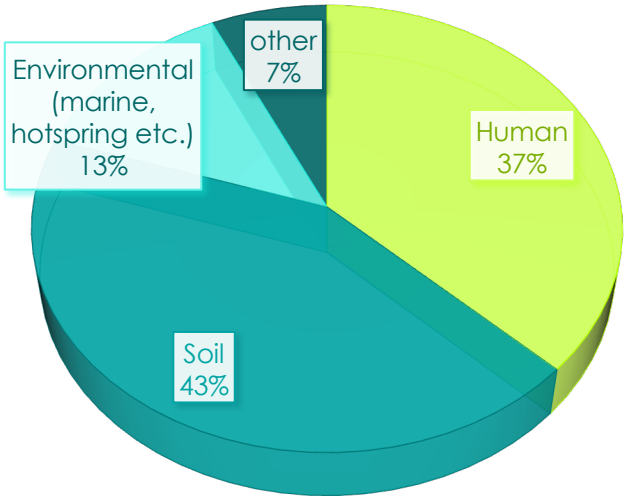
From 29,849 SAGs of ≥ medium quality using GTDB-Tk toolkit on genome assemblies

Diversity powered by nature

- Large collections of extremophiles with potentially novel enzyme activities and functional requirements
- Unique, free-to-operate, patentable sequences in accordance with the Nagoya Protocol
- Industry-wide applications, including healthcare, pharma, sustainability, food, materials, and chemical
- Highest Genomic IQ database available

56% from environmental samples

including soil, marine water, hot spring, mining site etc.



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bit-GEM: Unmatched microbial dataset redefining the frontier of genome-driven innovation

Comparison of genome clusters



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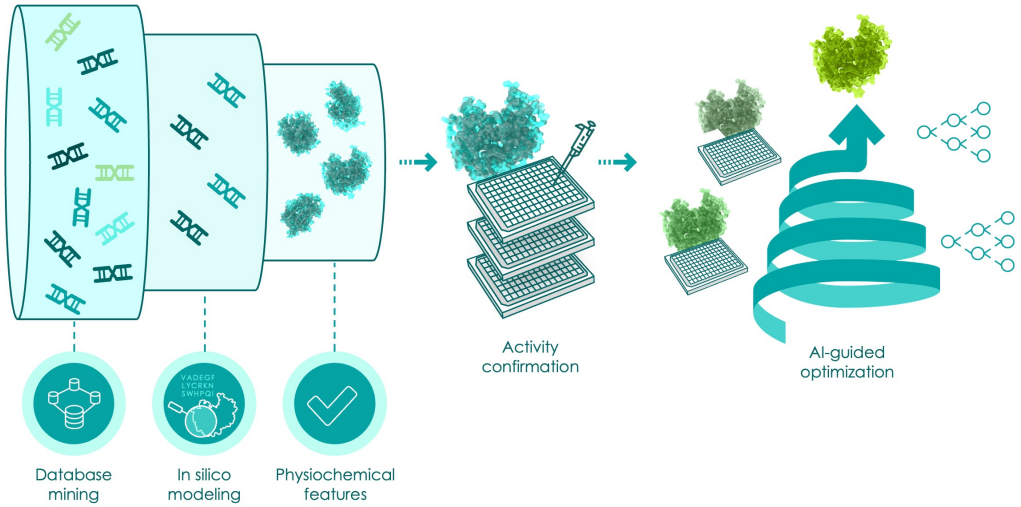
Microbe data plus AI makes faster, more robust enzyme engineering possible



Making years long processes possible within weeks to months

Microbes power the industries that will shape the future of our planet.

- Pharma/Life Science
- Food/Agriculture
- Energy
- Materials
- Chemicals
- Climate Resistance

bitBiome

In Silico toolbox

FROM BILLIONS OF SEQUENCES TO OPTIMIZED TARGETS

1 FOUNDATION
Data Foundation

Catalog and annotate the largest repository of microbial genomes

bit-GEM database



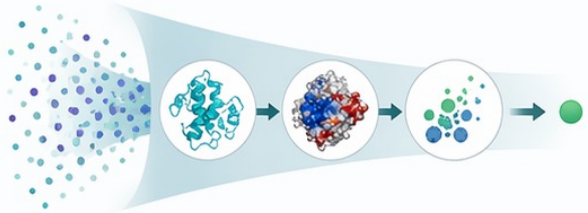
Genome-scale annotation
State-of-the-art algorithms with genome-context awareness

Protein function prediction
Advanced functional inference at scale

Taxonomic classification
High-resolution placement across the tree of life

2 DISCOVERY ENGINE
Sequence–Structure–Dynamics Analysis Suite

Traverse, filter, and select the ideal protein sequence



Structure & binding insights
3D modeling, surface & binding site analysis, docking

Function & selectivity
Affinity, specificity & selectivity prediction

Context-aware prediction
Genome neighborhood & environmental context

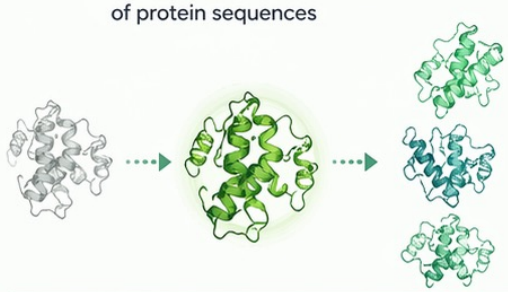
Developability models
Expressibility, solubility & stability prediction

Dynamics simulations
Physics-based MD to capture flexibility & conformations

Multi-criteria filtering
AI + physics scoring to rank best candidates

3 DESIGN ENGINE
AI Design & Optimization

AI-design and optimization of protein sequences



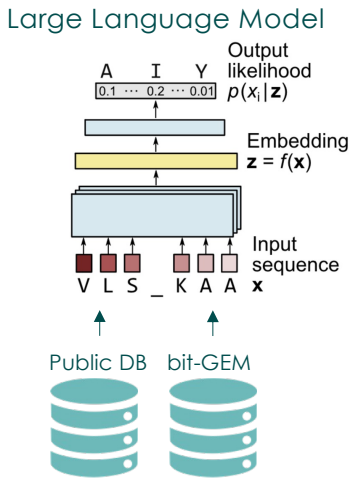
LLM-powered sequence generation
Fine-tuned models trained on bit-GEM generate high-quality, diverse sequences

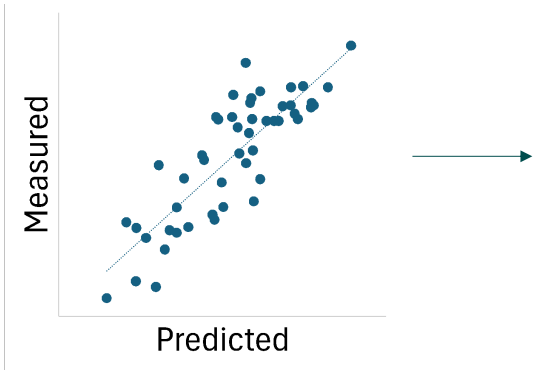
Evolution-guided design
Phylogenetic trees and ancestral sequence reconstruction for stable, promiscuous enzymes

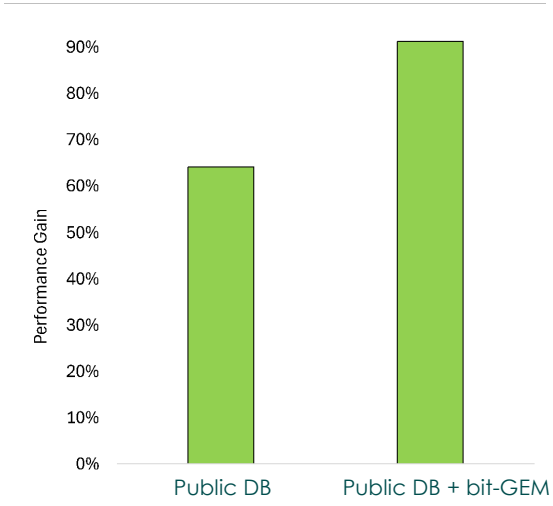
AI-guided optimization
Hotspot identification & residue-level mutations to improve stability and activity

A genome LLM built using the highest Genomic IQ database available

- Goal of a genome LLM is to predict effects of mutations for library design
- Result of model trained on our database is a higher probability of finding beneficial mutations with fewer cycles







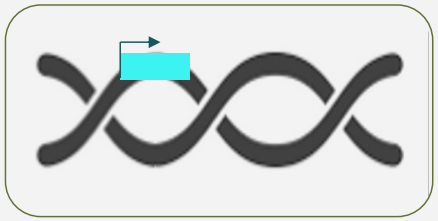
Number of screening cycles **decreased by 50%**

bitBiome

bit-EVO: Unique and Proprietary Genome Editing Platform

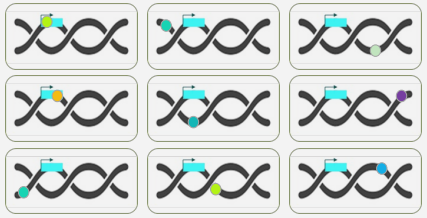
Enables large-scale modifications of genomes towards target outcomes

TECHNOLOGY



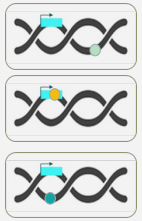
Initial strain with low productivity

Proprietary step to produce variant 'library' with each cell having a single unique targeted edit



Library of variants screened for increased activity

High-throughput screening



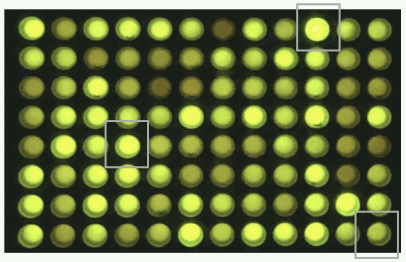
Strains with higher productivity

APPLICATION EXAMPLE

Initial strain with low GFP productivity



Variant 'library' with each cell having a single unique targeted edit



Screened by fluorescence



Strains with **20X improved** productivity

bitBiome

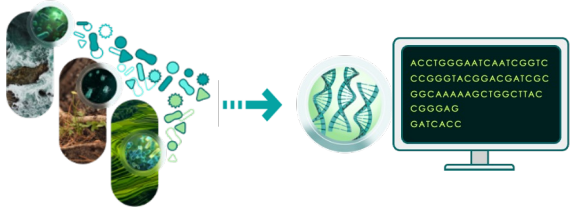
bit-EVO results in proprietary high-productivity strains providing the best starting platform for further improvements

Unique combination of expertise & capabilities in bitBiome

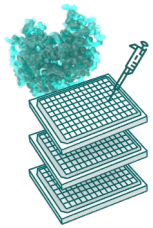
Full suite of technologies from data to product

Discovery | **Design** | **Build · Test · Learn** | **Manufacturing**

1. **Environmental microbes**
2. **Microbial Sequencing**
3. **Genome database**
4. **In-silico (bio- and chemo-info)**
5. **Screening and engineering**
6. **Scale-up, QC, Supply chain regulation**











SEQUENCE
bit-MAP®

CATALOG
bit-GEM

EDIT
bit-EVO

bitBiome

Case Studies



bitBiome

bitBiome projects have tackled a wide variety of functional parameters and scales

Identifying the best starting point possible

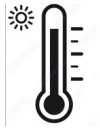
Discovery



Stability



Heat



Solvents



pH



Efficient *in silico* and *in vitro* protein improvement

Engineering



Cofactor swapping



Substrate expansion



Inhibitor resistance



Protein production at R&D scales and beyond

Production



Fermentation



Secretion



Host selection



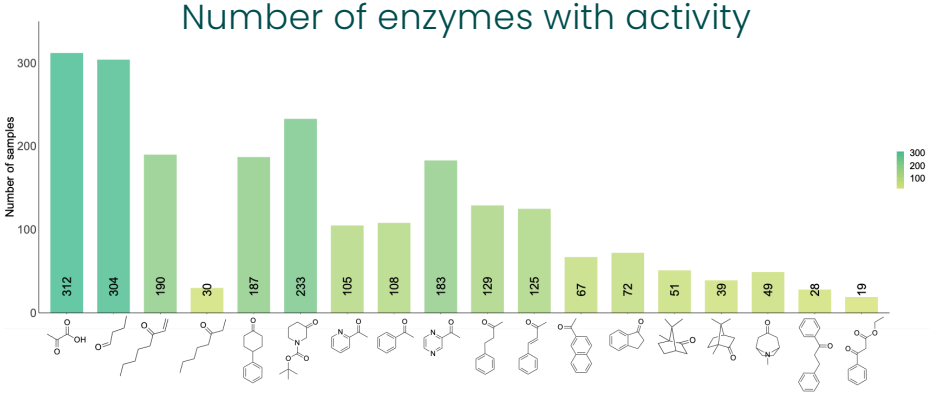
bitBiome

Transaminase Enzyme Screening Kit

IN PARTNERSHIP WITH TWIST BIOSCIENCE



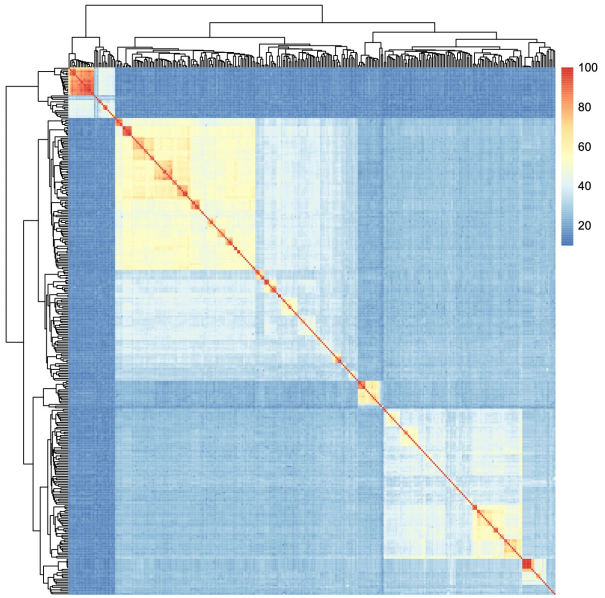
Number of enzymes with activity



371 transaminases were identified and tested with 18 different substrates.

The sequence similarity network shows the high level of sequence diversity among the 301 active sequences

Sequence Similarity Network

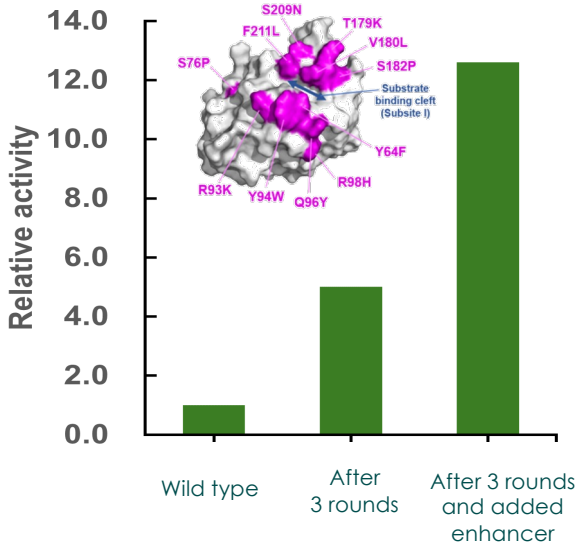


bitBiome TWIST BIOSCIENCE

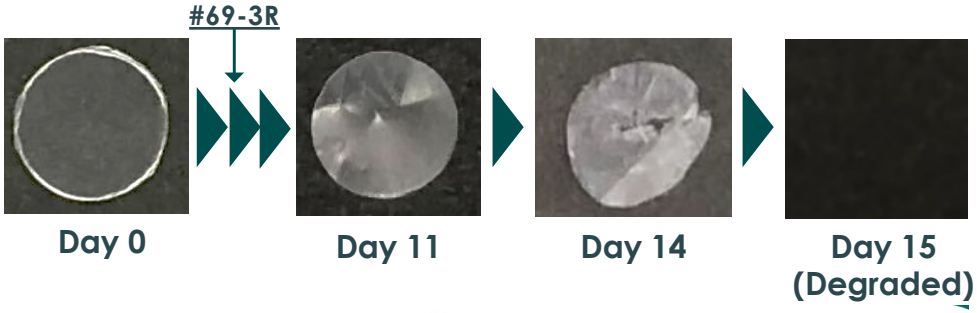
bitBiome identified and improved a novel PET degrading enzyme

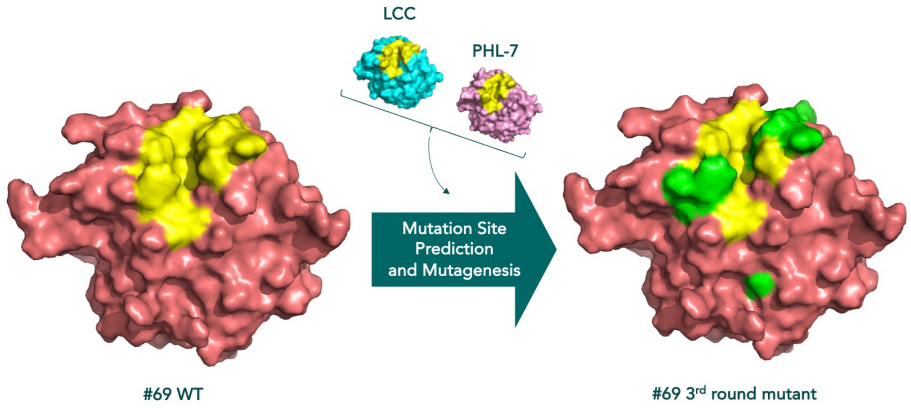
ENZYME IDENTIFIED FROM SOIL-BASED MICROBIAL SEQUENCES

Achieved 13x improvement



bitBiome's modified enzyme completely breaks down PET films





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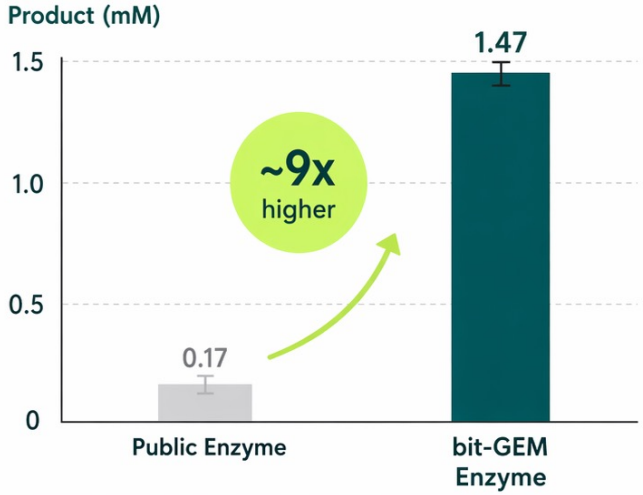
bit-GEM Identified a natural enzyme with higher productivity than current best-in-class from environment

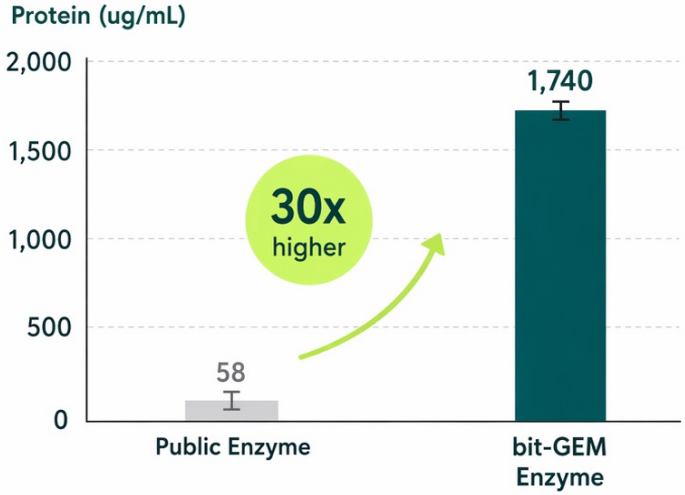
BEST CANDIDATE RIGHT FROM THE DATABASE

9-fold higher activity than publicly available enzyme



~9-fold increase in product formation compared to the public enzyme.

Significant improvement in expression in *E. coli*



~30-fold increase in soluble protein expression compared to the public enzyme.

Data shown as mean ± SD from independent replicates.

Global Team, Global Reach



bitBiome

Founded in November 2018.
Raised > $45m in equity and grant.

Headquartered in Japan,
With presence in the US and the UK

$4.5m Revenue in 2025,

Unique proprietary platform addressing all forms of bio-manufacturing
Allowing flexibility towards the most efficient design

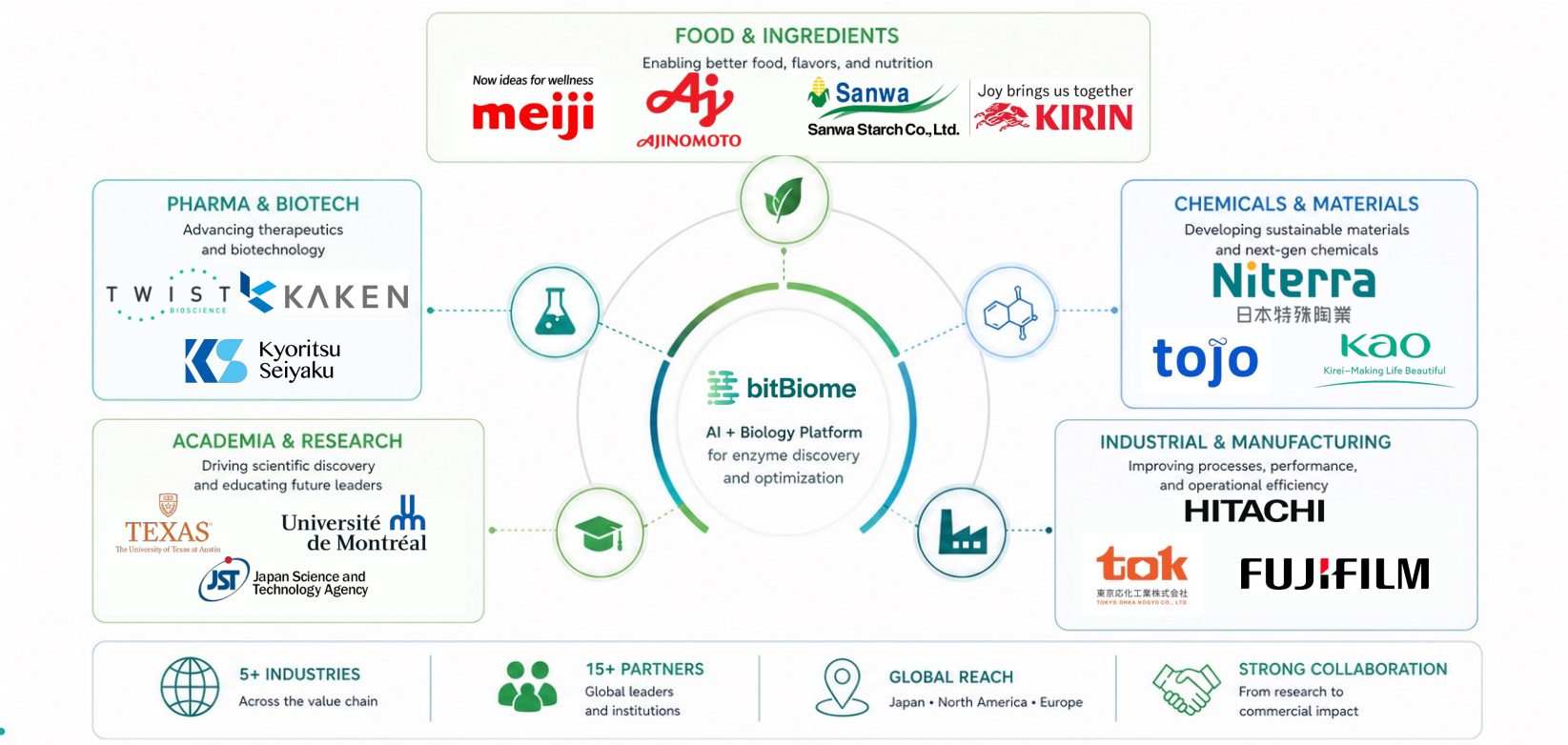
State-of-the-art facilities in Tokyo
Significant cost advantage with operations in Japan

A truly global company
A third of our 50+ employees are international talents, speaking **>20** languages

Reputation:
First Japanese company to be on the "Grow Everything" podcast, and **Forbes Asia 100 to Watch**

Trusted by leaders across industries

Powering enzyme innovation from discovery to commercial impact



What they say about bit-GEM and bit-EVO



"TOK is committed to achieving carbon neutrality and net zero emissions by 2025. As a result, we have decided to work with bitBiome due to their **extensive knowledge in enzyme discovery and unique natural enzyme sequence library**. Their speed of development and R&D knowledge was exceptional, and we have full confidence in their abilities to help us achieve our goals now and for the future."

TOK (Tokyo Ohka Kogyo)



"We are confident that by integrating bitBiome's **unique gene database and advanced *in silico* enzyme exploration** technologies, including surface feature analysis, with our AminoScience® technologies, we can unlock new value. This collaboration will **accelerate the development of innovative products** and solutions, delivering enhanced value to our customers and partners."

Shintaro Iwatani, PhD,
The head of Biosolutions Labs.,
Ajinomoto Co., Inc.

bitBiome

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Thank you

info@bitbiome.bio

