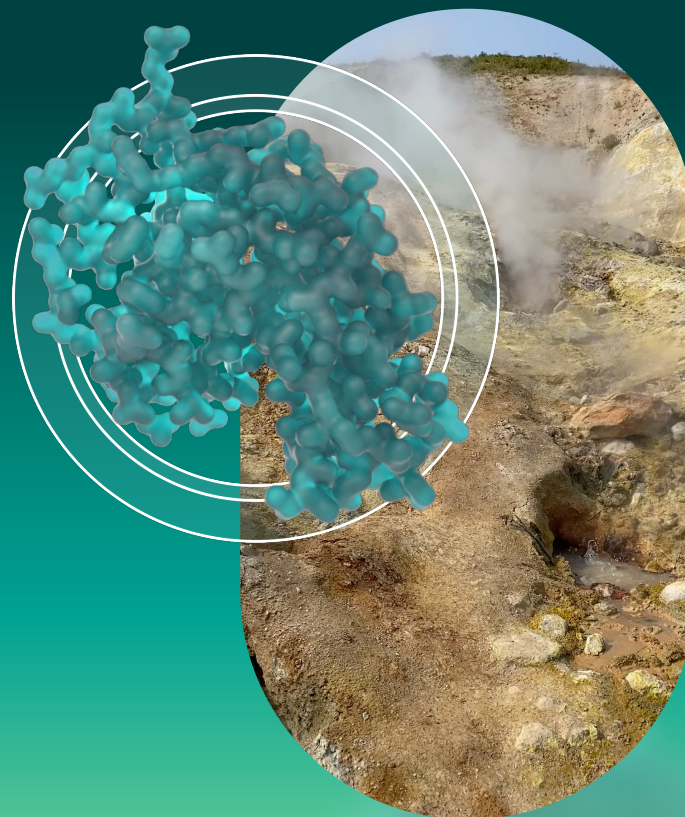




Discovery and Engineering using bitBiome's Microbial Genome Database



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



SEQUENCE

bit-MAP

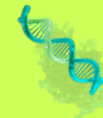
The **one and only single-cell sequencing** for microbes that's 100x more efficient than conventional methods



CATALOG

bit-GEM

The **world's most diverse database**—3 billion + sequences and growing—built on single-cell sequencing of microbes from natural samples



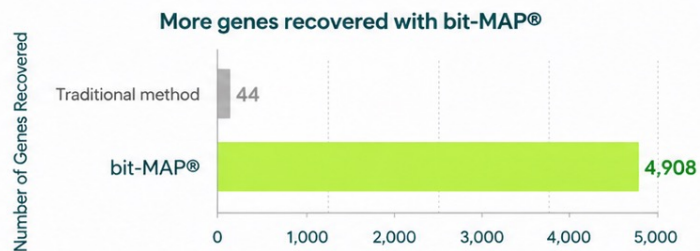
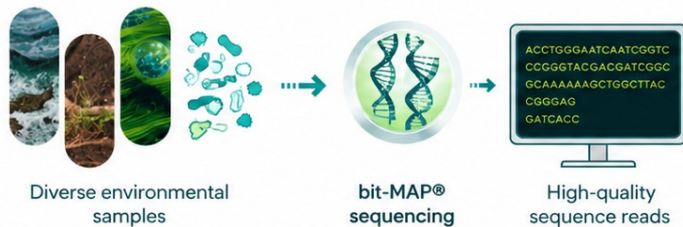
Edit

bit-EVO

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

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

bit-MAP[®] sequencing



112X more non-redundant genes
from six different environmental samples

bit-GEM database



>3 B
fully annotated genes

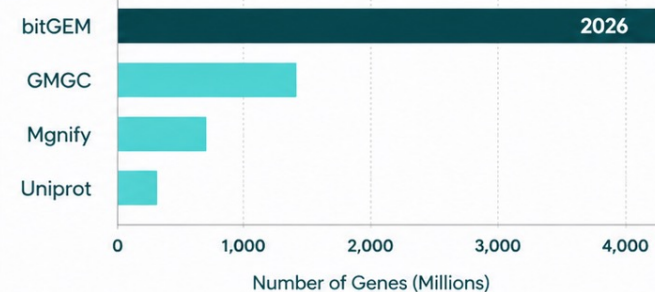


>1 M
sequenced genomes



Global diversity
across environments

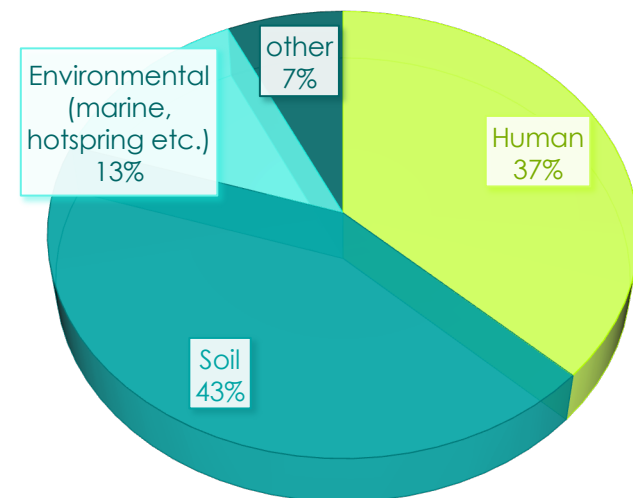
Largest and most comprehensive microbial resource



Diversity powered by nature

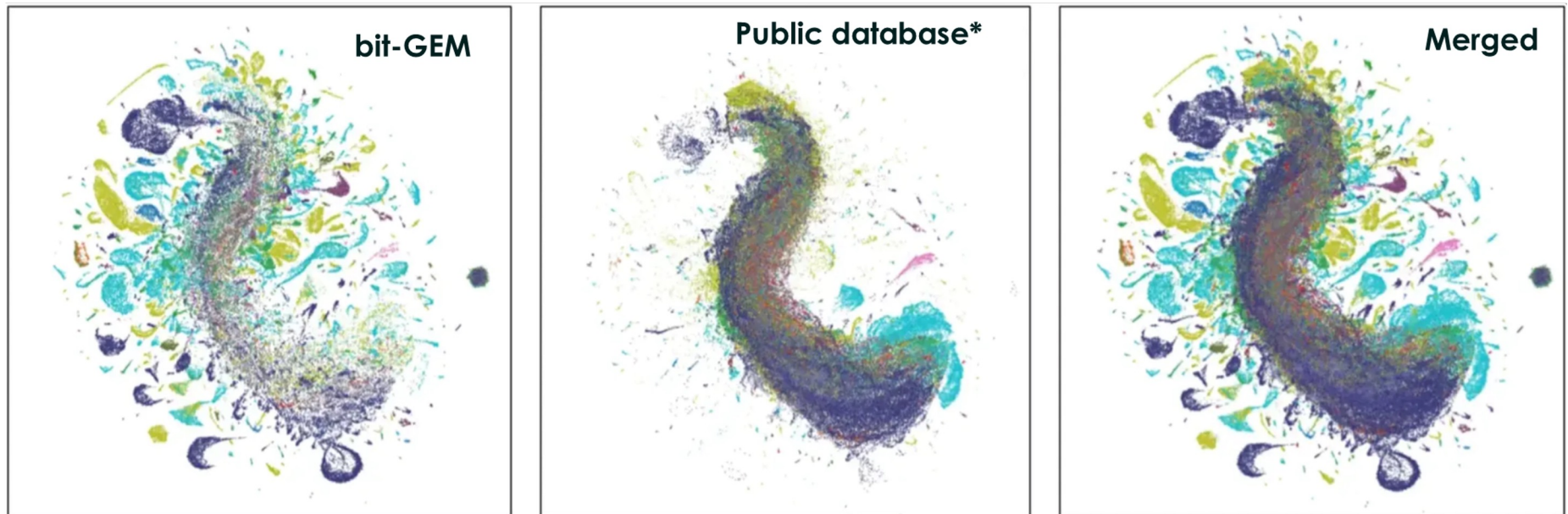
- Large collections of extremophiles with potentially novel enzyme activities and functional requirements
- Unique, free-to-operate, patentable sequences in accordance with the Nagoya Protocol
- Industry-wide applications, including healthcare, pharma, sustainability, food, materials, and chemical
-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

56% from
environmental samples
including soil, marine water,
hot spring, mining site etc.

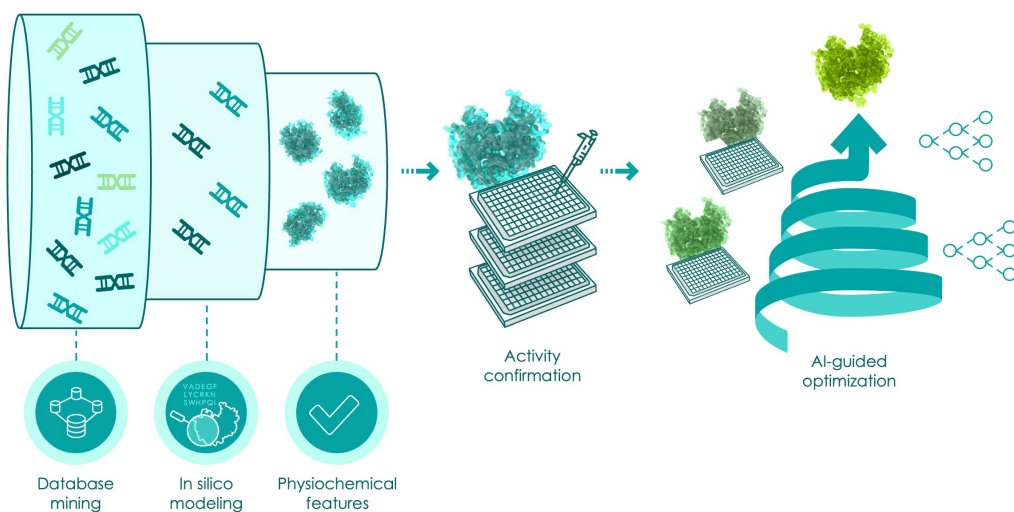


bit-GEM: Unmatched microbial dataset redefining the frontier of genome-driven innovation

Comparison of genome clusters



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



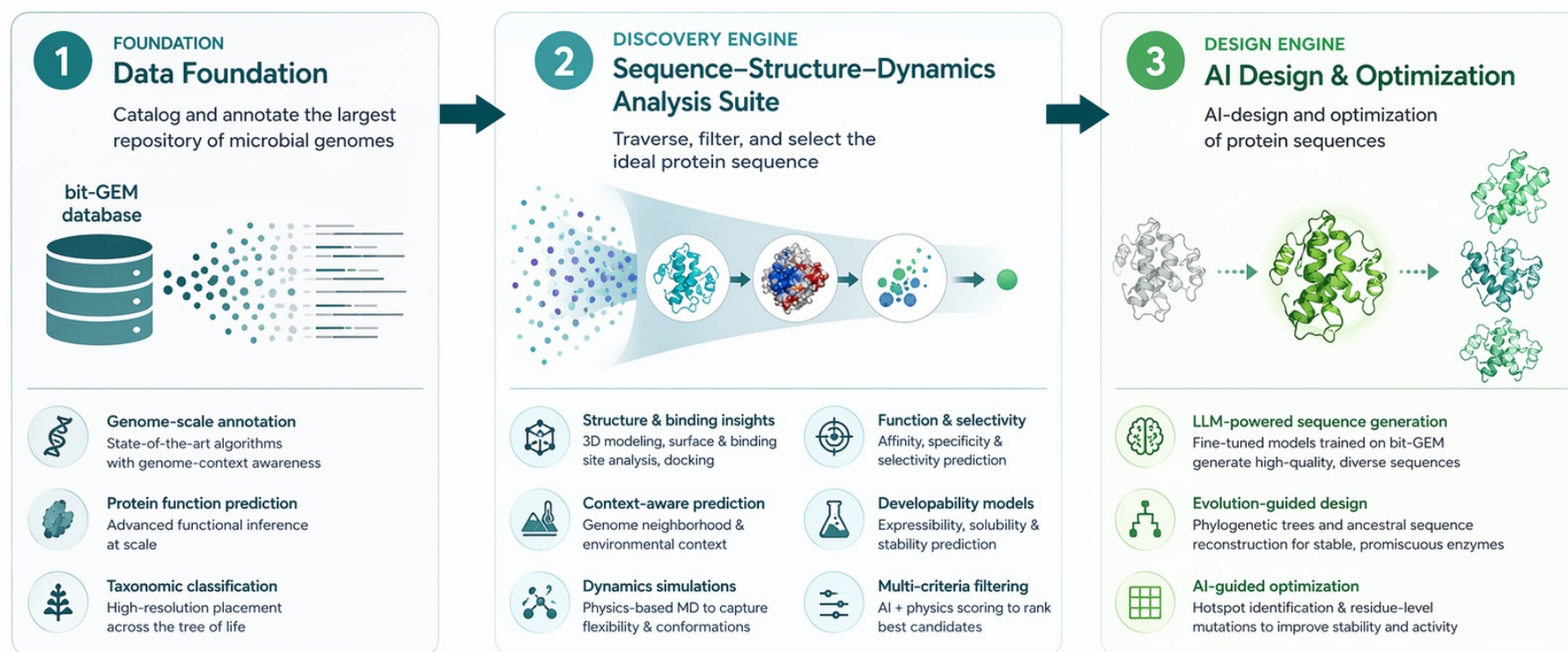
Making years long processes possible within weeks to months

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

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

In Silico toolbox

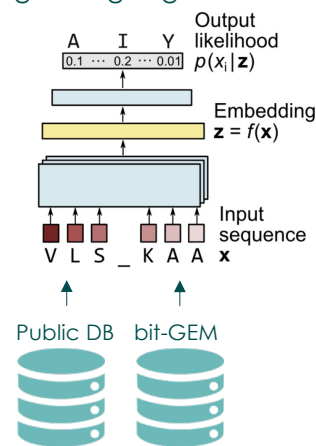
FROM BILLIONS OF SEQUENCES TO OPTIMIZED TARGETS



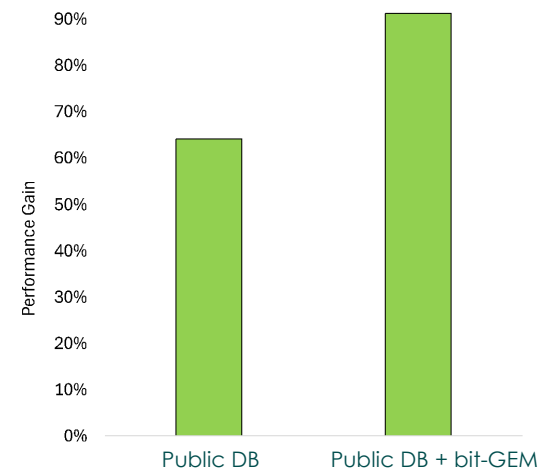
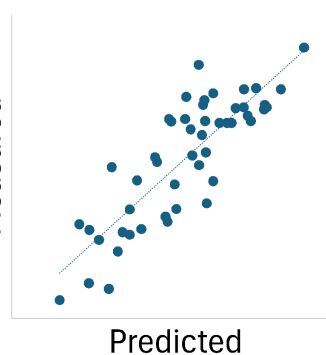
A genome LLM built using the highest Genomic IQ database available

- 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

Large Language Model



Measured

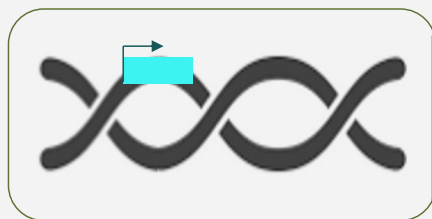


Number of screening cycles **decreased by 50%**

bit-EVO: Unique and Proprietary Genome Editing Platform

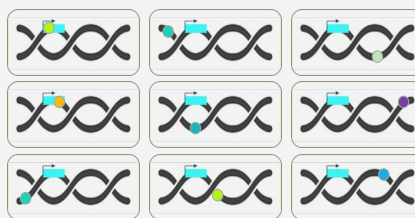
Enables large-scale modifications of genomes towards target outcomes

TECHNOLOGY



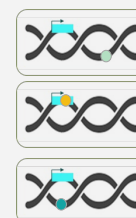
Initial strain with low productivity

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



Library of variants screened for increased activity

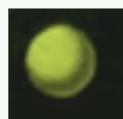
High-throughput screening



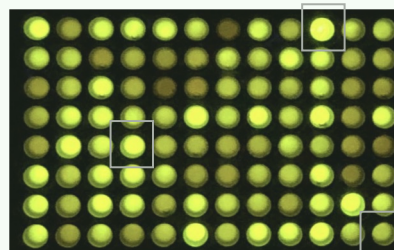
Strains with higher productivity

APPLICATION EXAMPLE

Initial strain with low GFP productivity



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



Screened by fluorescence



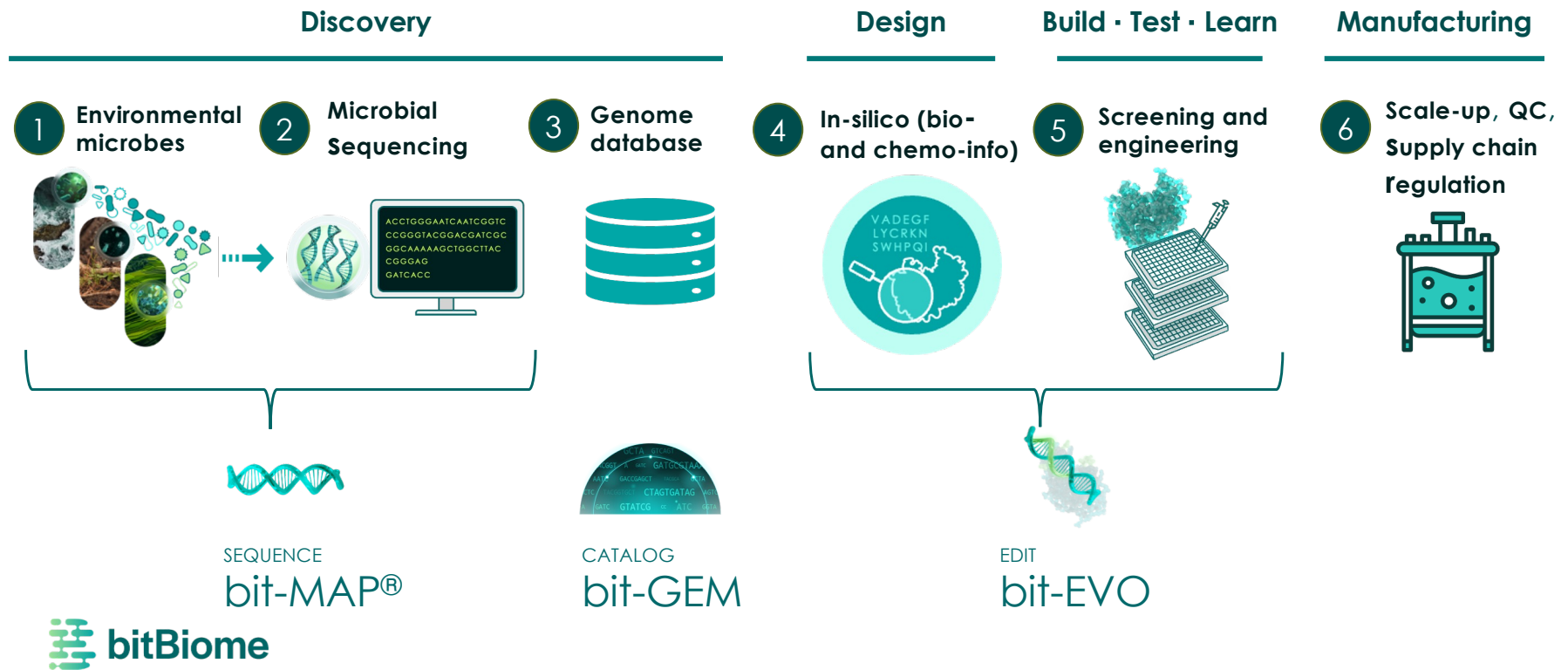
Strains with **20X improved** productivity



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



Case Studies

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

Identifying the best starting point possible

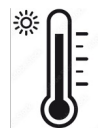
Discovery



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

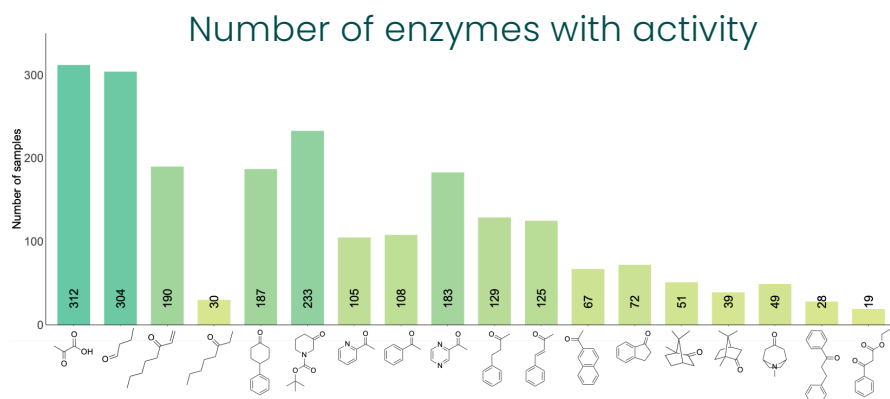


Host selection



Transaminase Enzyme Screening Kit

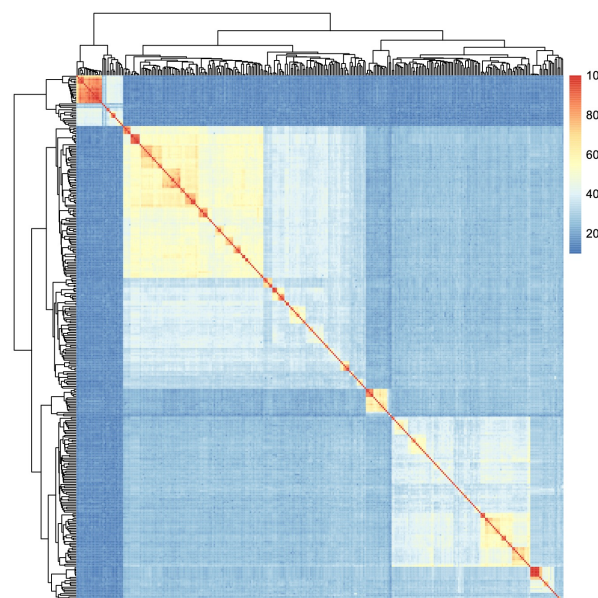
IN PARTNERSHIP WITH TWIST BIOSCIENCE



371 transaminases were identified and tested with 18 different substrates.

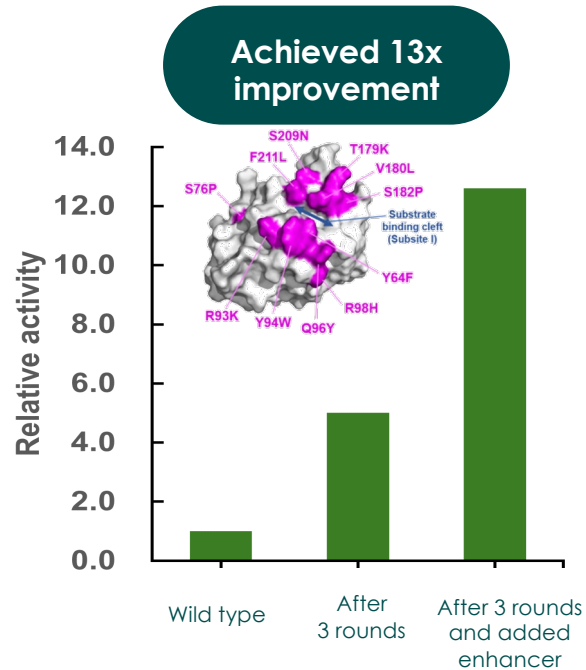
The sequence similarity network shows the high level of sequence diversity among the 301 active sequences

Sequence Similarity Network

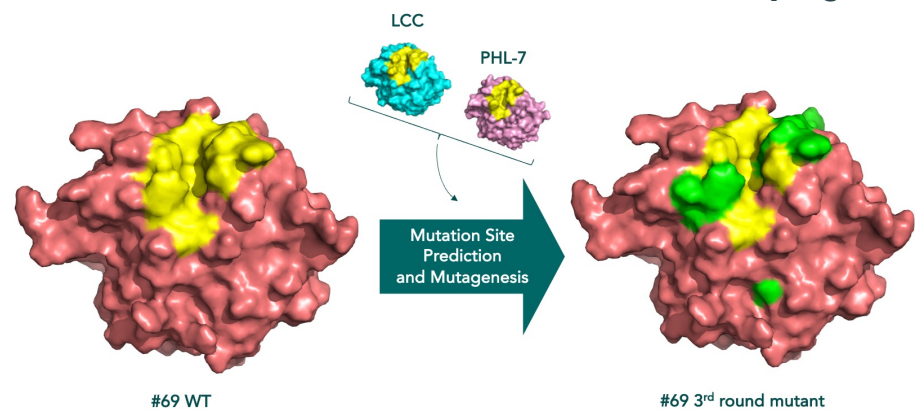


bitBiome identified and improved a novel PET degrading enzyme

ENZYME IDENTIFIED FROM SOIL-BASED MICROBIAL SEQUENCES



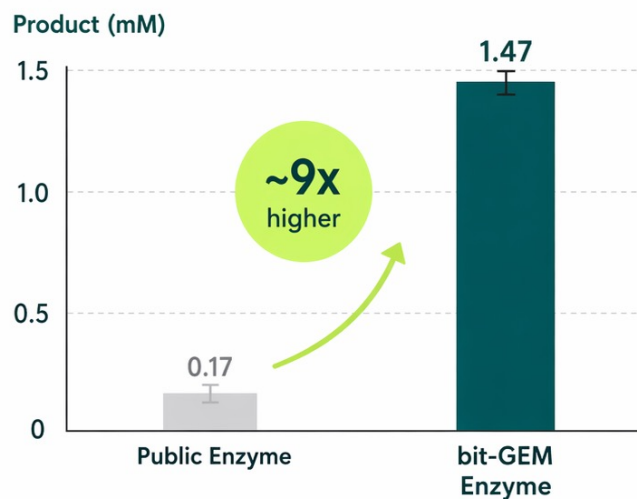
bitBiome's modified enzyme completely breaks down PET films



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

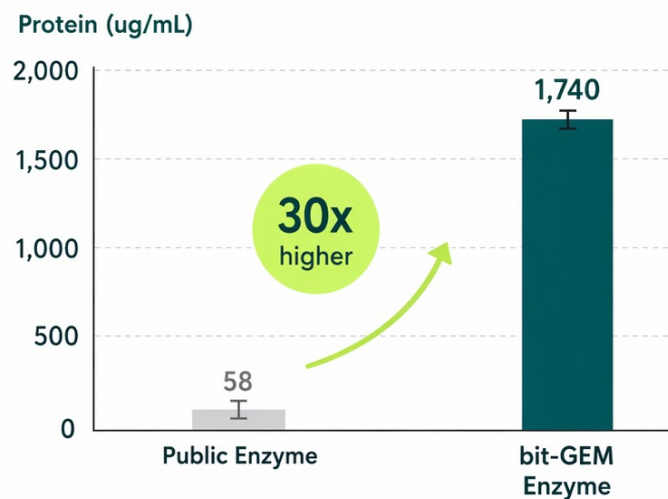
BEST CANDIDATE RIGHT FROM THE DATABASE

 **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.

Global Team, Global Reach

● Footprint
● Clients/Partners




40+
Employees


25%+
International
Talent


10+
Languages
Spoken


Global
Reach



Founded in November 2018.
Raised **> \$25m** 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



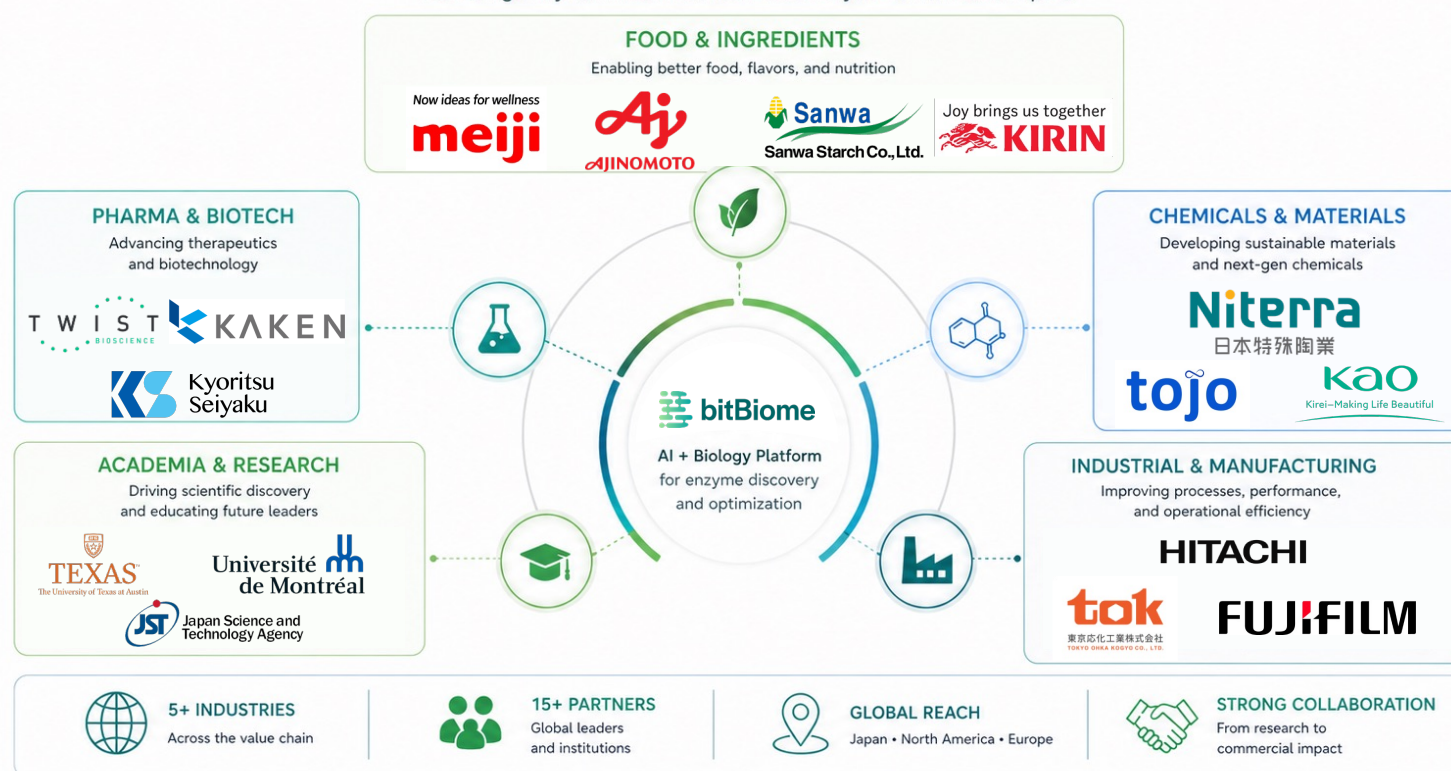
A truly global company
A quarter of our 40+ employees are international talents, speaking **>10** languages



Reputation:
First Japanese company to be on the "Grow Everything" podcast, and **Forbes Asia 100 to Watch 16**

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.



Thank you

info@bitbiome.bio

