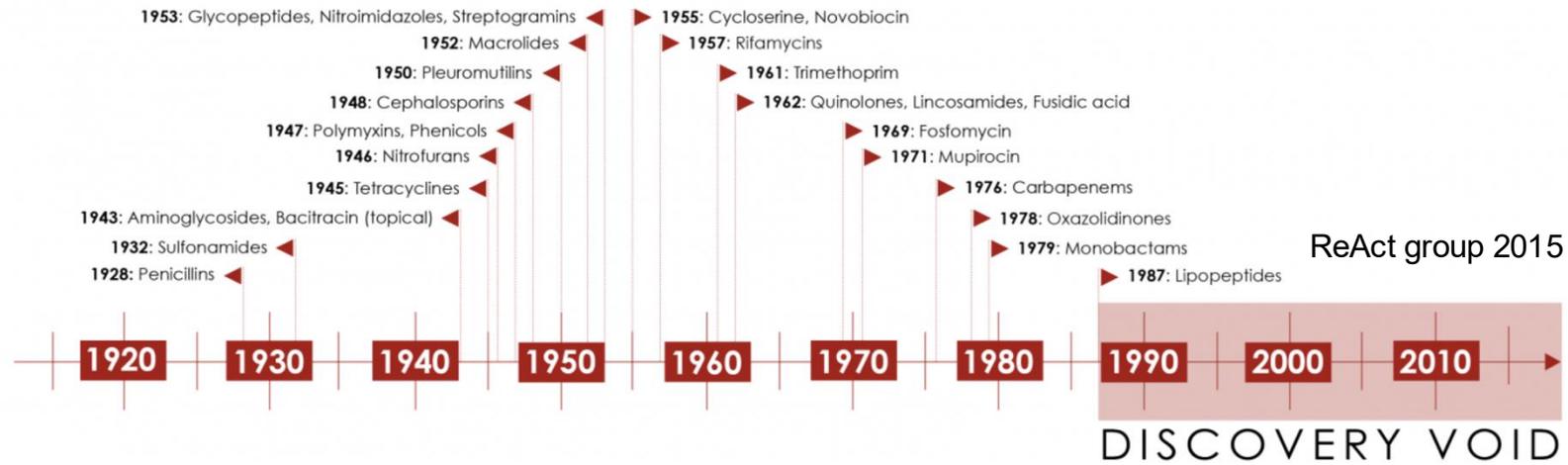


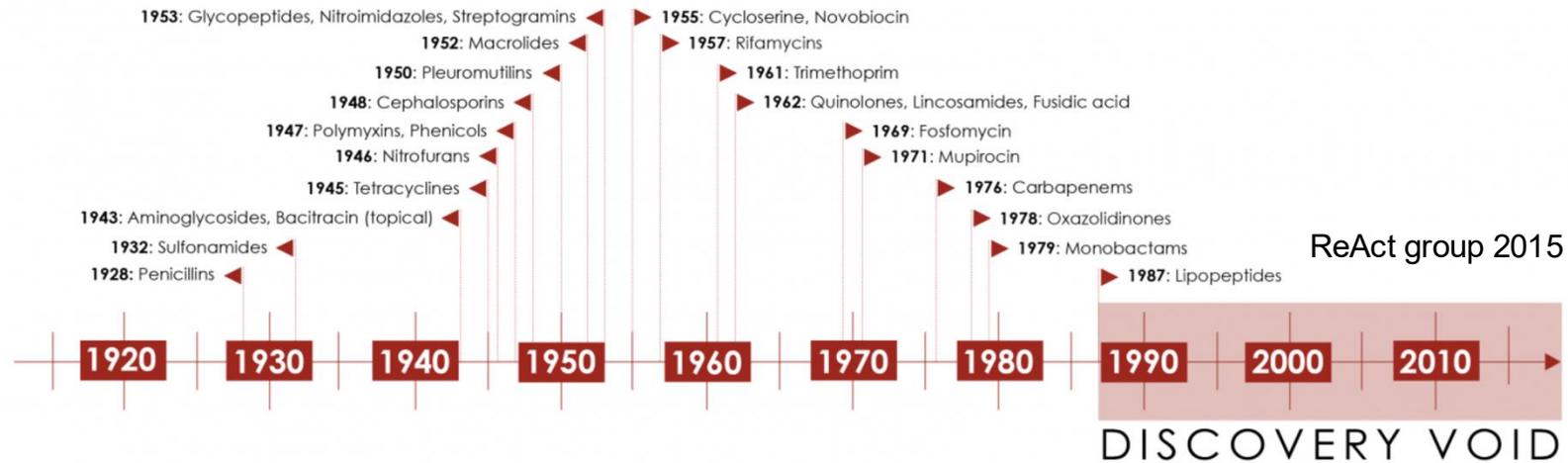
De novo antimicrobial peptides by integrating deep learning and synthetic biology

Amir Pandi

The shortage of new antibiotics, combined with rising antimicrobial resistance, a critical global health threat of the 21st century



The shortage of new antibiotics, combined with rising antimicrobial resistance, a critical global health threat of the 21st century



- **7.7 million** deaths yearly from bacterial infections:
 - **4.95 million** linked to drug-resistant pathogens.
 - **1.27 million** directly caused by antibiotic-resistant bacteria.

Okeke, I. N. *et al. Lancet* (2024)

- By 2050, antimicrobial resistance (AMR) could cause **10 million** deaths per year globally

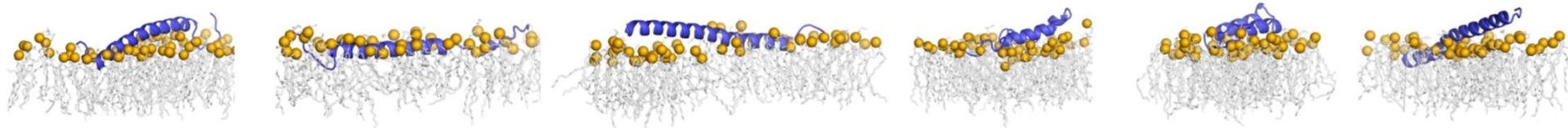
AMR collaborators *Lancet* (2022)

Antimicrobial peptides (AMPs) offer a promising solution: low propensity for resistance and great potential in therapies, food and biomaterials

Unmodified ribosomal antimicrobial peptides (AMPs)

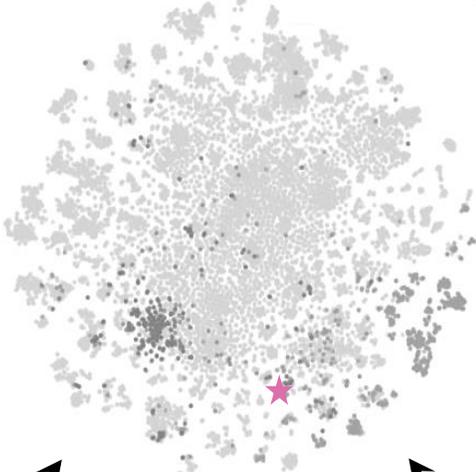
- Low emergence of resistance
- > 3000 AMPs discovered across all domains of life
- Ease of development (natural amino acid subunits)

Lazzaro *et al.*, Science, 2020

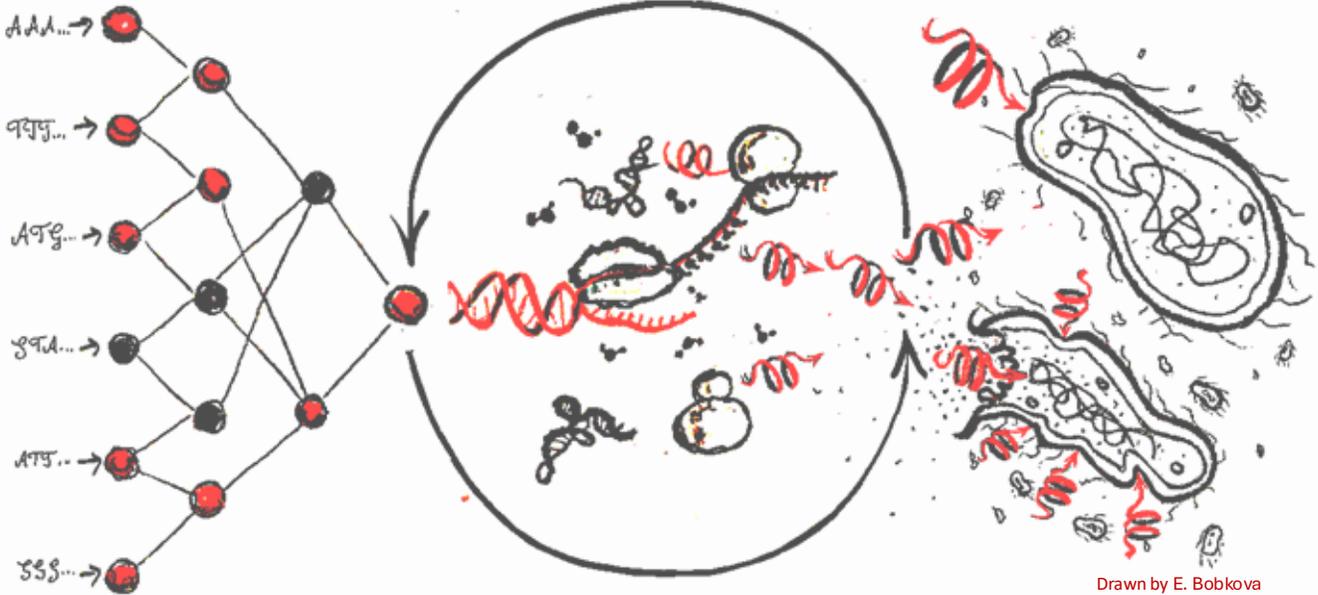


Design of *de novo* antimicrobial peptides (AMPs) to tackle antimicrobial resistance

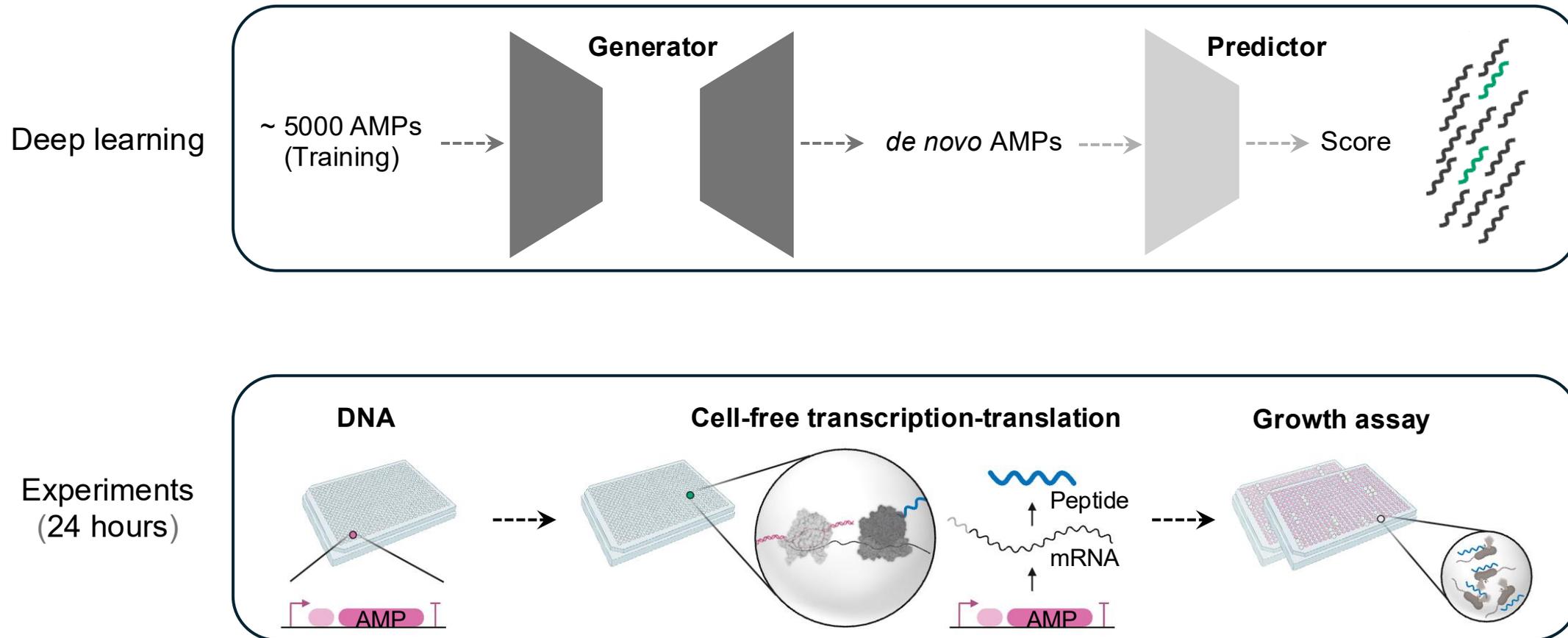
Generate new AMPs by deep learning



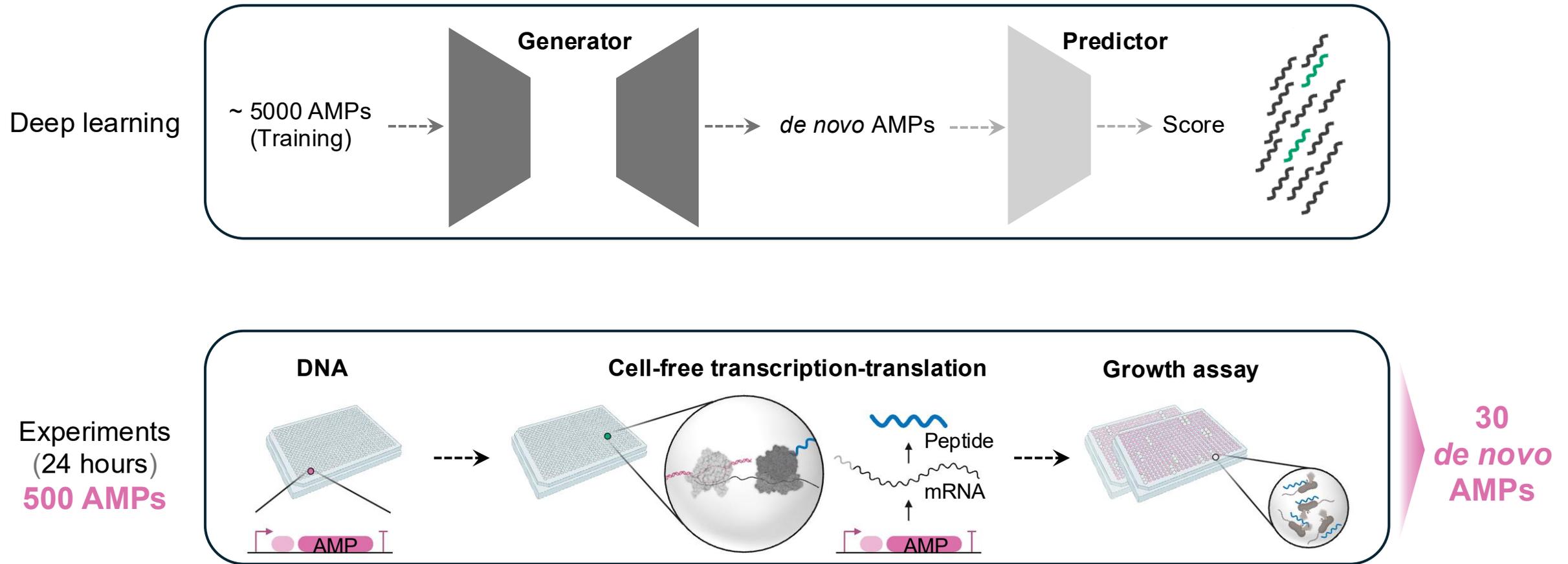
Massive sequence space



Combination of deep learning and cell-free biosynthesis enables rapid development of de novo AMPs

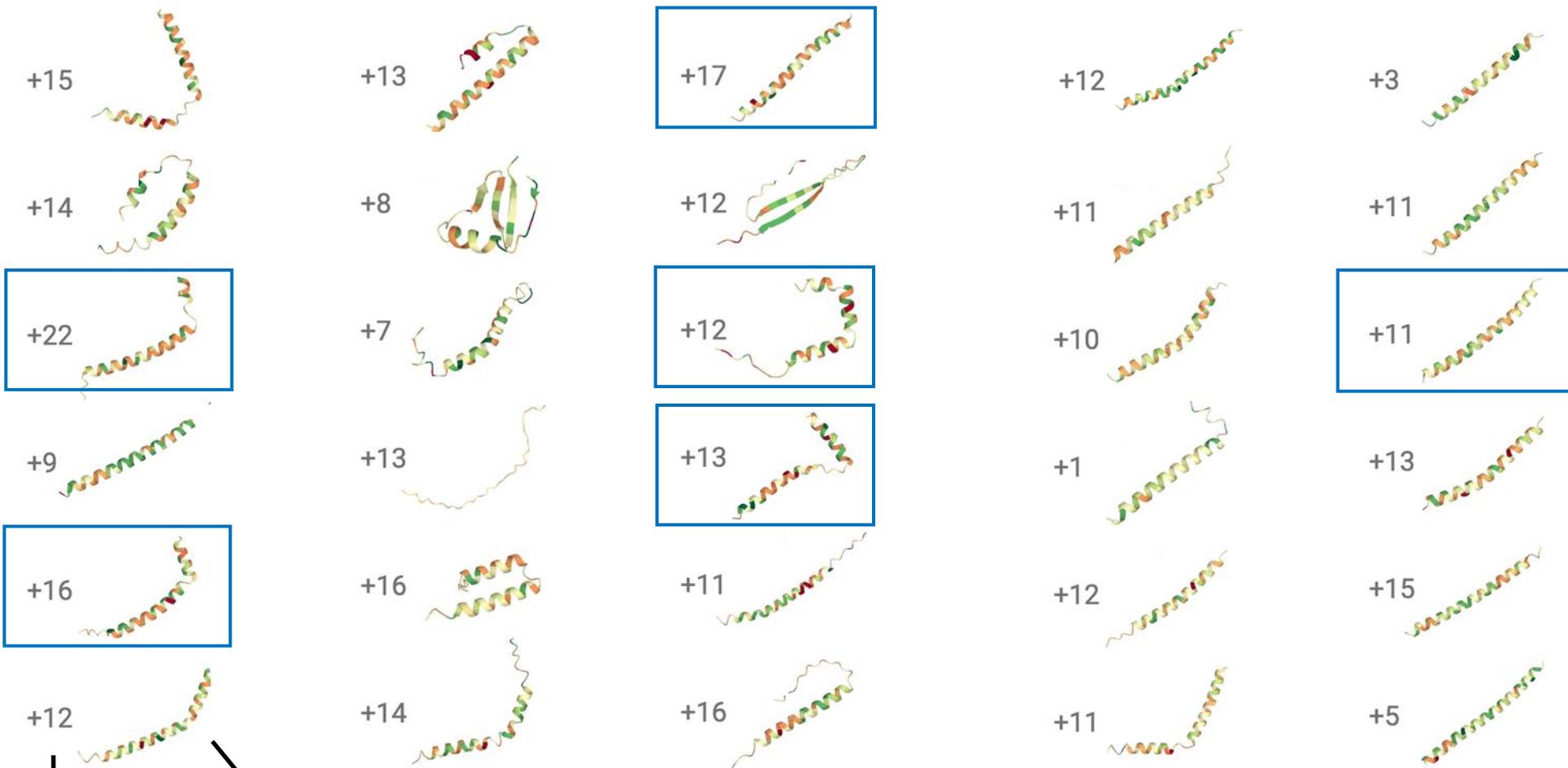


Combination of deep learning and cell-free biosynthesis enables rapid development of de novo AMPs



In 5 rounds, total of 500 AMPs tested,
with success rates of 0 (round 1) to 12.6% (round 5)

30 *de novo* AMPs were identified out of 500 candidates screened experimentally



Net charge By AlphaFold

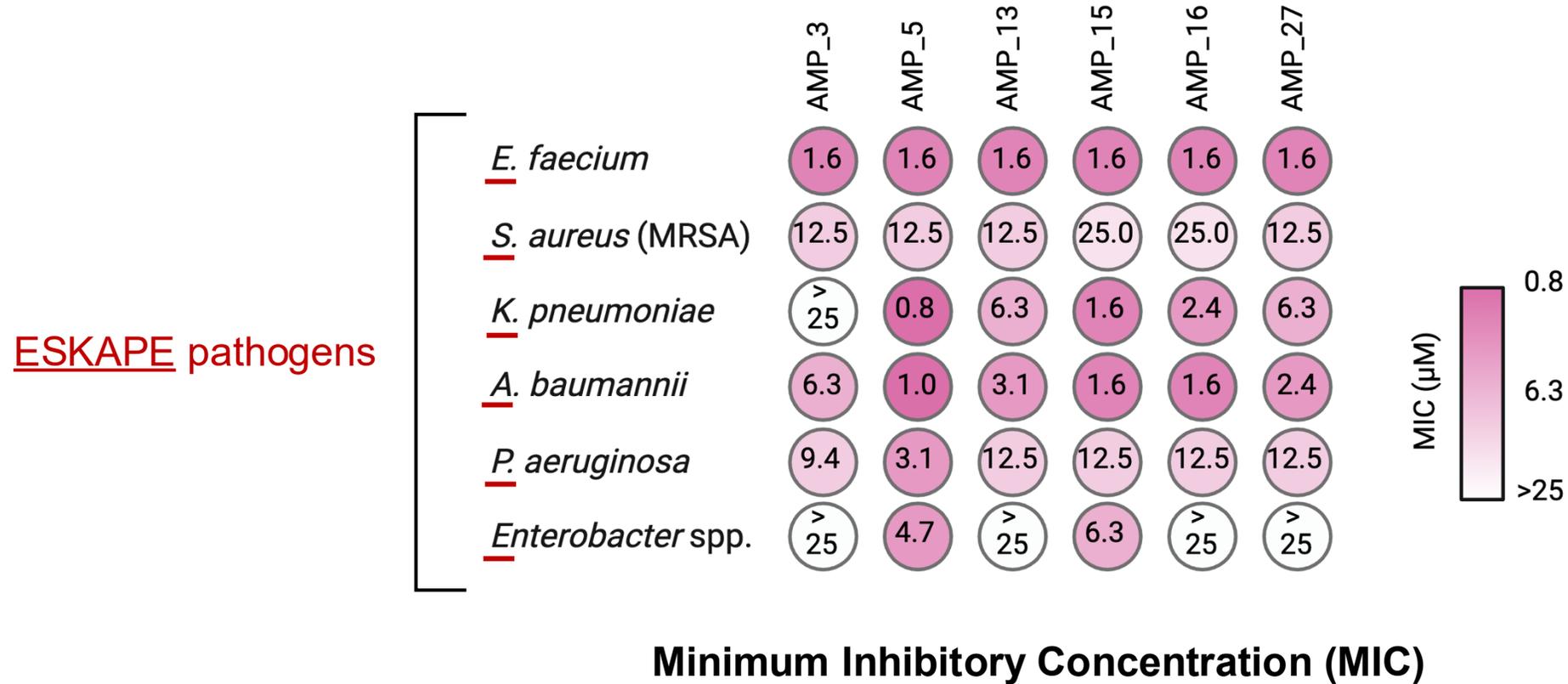
AMP amino acids

Highly hydrophilic

Highly hydrophobic

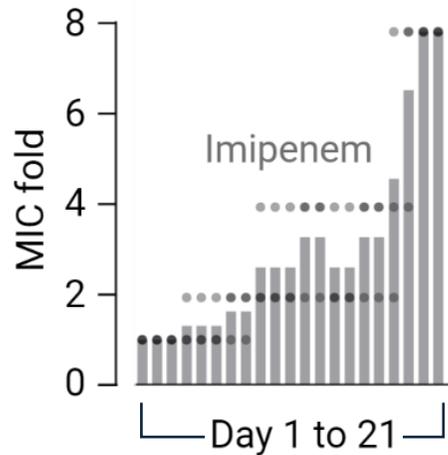
Low toxicity & broad-band activity against ESKAPE pathogens *in vitro*

Six *de novo* AMPs showed broad-spectrum activity *in vitro*



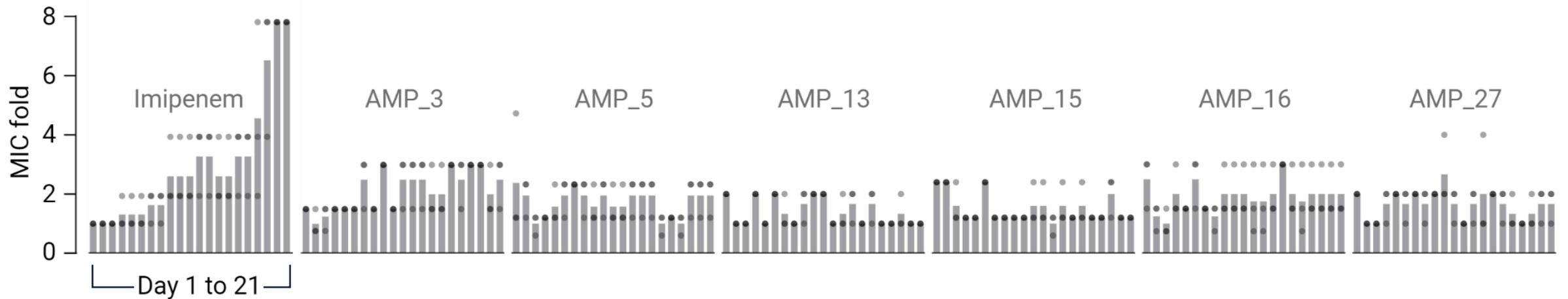
E. coli* did not evolve resistance against *de novo* AMPs, *in vitro

21 days daily passage with fresh media and AMP



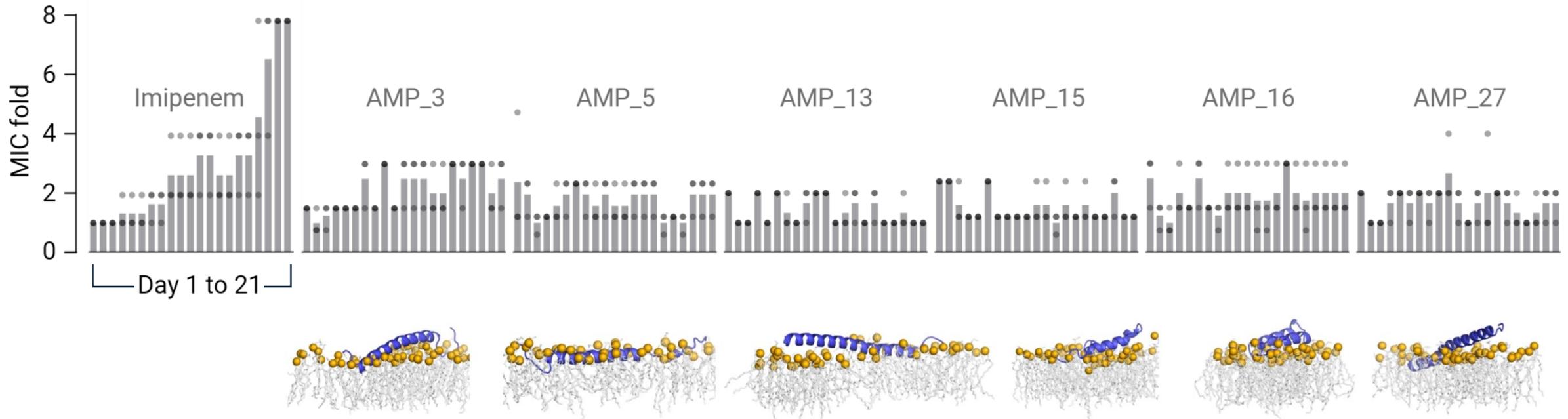
E. coli* did not evolve resistance against *de novo* AMPs, *in vitro

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E. coli* did not evolve resistance against *de novo* AMPs, *in vitro

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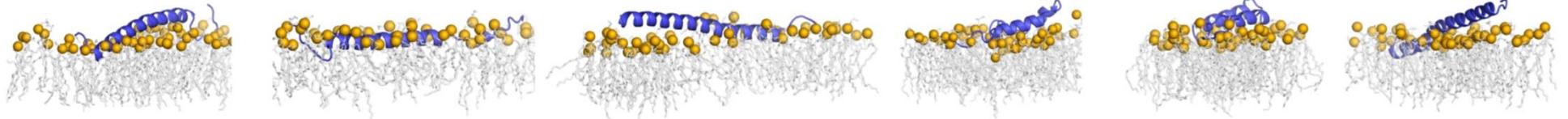
All-atom molecular dynamics simulation for 1 μ s

Limitations of (unmodified ribosomal) AMPs

Protease instability

Lack of antimicrobial specificity

Simple mode of action



Methods and features to put antimicrobial peptides (AMPs) into effect

Challenges

Solutions

Methodological

- Datasets and models
- Expression of de novo peptides
- AMP synthesis/purification

AMP features

- Protease stability
- Pathogen specificity
- Mechanism of action

Methods and features to put antimicrobial peptides (AMPs) into effect

Challenges

Solutions

Methodological

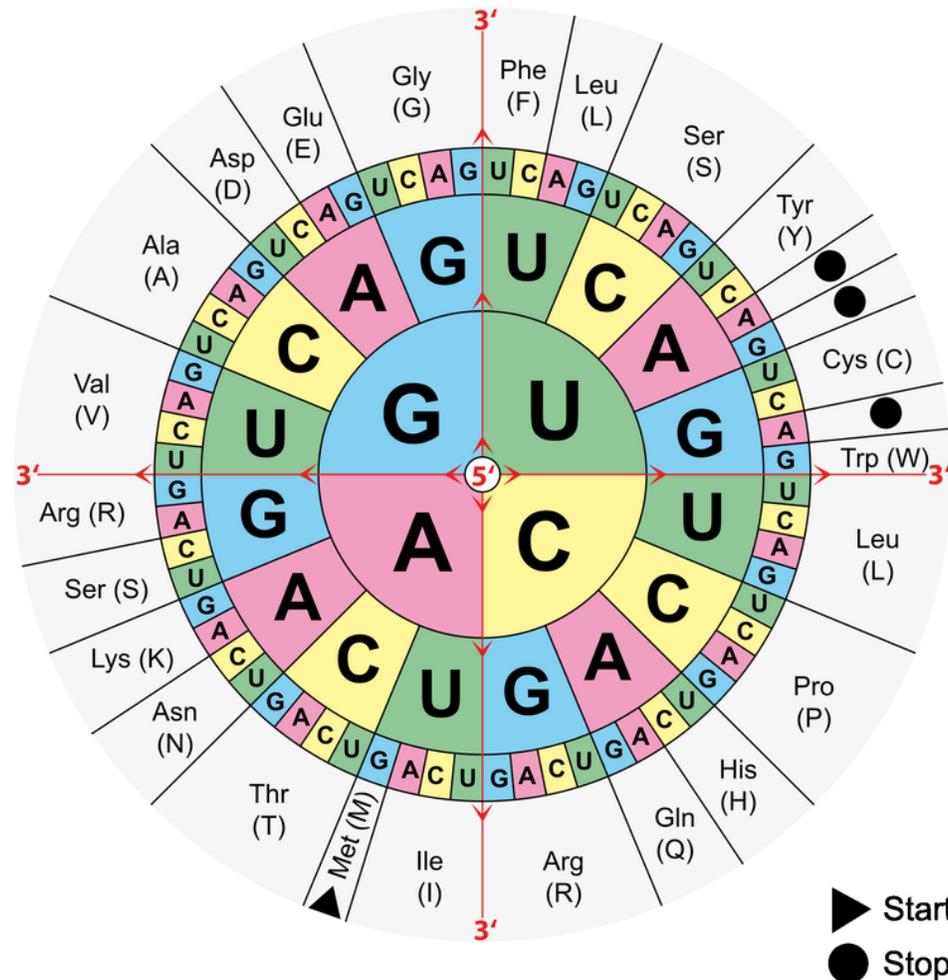
- Datasets and models
- Expression of de novo peptides ----->
- AMP synthesis/purification
- Codon language AI for DNA design

AMP features

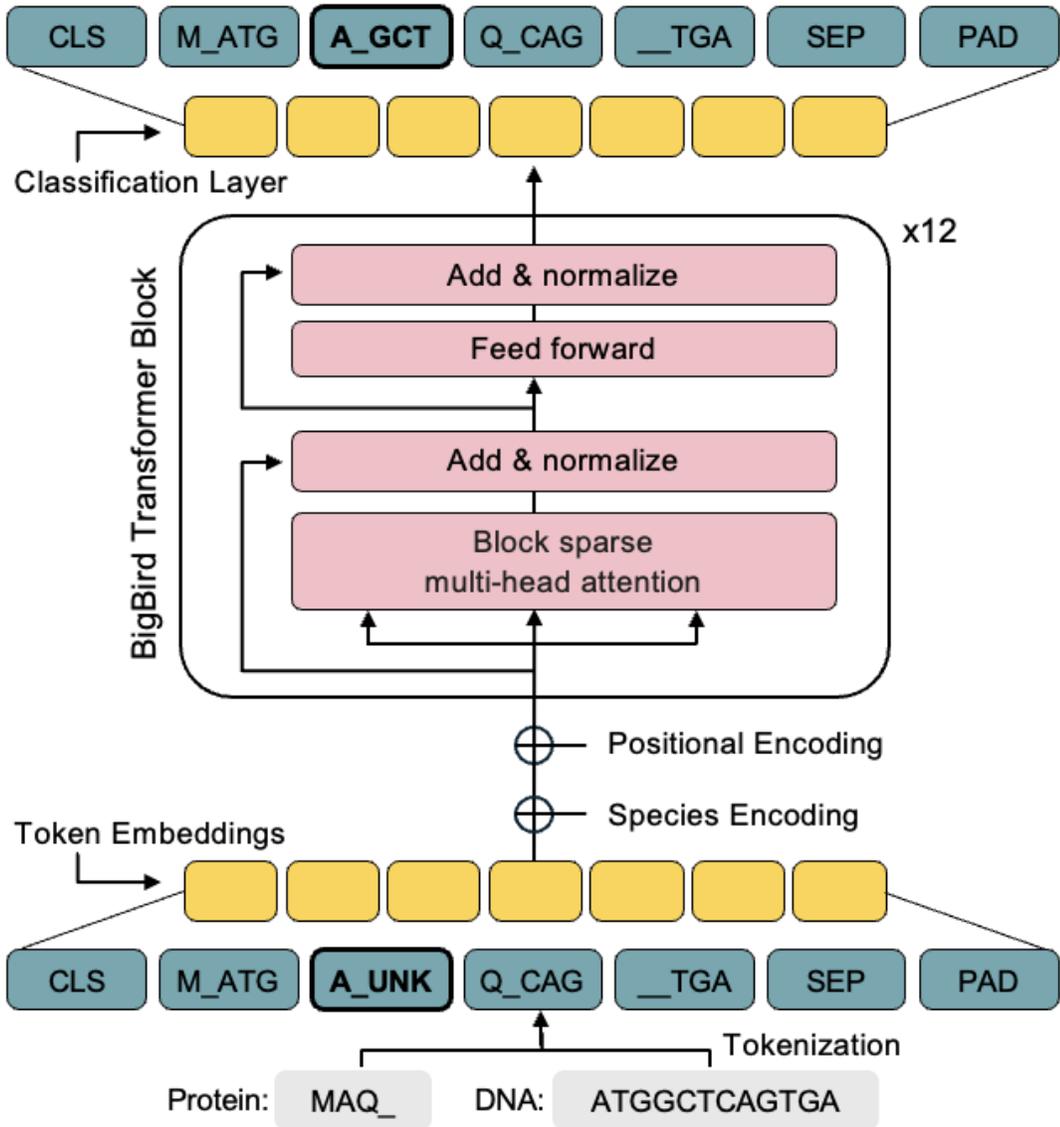
- Protease stability
- Pathogen specificity
- Mechanism of action

Codons are universal but degenerate: different species have varied preferences

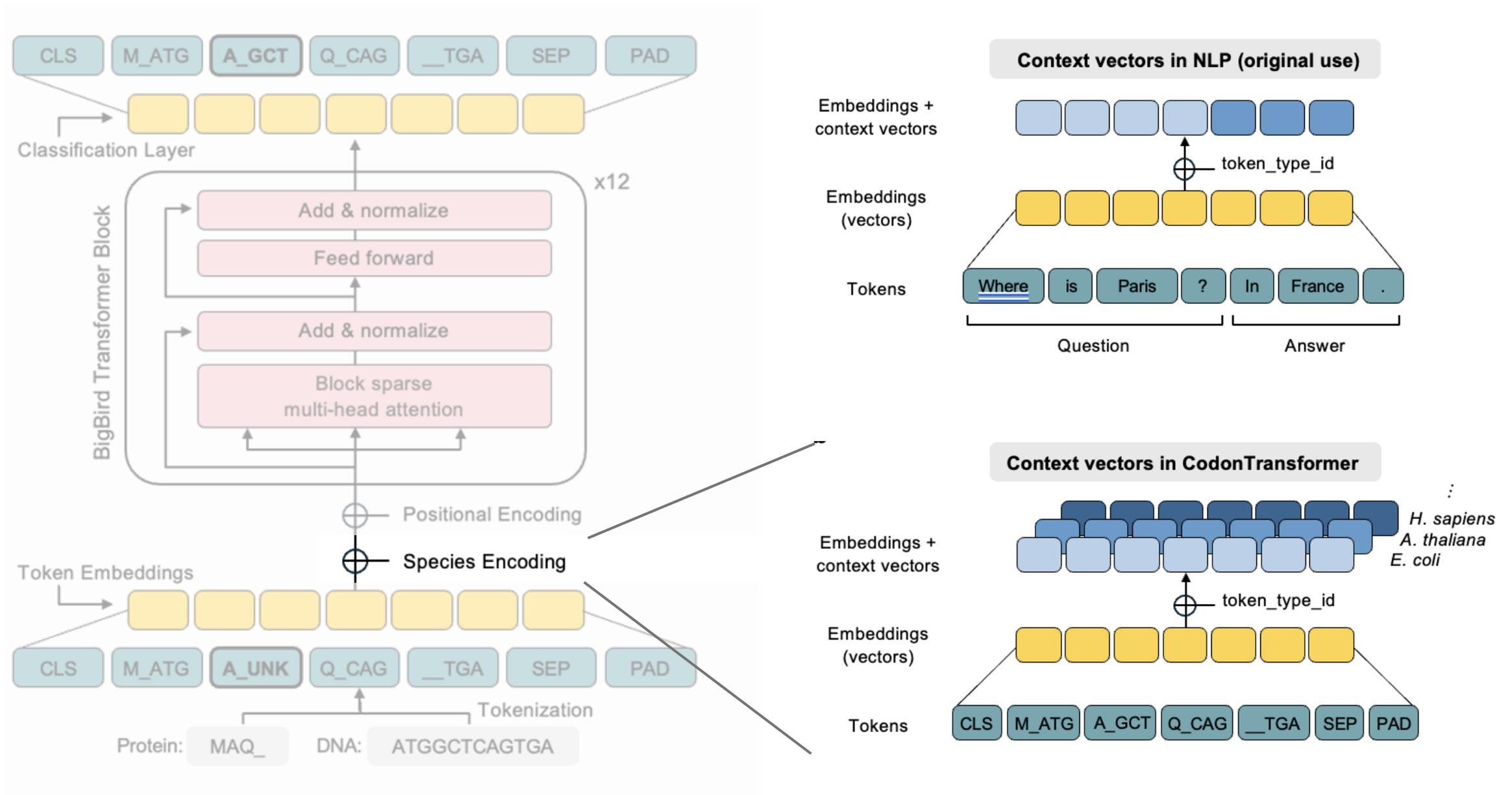
Importantly, de novo proteins/peptides do not have a natural DNA



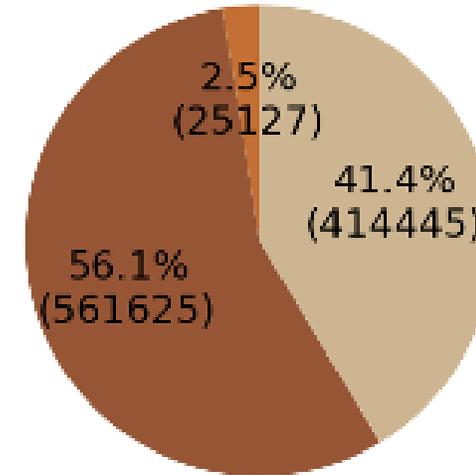
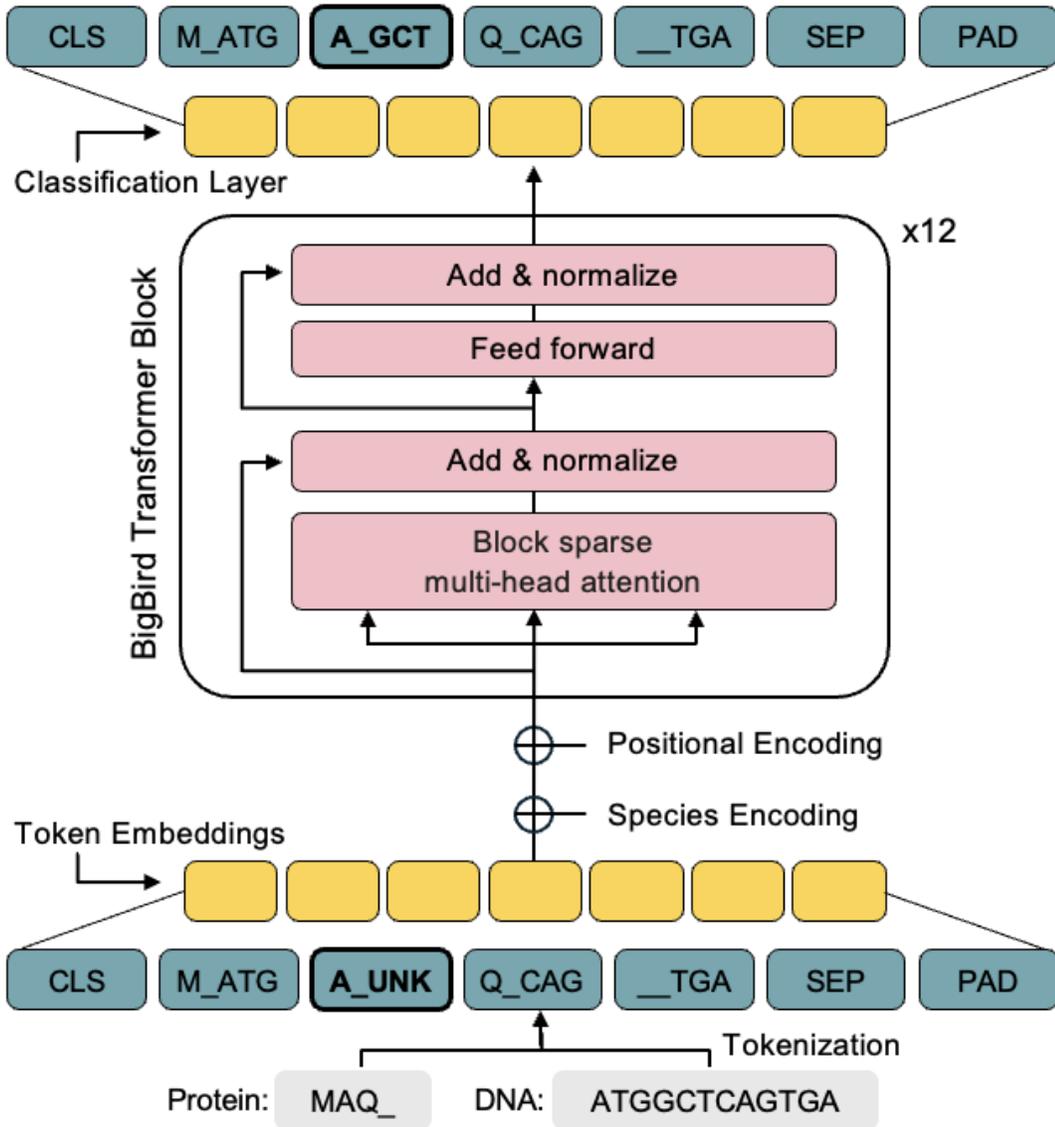
CodonTransformer: A multispecies context-aware neural network for codon optimization



CodonTransformer: A multispecies context-aware neural network for codon optimization

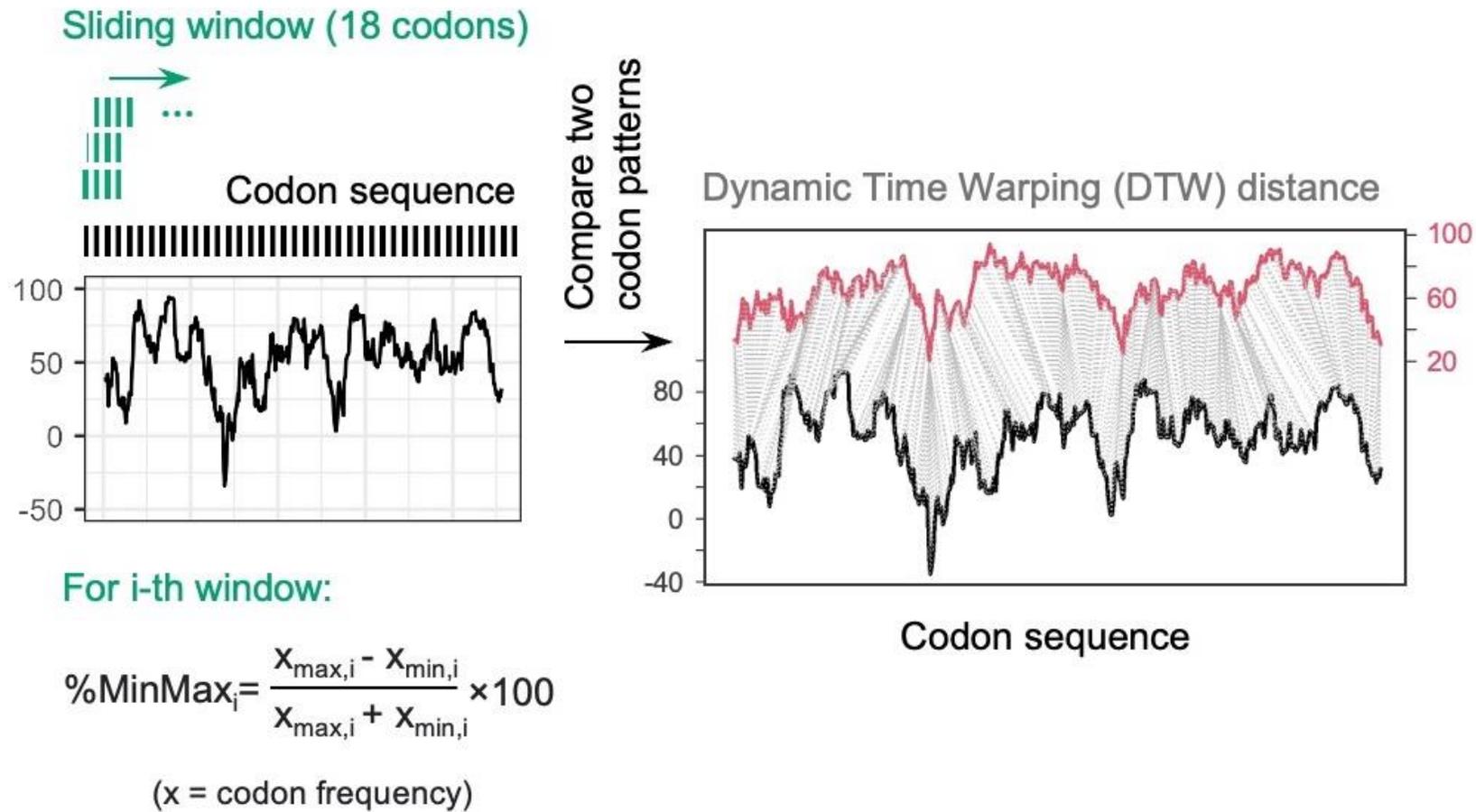


CodonTransformer: A multispecies context-aware neural network for codon optimization



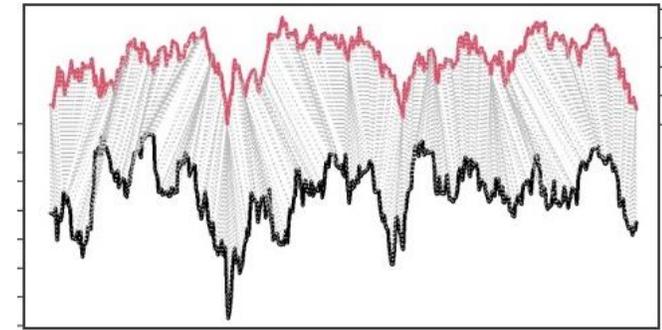
Base model Training with ~ 1 million genes
 (🕒 Archaea, 🌐 Eukarya, 🦠 Bacteria)

CodonTransformer generates natural-like DNA sequence patterns

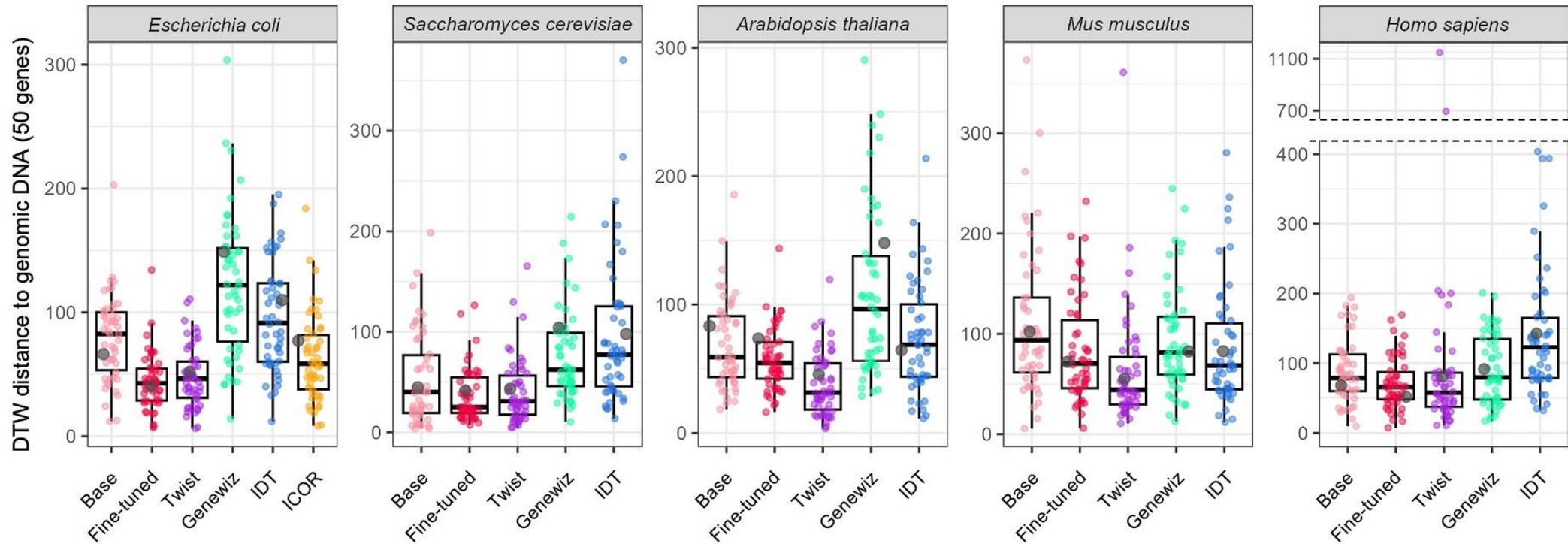


CodonTransformer generates natural-like DNA sequence patterns

Dynamic Time Warping (DTW) distance



Codon sequence



Methods and features to put antimicrobial peptides (AMPs) into effect

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- Datasets and models
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AMP features

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- Pathogen specificity
- Mechanism of action

Methods and features to put antimicrobial peptides (AMPs) into effect

Challenges

Solutions

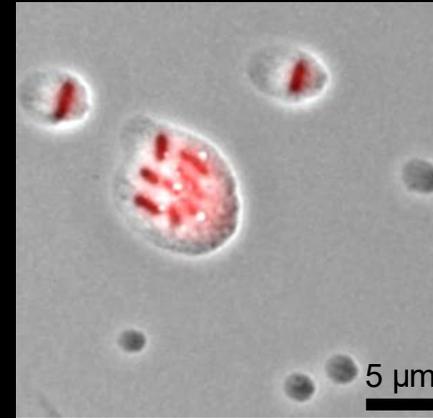
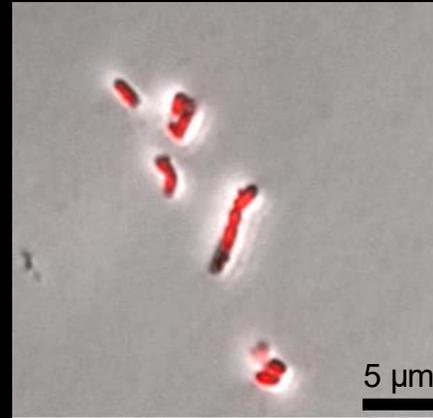
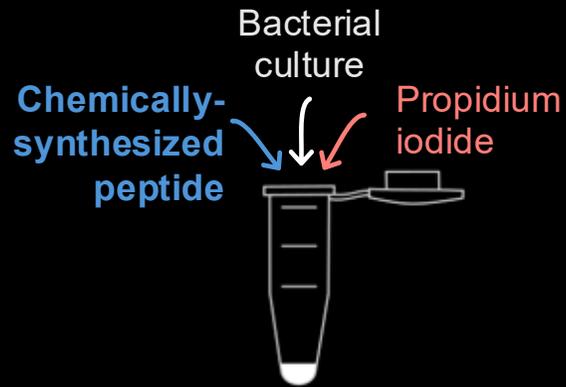
Methodological

- Datasets and models
 - Expression of de novo peptides ----->
 - AMP synthesis/purification
- Codon language AI for DNA design

AMP features

- Protease stability
 - Pathogen specificity
 - Mechanism of action ----->
- Discovery of a new feature

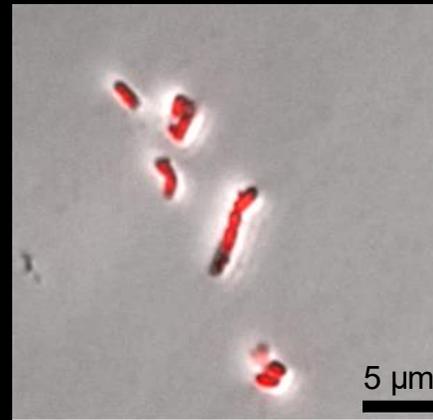
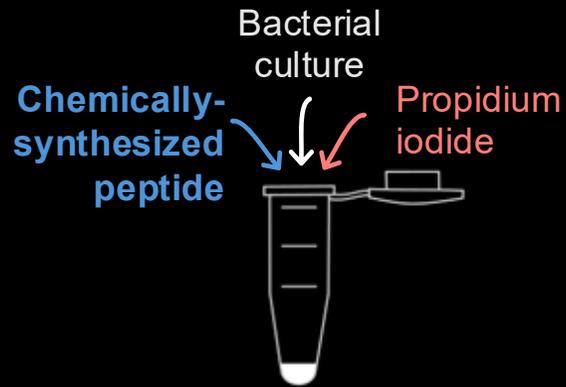
Discovery of a novel AMP feature



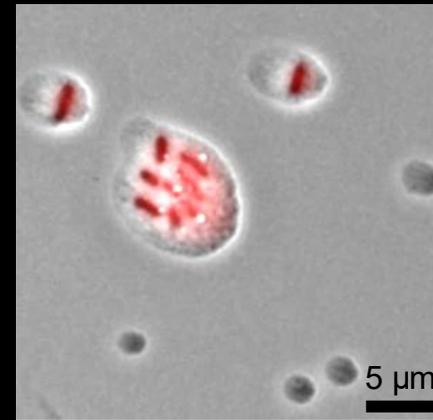
→ Forms droplets *in vitro*, engulfs and kills bacteria

Discovery of a novel AMP feature

Liquid-liquid phase separation (LLPS)

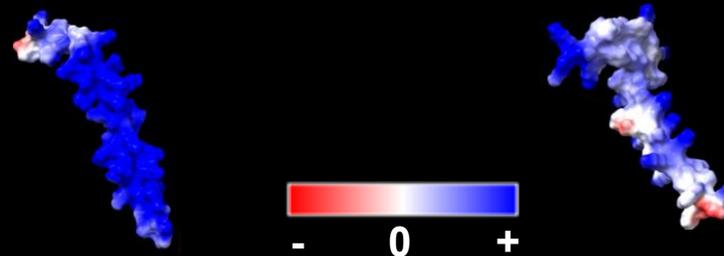


AMP without LLPS

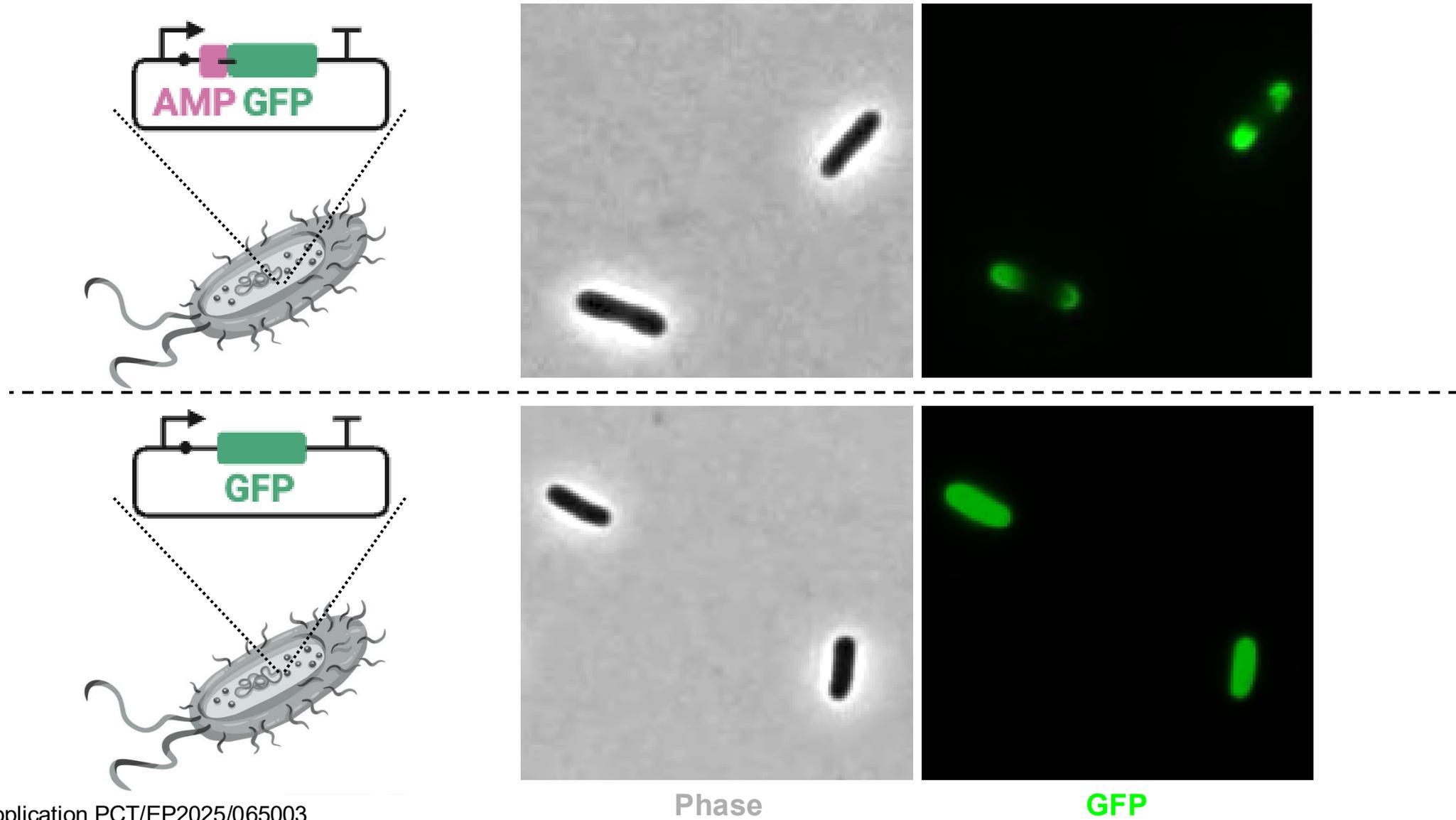


L1AMP (with LLPS)

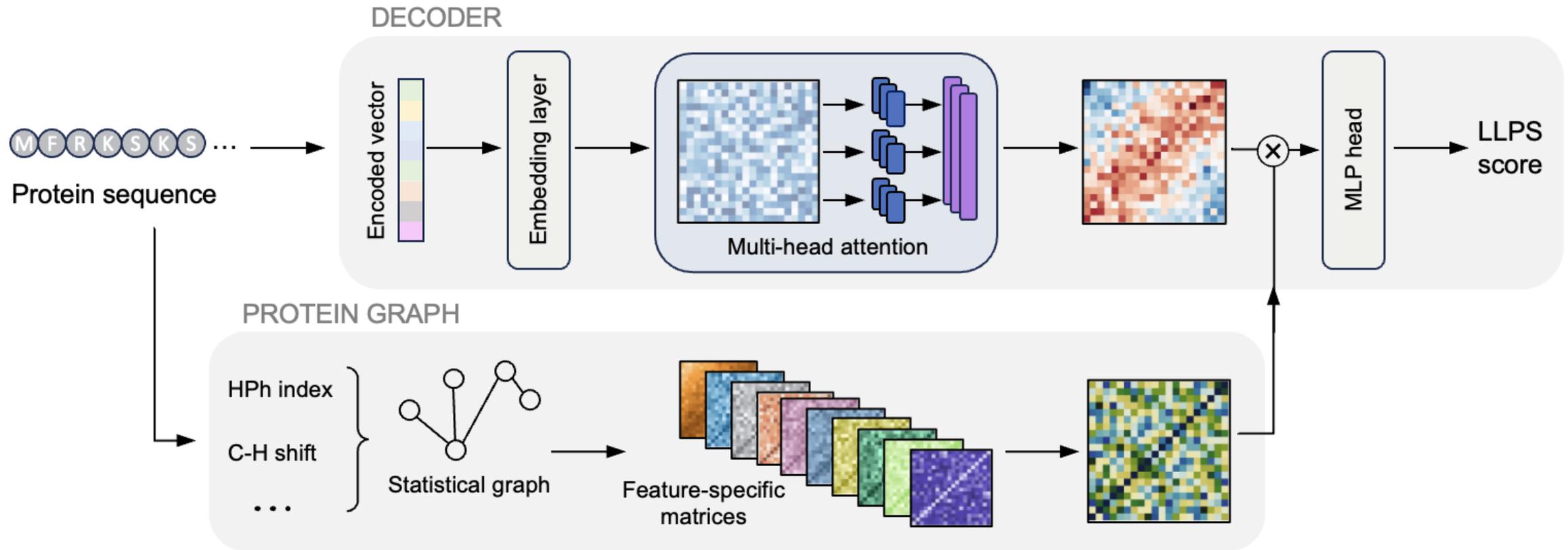
→ Forms droplets *in vitro*, engulfs and kills bacteria



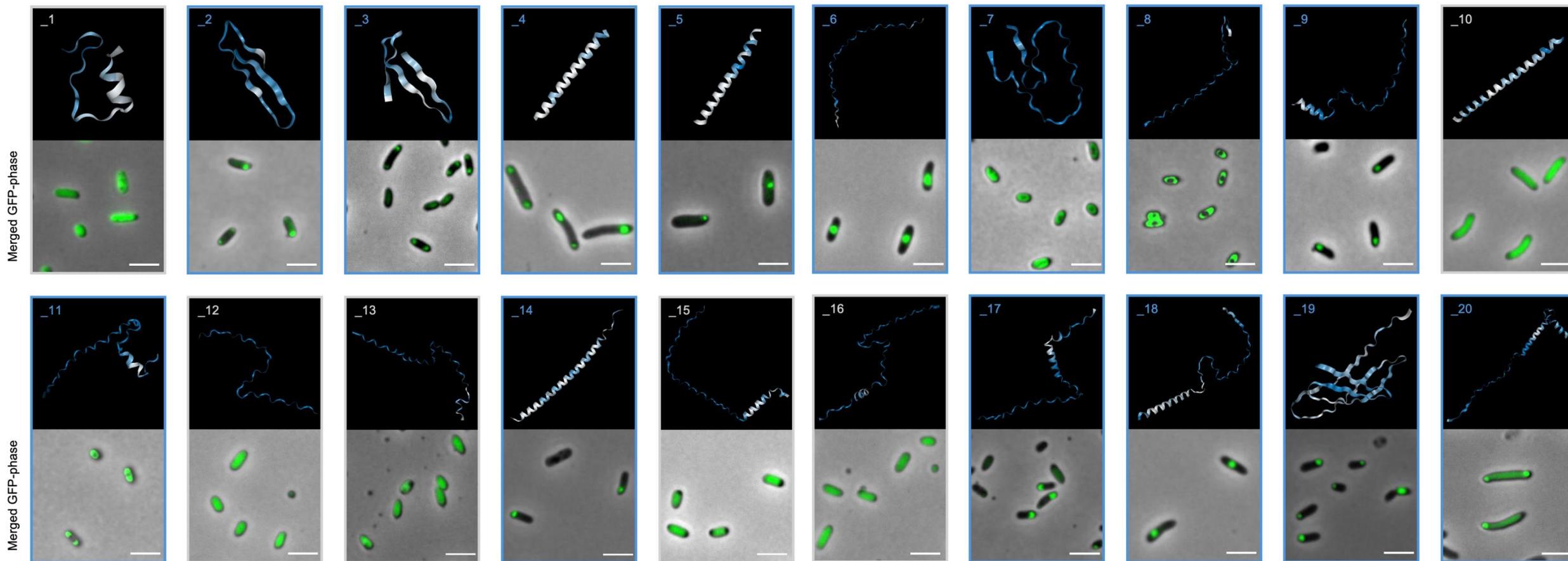
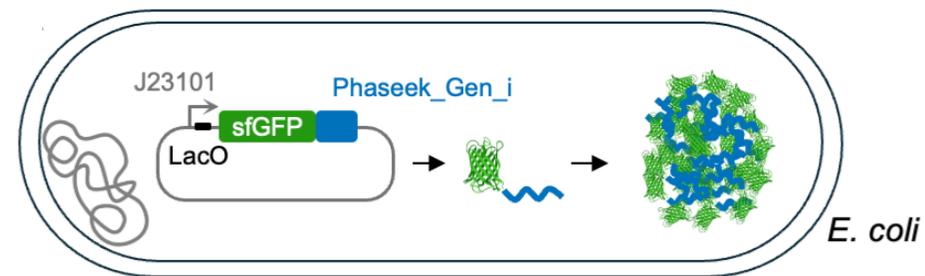
L1AMP phase-separates when expressed in *E. coli* fused to GFP

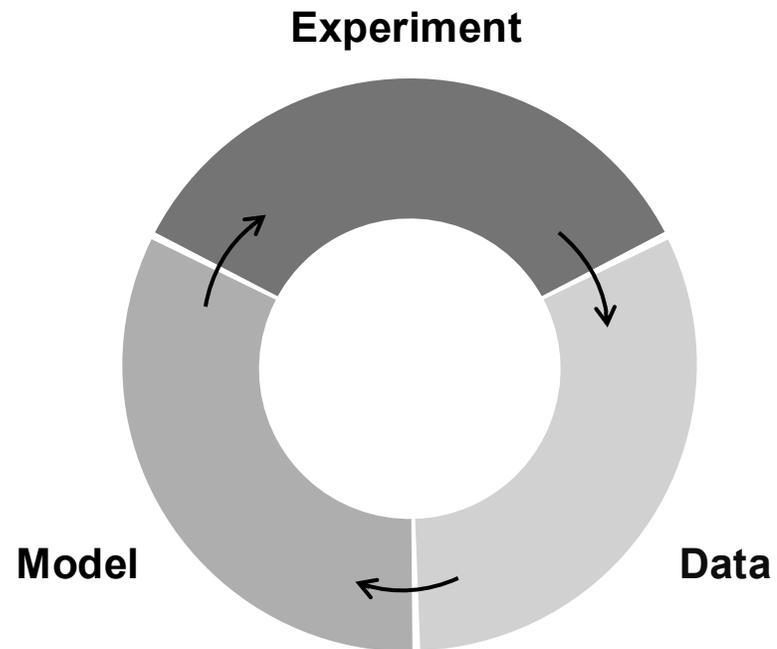
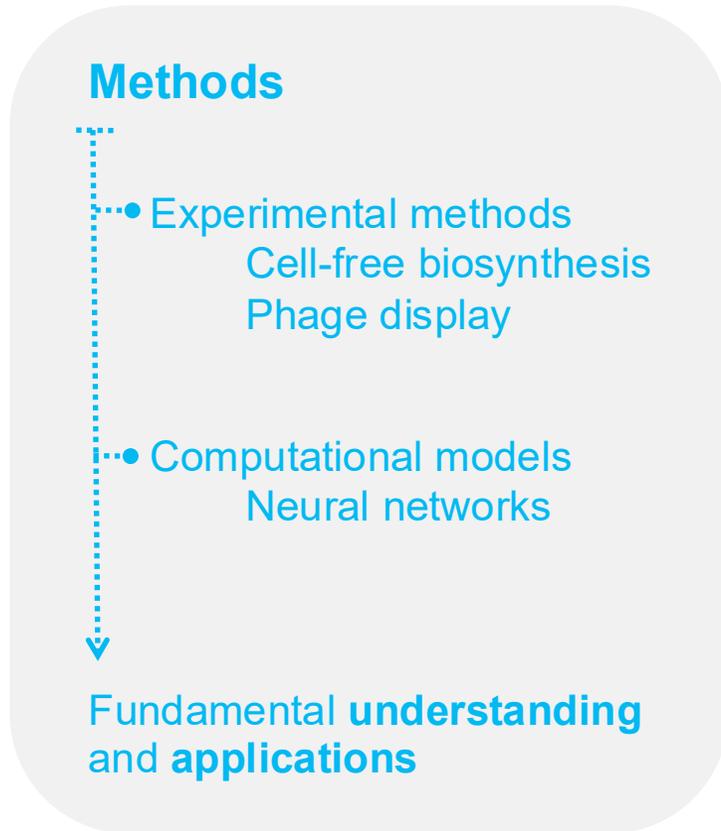


Phaseek: a hybrid model for multiscale prediction of protein liquid-liquid phase separation



Phaseek can be used to generate new phase-separating peptides





Protease stability

Antimicrobial specificity

Mode of action

- Inspired by the natural examples
- Learning their underlying language
- Inexhaustible design of candidates with “tailored properties” that nature did not have the selective pressure to explore.



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Ariel Lindner

Collaborators:

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D. Adam
C. Diehl
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V. Gureghian
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AM. Cheraghali

MAX PLANCK INSTITUTE
FOR TERRESTRIAL MICROBIOLOGY



Max-Planck Institute, Marburg
Tobias Erb

Collaborators:

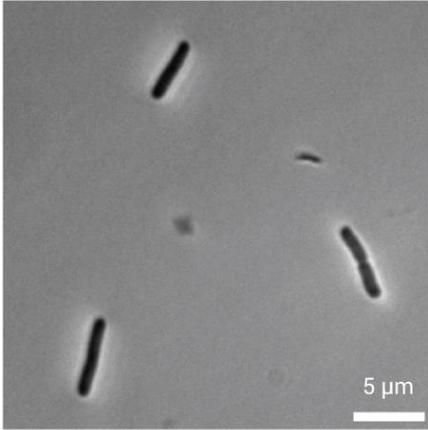
Dep. Chemistry, University of Marburg:
Prof. O Vazquez, Dr. F Abendort, VT Trinh

Bundeswehr Institute for Microbiology, Munich
Dr. H von Buttlar, Dr. D Adam, P Braun

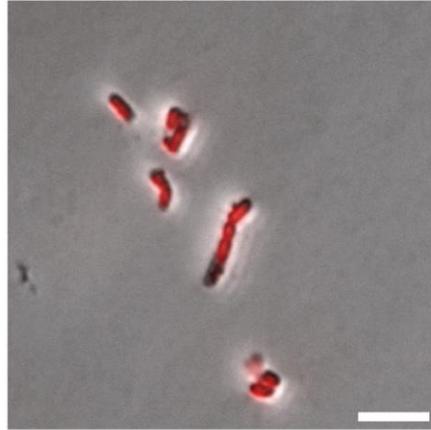
Funding:



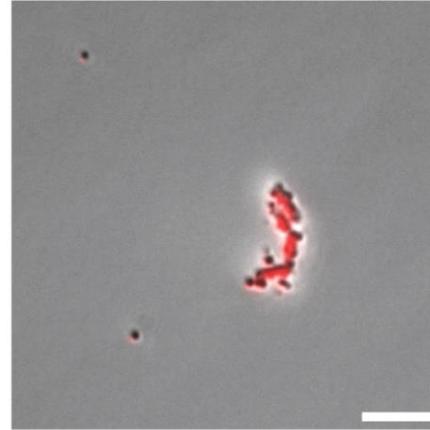
d Untreated *E. coli* (control)



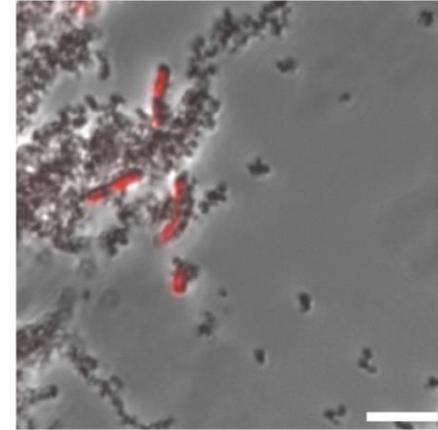
AMP_3



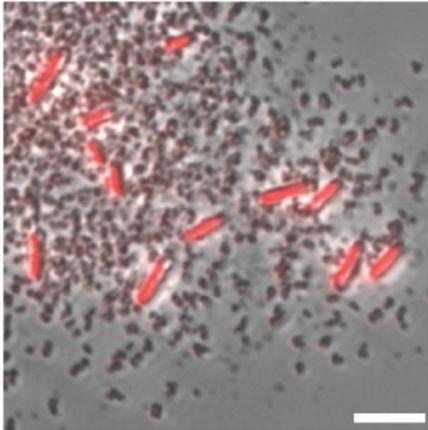
AMP_5



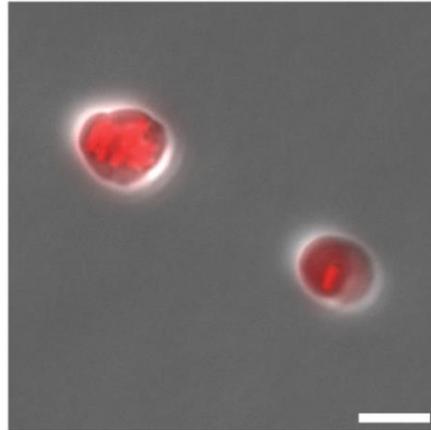
AMP_13



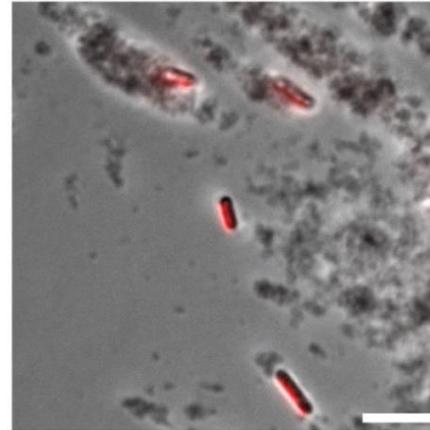
AMP_15



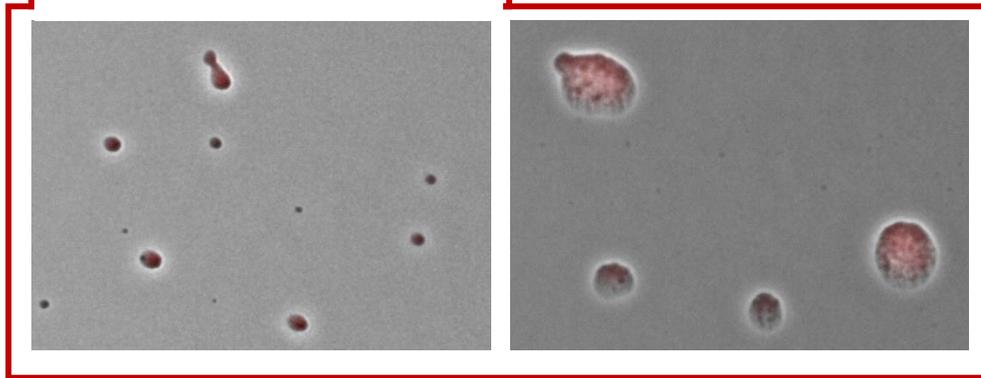
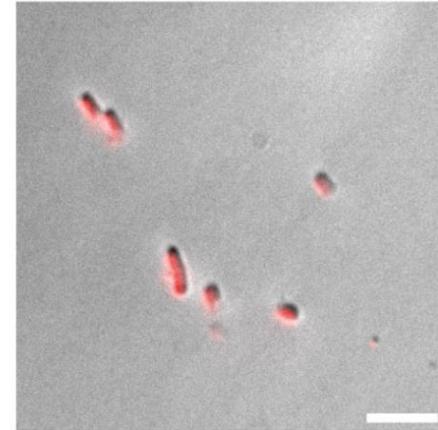
AMP_16



AMP_27



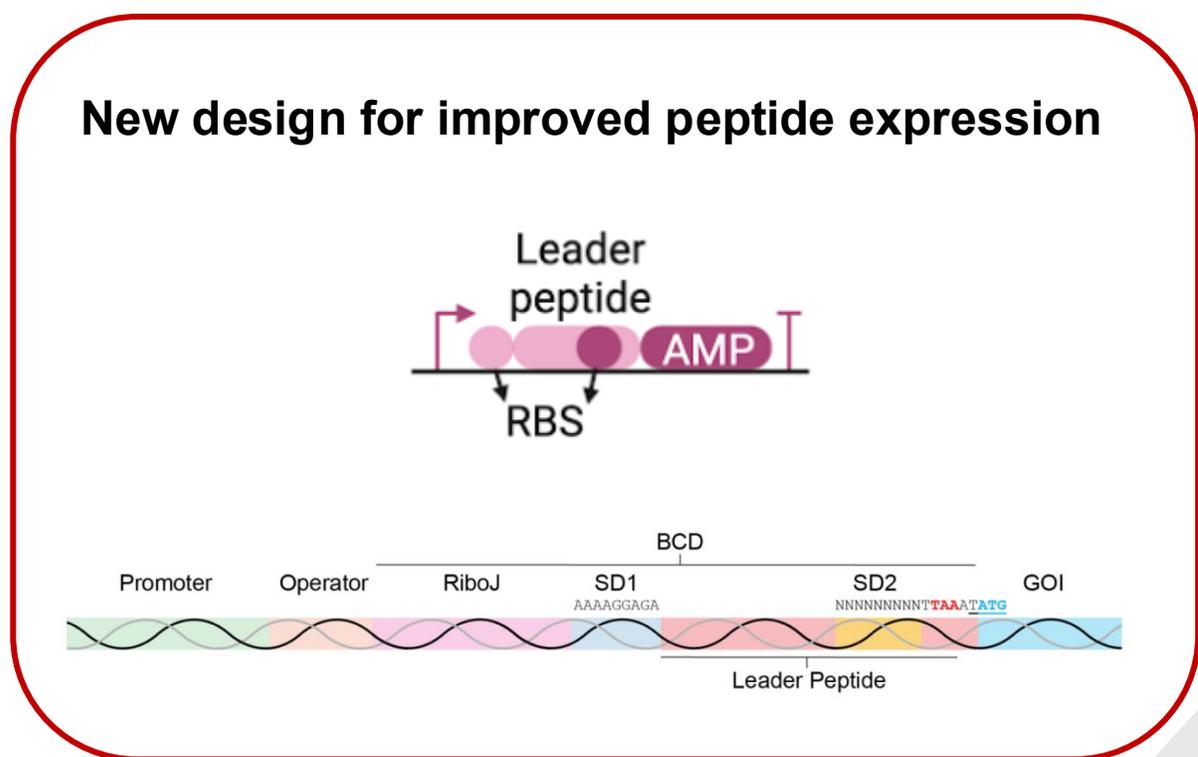
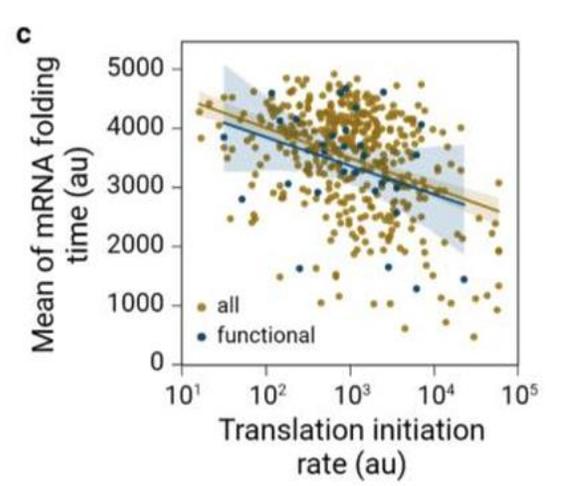
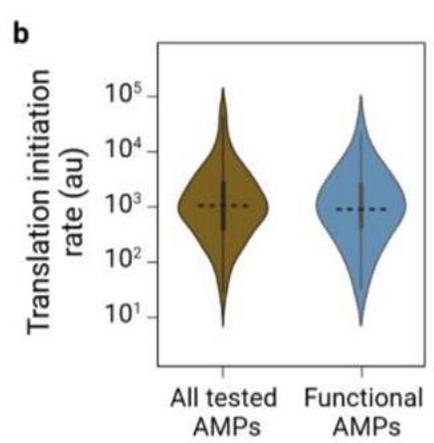
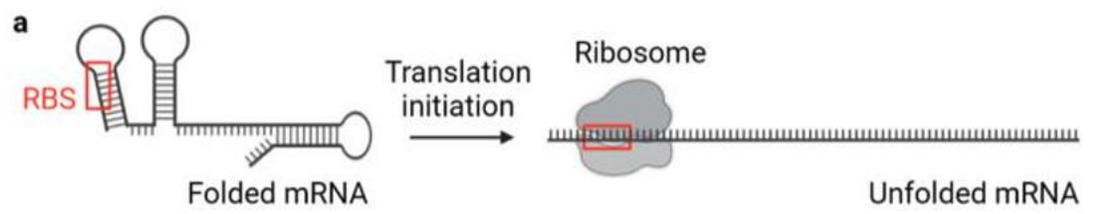
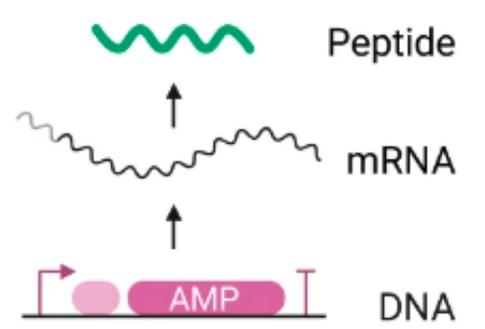
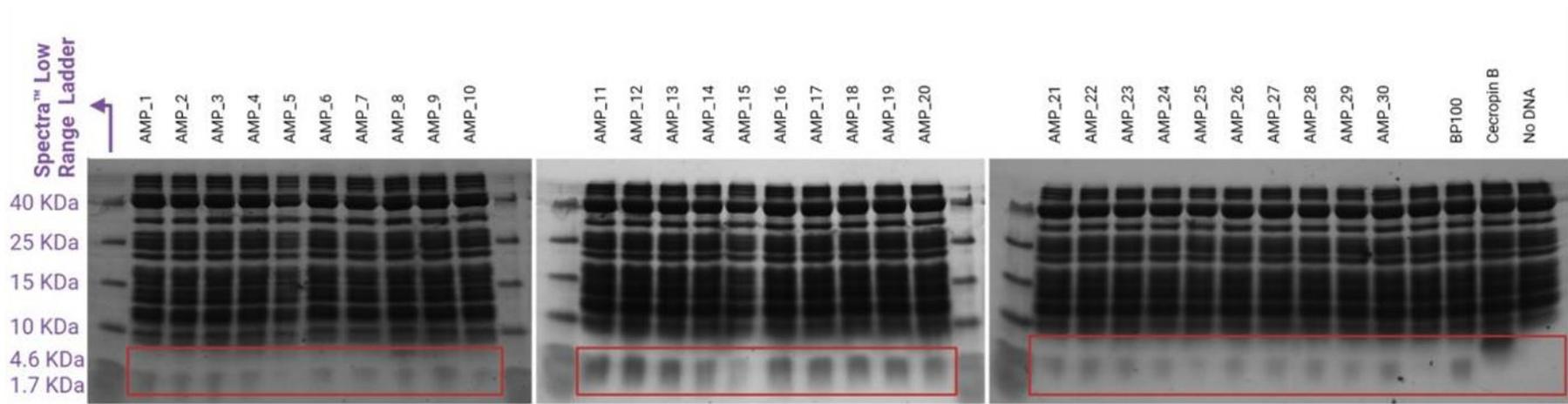
Cecropin B



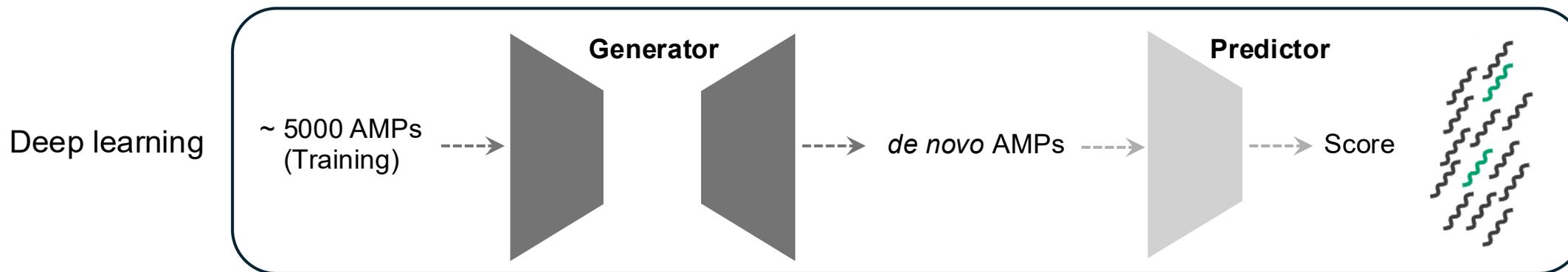
No cell (only L1AMP)

Supplementary Table 4: Rounds of AMP generation, filtering, and prioritization with different models/approaches and numbers.

	round 0	round 1	round 2	round 3	round 4
Generator	VAE_v0	VAE_v0	VAE_v1	VAE_v1	VAE_v2
Sampling	Optimized Cecropin B*	random	random	random	random
Regressor	CNN reg_v0	CNN reg._v0	CNN reg._v1	CNN reg._v2 + Toxicity classifier	CNN reg._v2 + RNN reg._v0
All generated peptides	100	100,000	100,000	200,000	150,000
Viable peptides	100	9,220	9,117	18,218	29,457
MIC-predicted and experimentally tested	50	50	150	100	150
Functional peptides discovered	0	2	9	0	19
Efficiency (%)	0	4	6	0	12.6

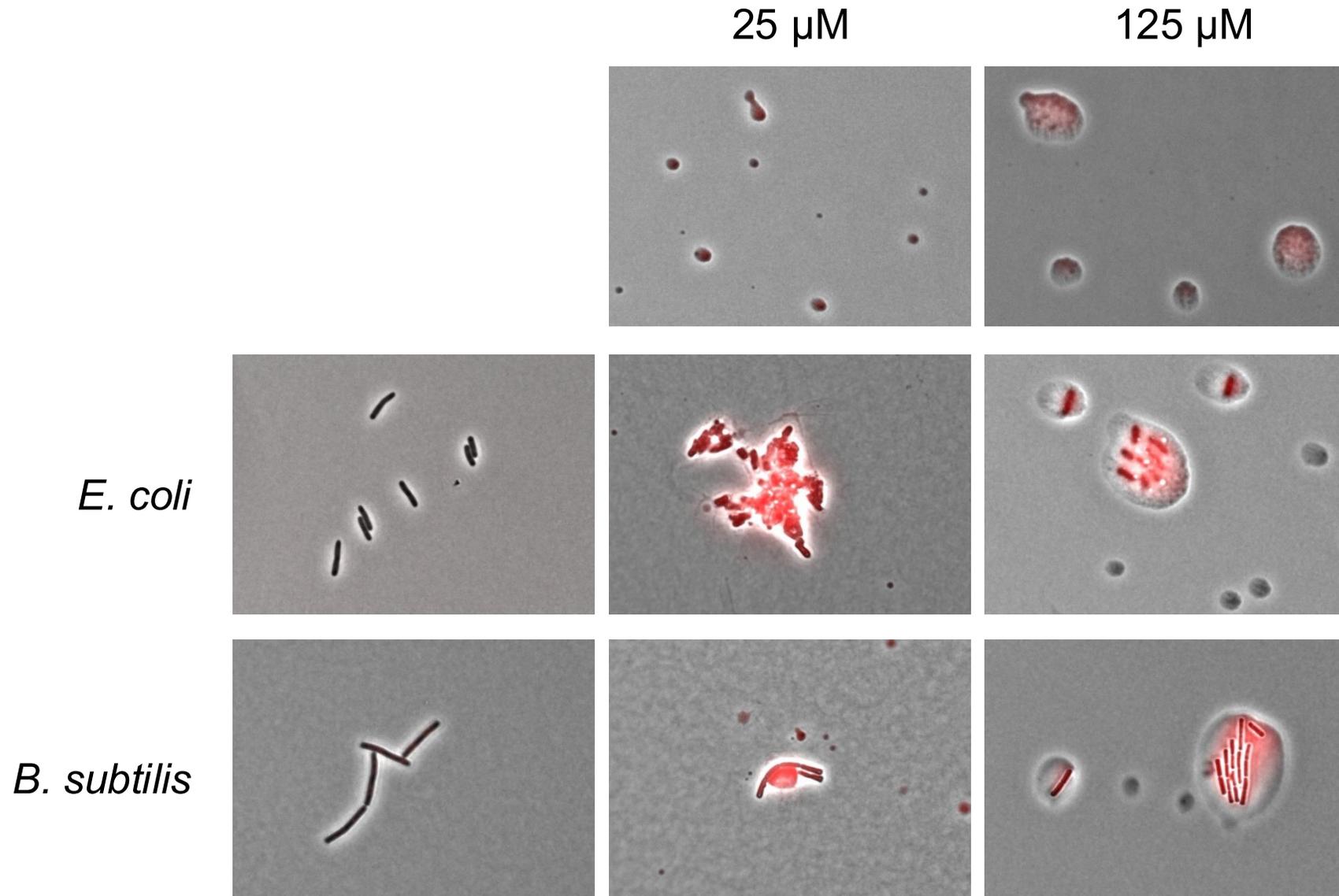


Combination of deep learning and cell-free biosynthesis enables rapid development of de novo AMPs



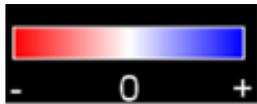
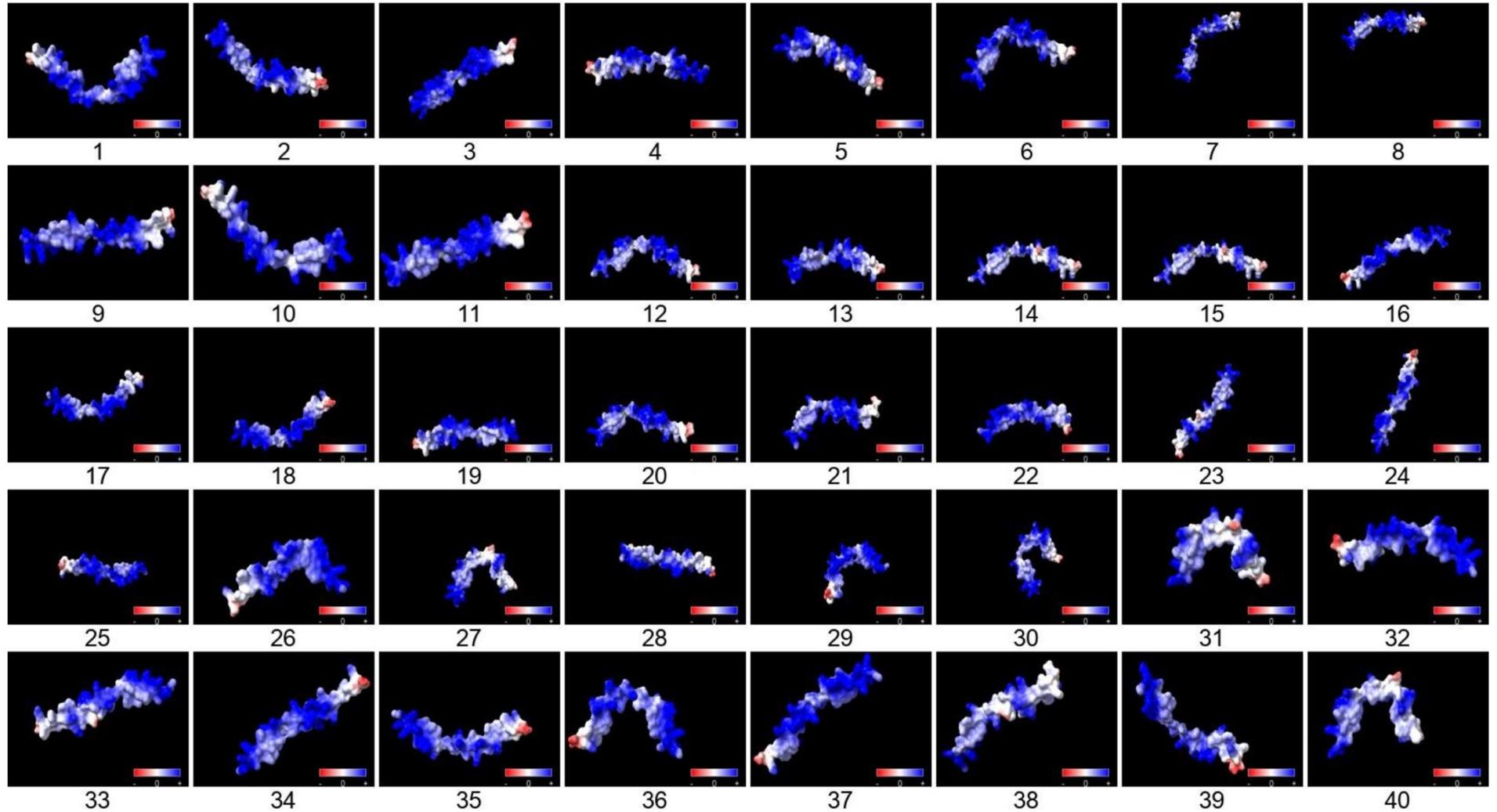
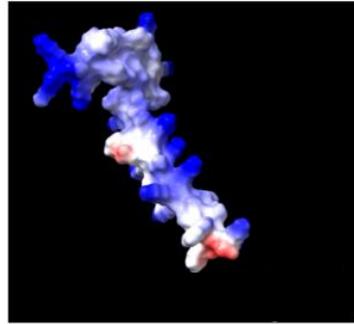
	Chemical synthesis	Cell-free biosynthesis	Cell-based biosynthesis
Cost	High	Moderate	Inexpensive
Speed	Slow	Fast	Moderate
Purity	Good	Low	Good

LLPS and bacterial killing by chemically synthesized AMP

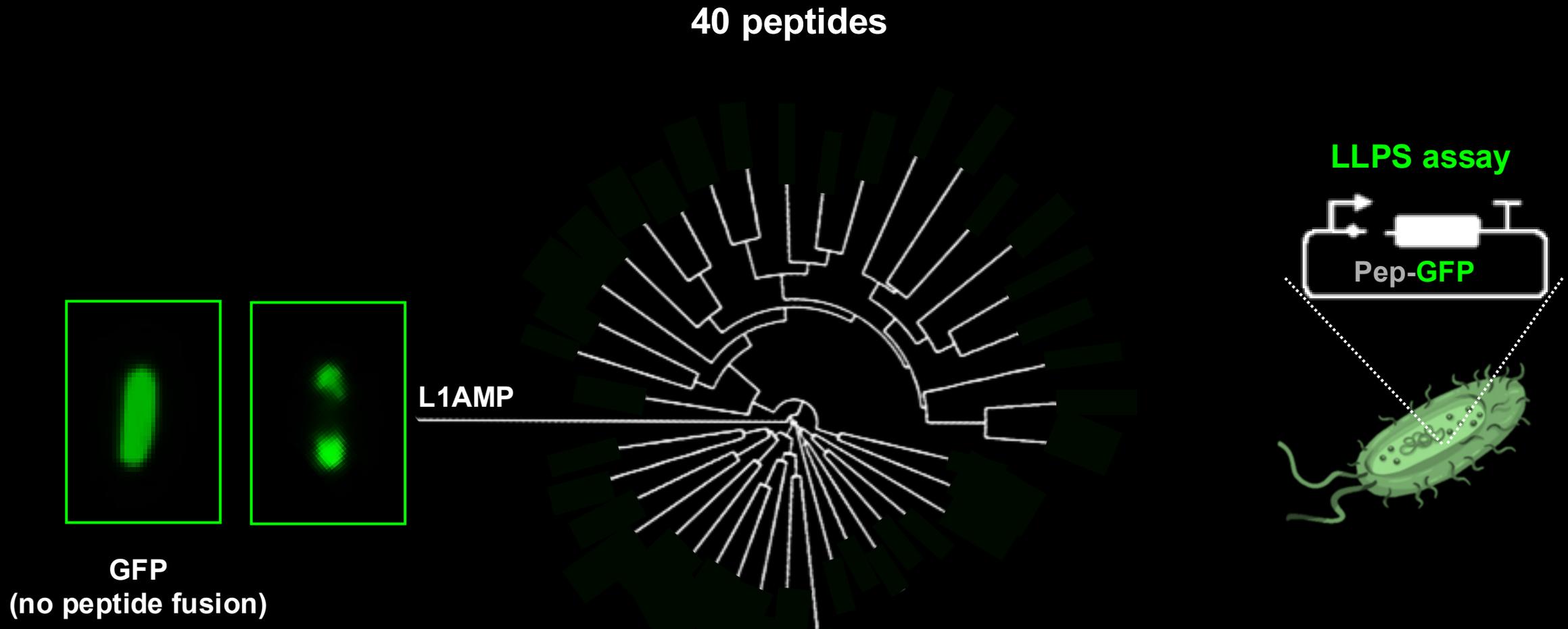


40 *de novo* AMPs were generated from L1AMP using the generative model

L1AMP

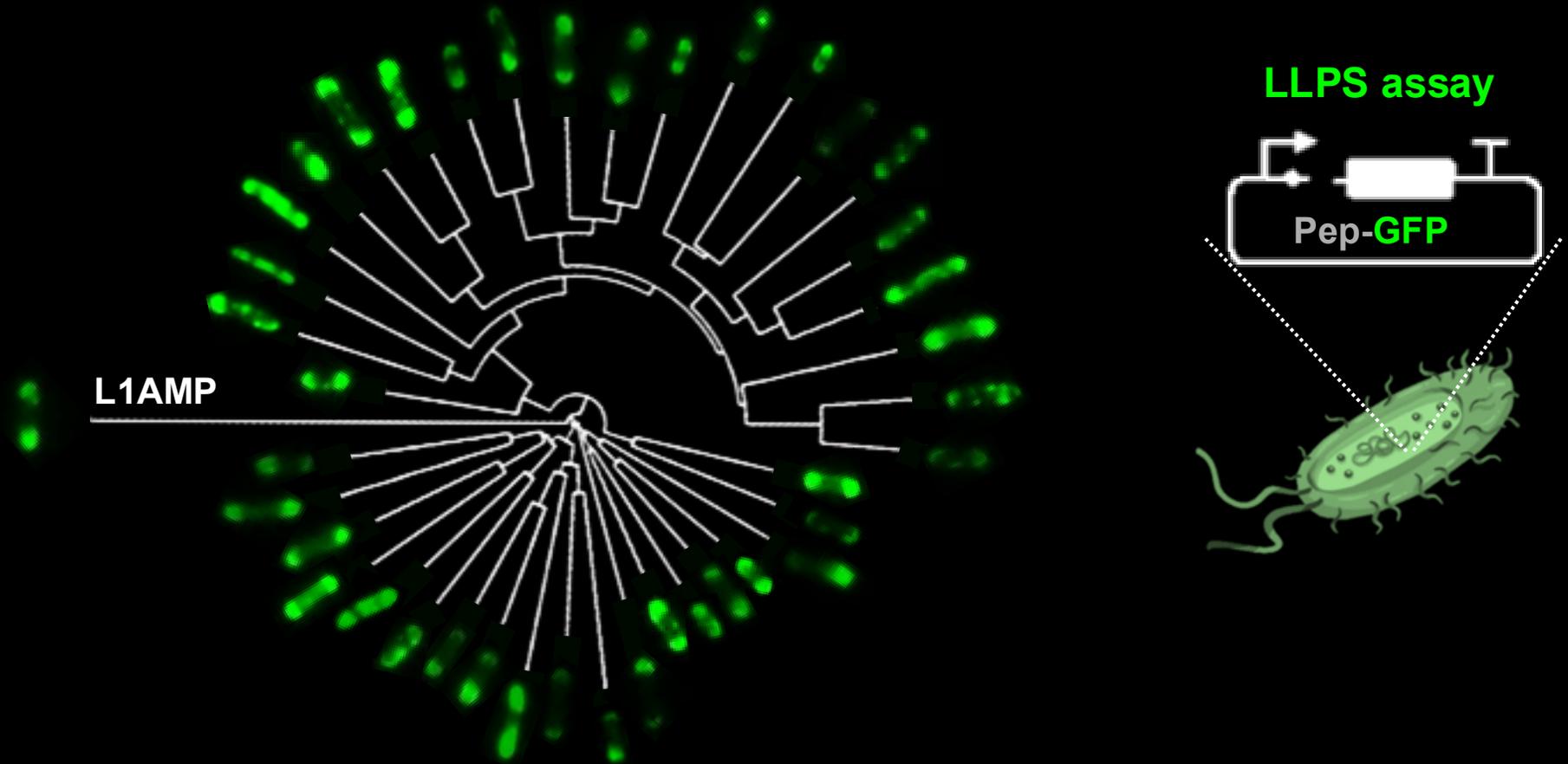


Discovery of a novel AMP feature



Discovery of a novel AMP feature

40 peptides

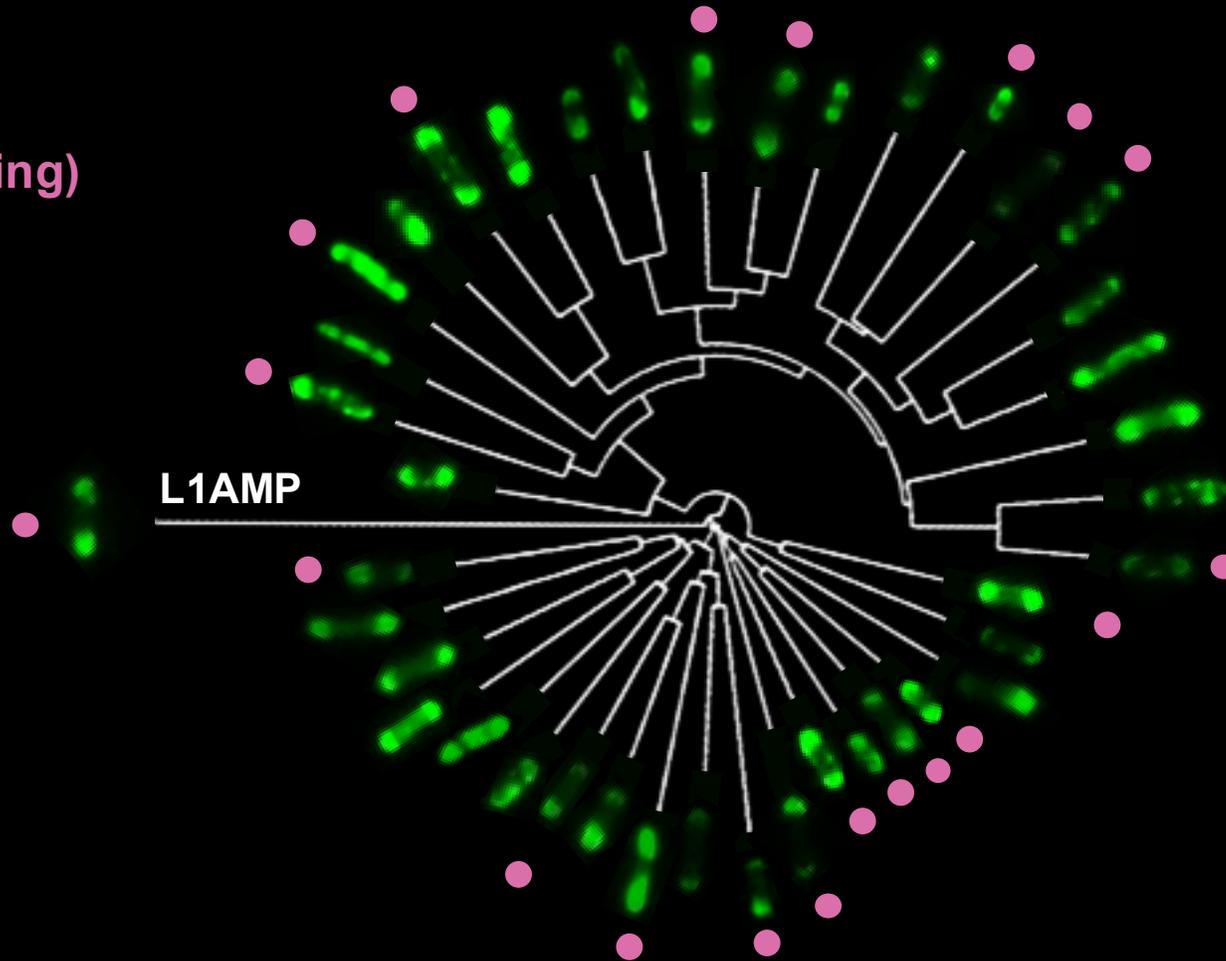


L1AMP-derived peptides show **LLPS** behavior

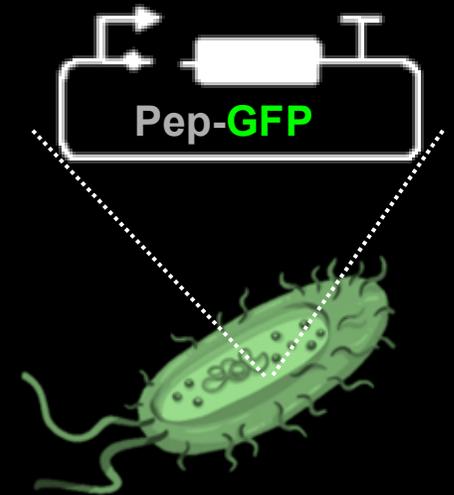
Discovery of a novel AMP feature

40 peptides

AMP activity
(Cell-free screening)

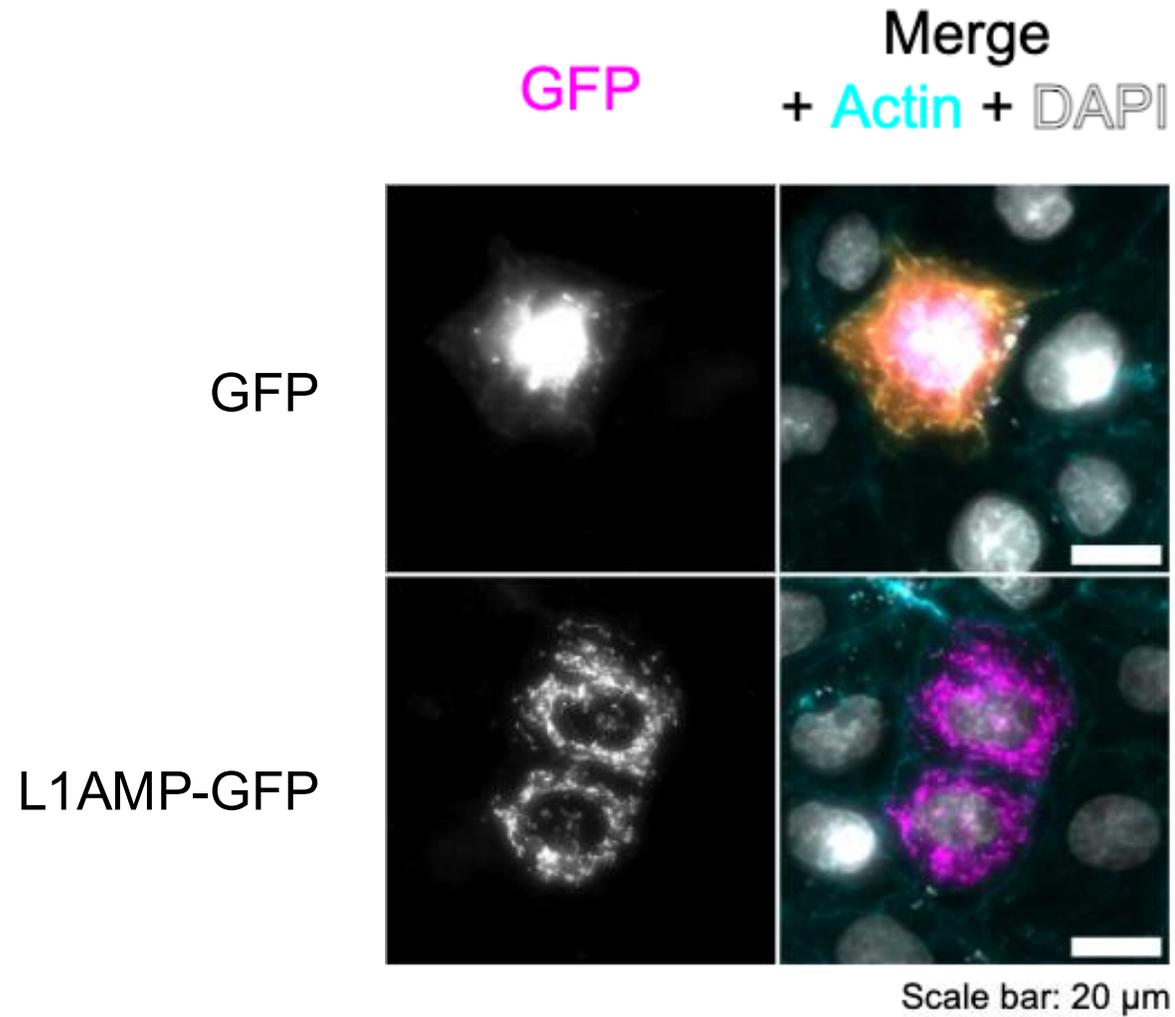


LLPS assay



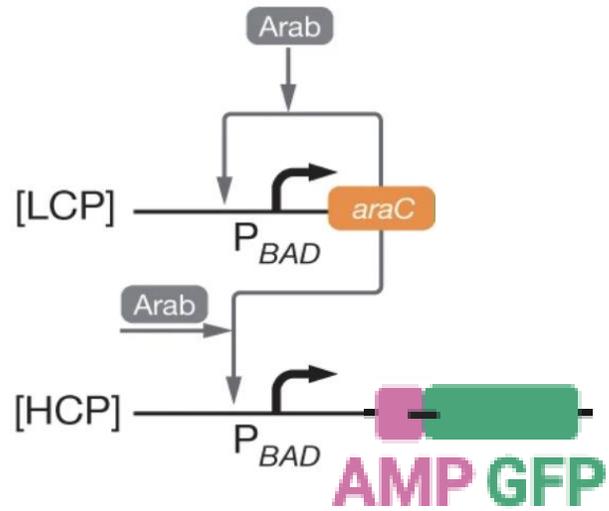
19 show both **LLPS** and **antimicrobial** behaviors

L1AMP phase-separates in human cells (TC7)



Thomas Petit, Alice LEBRETON lab
(ENS Paris)

Different expression levels of L1AMP-GFP



Daniel *et al.* 2013 *Nature*

Increasing concentration of inducer

