

Treatment Options for Carbapenem Resistance AND Antimicrobial Peptide Design with AI

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Koç University

Fig. 2. Pathogens prioritized in the 2024 BPPL update as compared with the 2017 BPPL

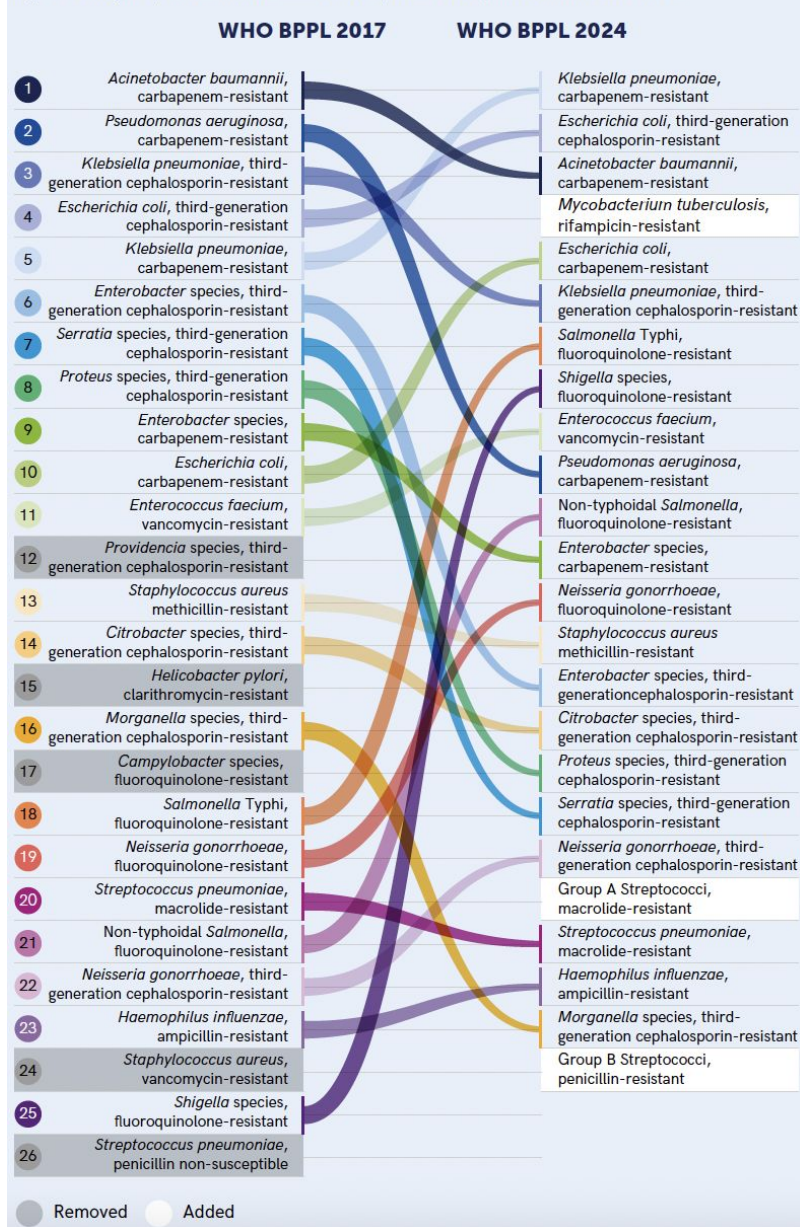
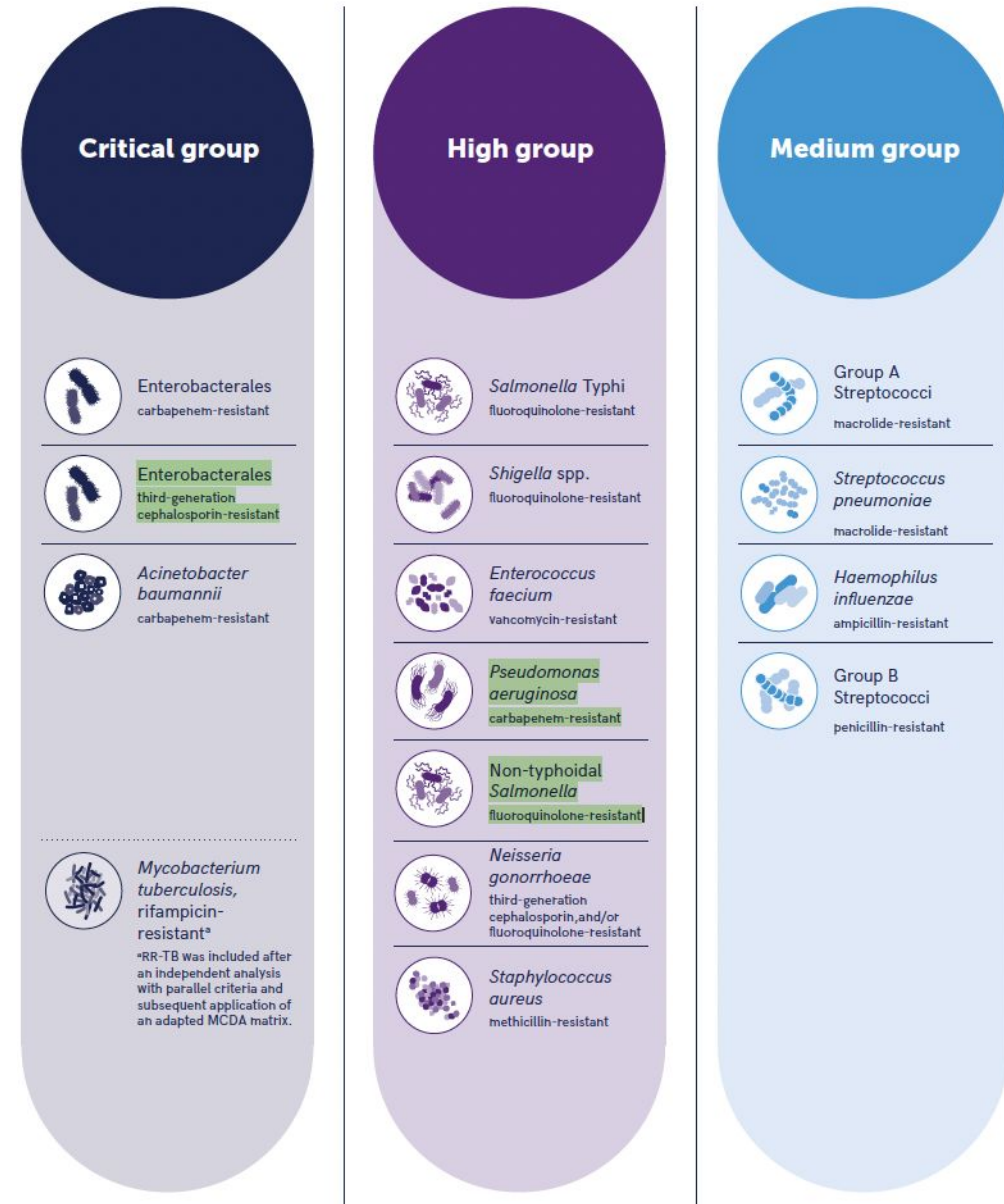
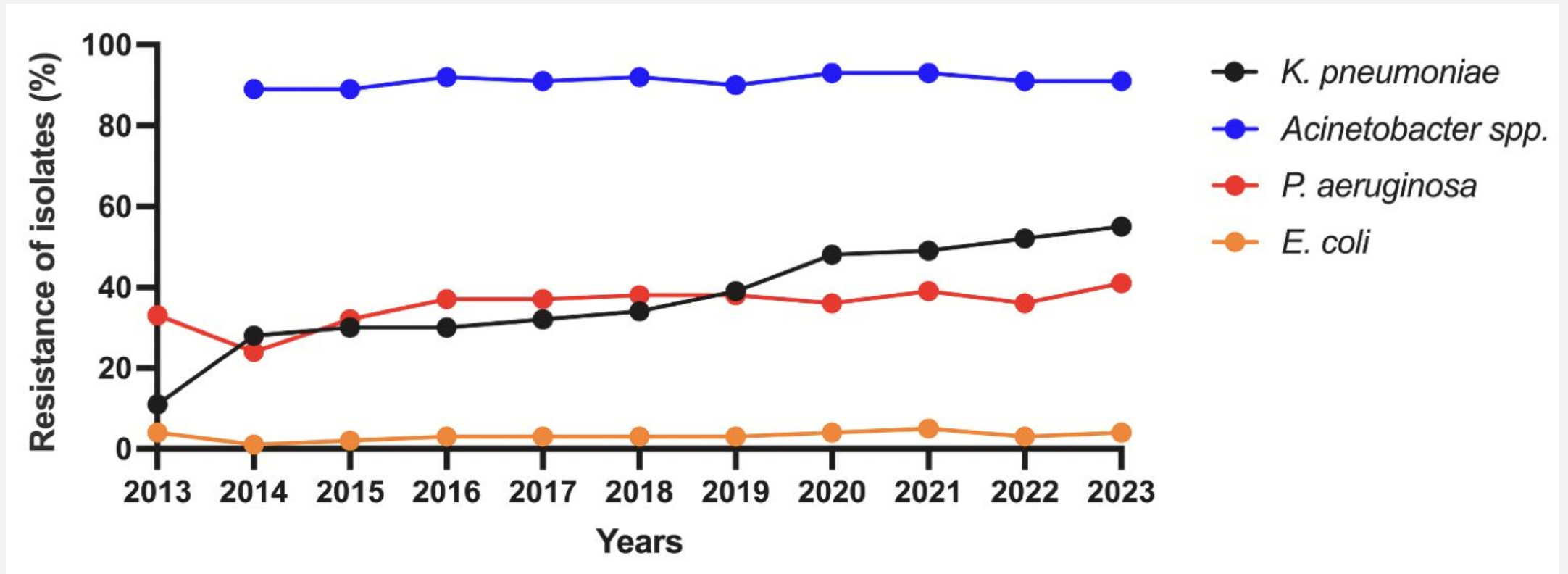


Fig 4. WHO Bacterial Priority Pathogens List, 2024





Increasing Antimicrobial Resistance in Türkiye



Alhan Ö, Özger HS, Karatuna O, Azap ÖK, Madran B, Keske Ş, Çınar G, Akdemir İ, Ergönül Ö. Antibiotic resistance in Türkiye: what has been done and what needs to be done urgently? Clin Microbiol Infect. 2025

Nightmare Scenario

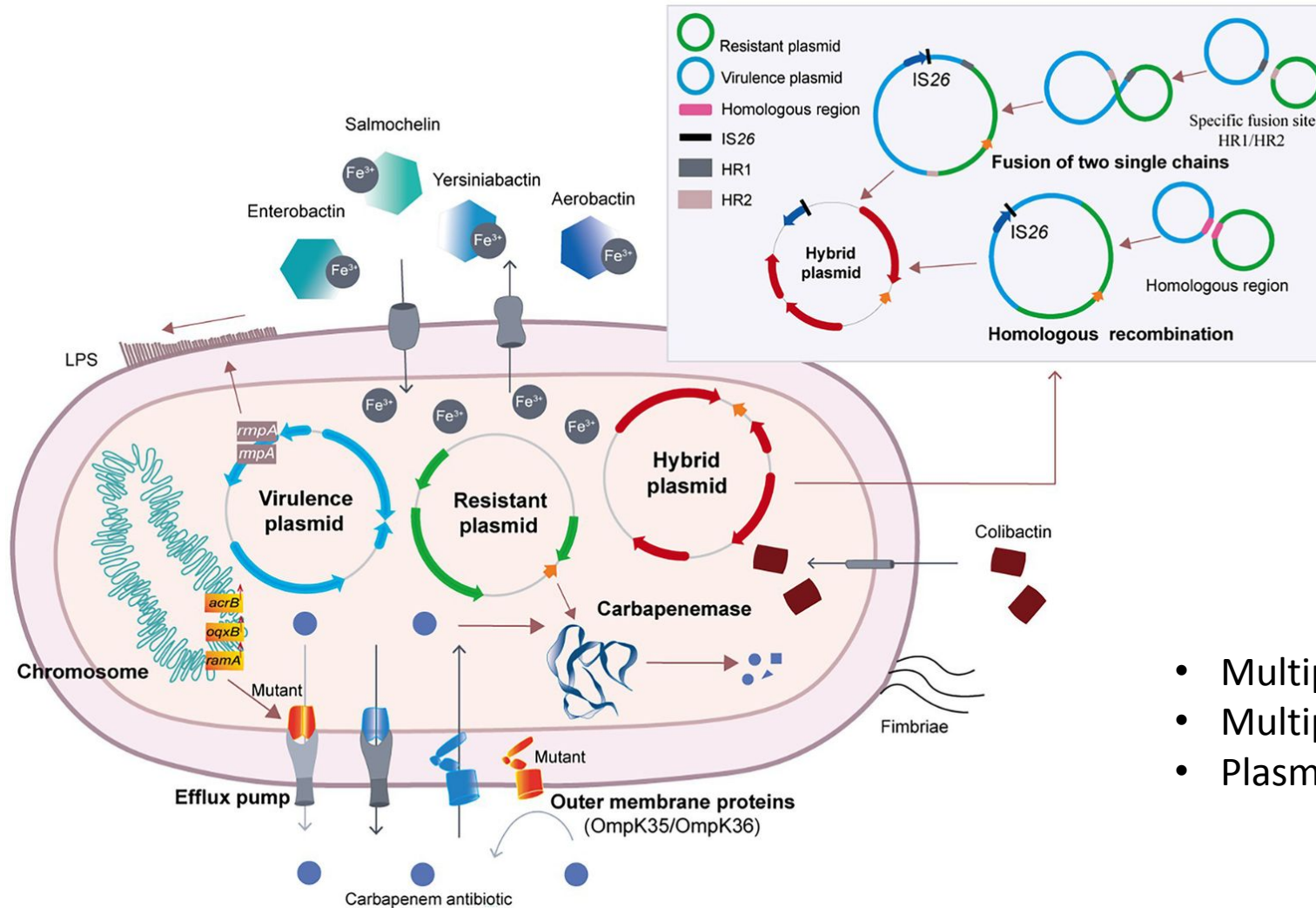
High resistance + hypervirulence

These strains combine:

- **Carbapenem resistance** (e.g., *blaKPC*, *blaNDM*, *blaOXA-48*)
- **Hypervirulence genes** (e.g., *rmpA*, *iucA*, *ybtA*)

This makes them both harder to treat and more capable of causing severe, rapidly progressing infections.

Carbapenem-resistant *Klebsiella pneumoniae* is a global threat

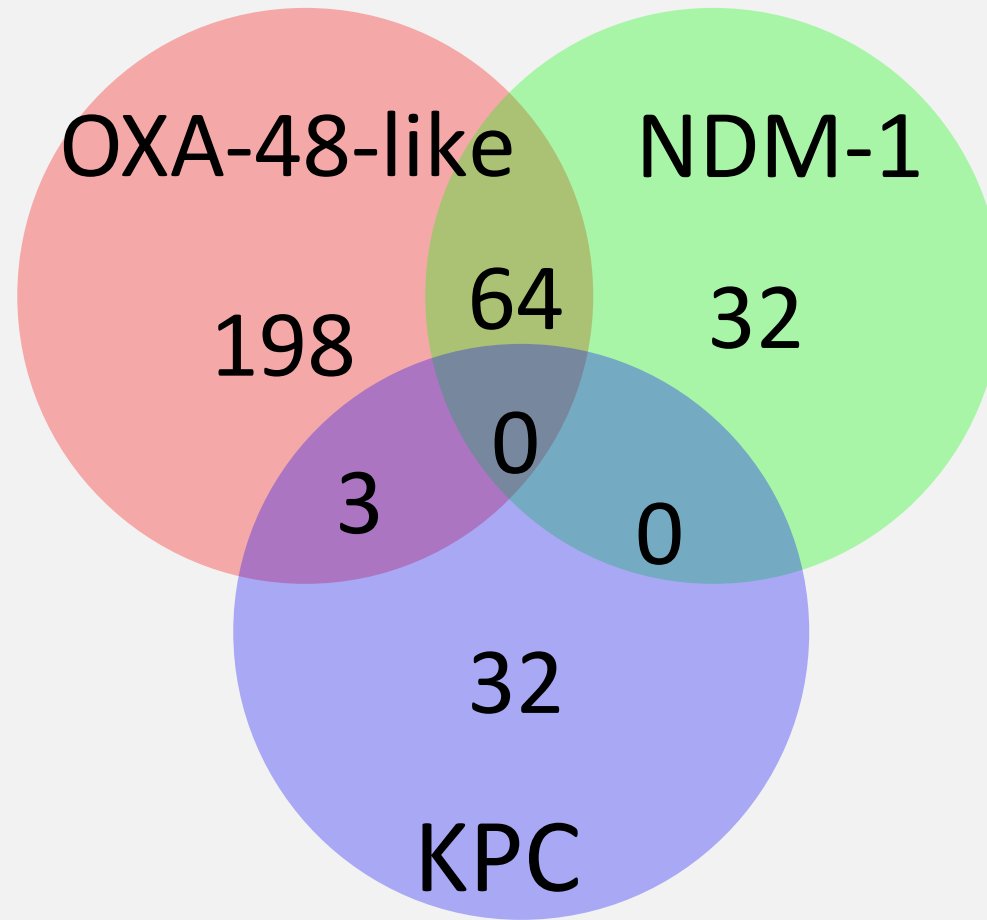


(Han et al., 2022, Front Microbiol)

- Multiple virulence factors
- Multiple antibiotic resistance mechanisms
- Plasmids for transfers

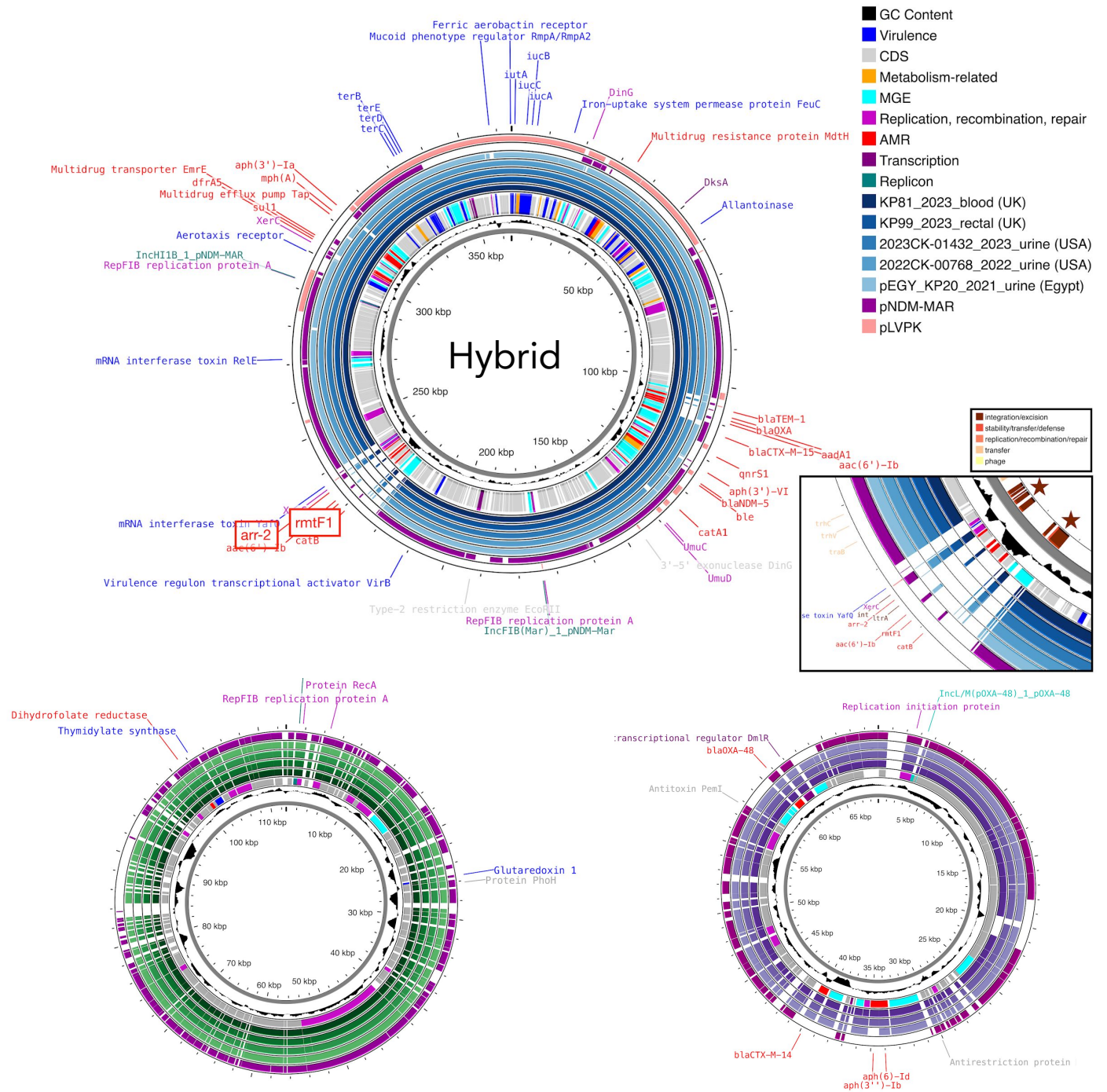


Molecular Features of Carbapenem Resistant *Klebsiella pneumoniae*, n=427



Specific subtype, ST147,
is disseminating in Türkiye
that carries a hybrid
plasmid with multiple
virulence and AMR
factors, including NDM-5

All in a single isolate!



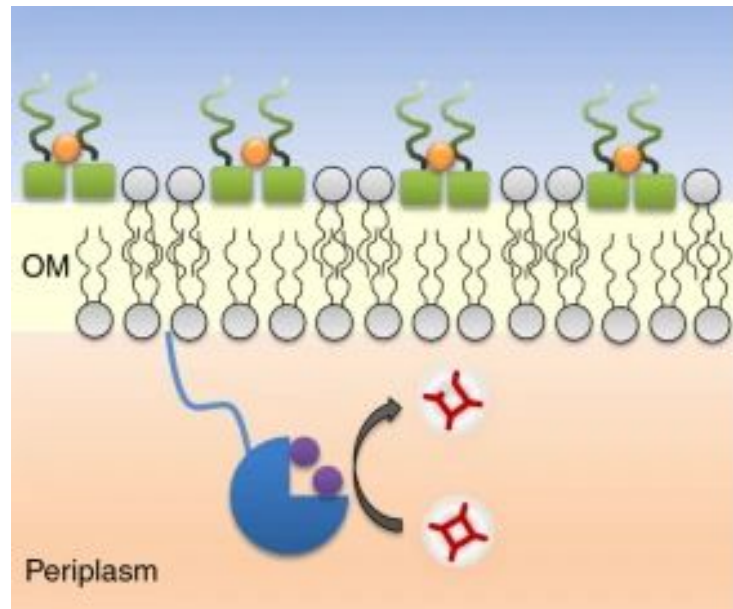
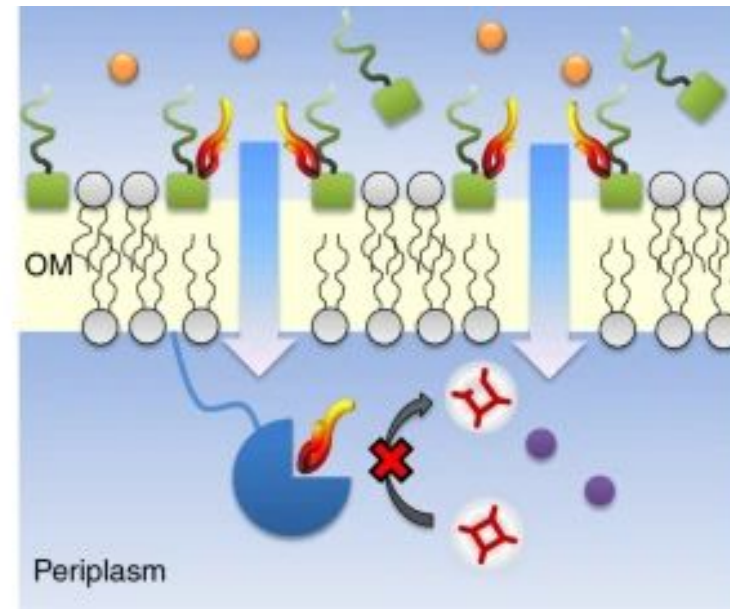
Antimicrobial Peptides (AMP)

- short peptides made by many organisms, including humans, animals, plants, and microbes
- 10-50 amino acids
- they can act against drug-resistant bacteria

LL-37 *human cathelicidin*

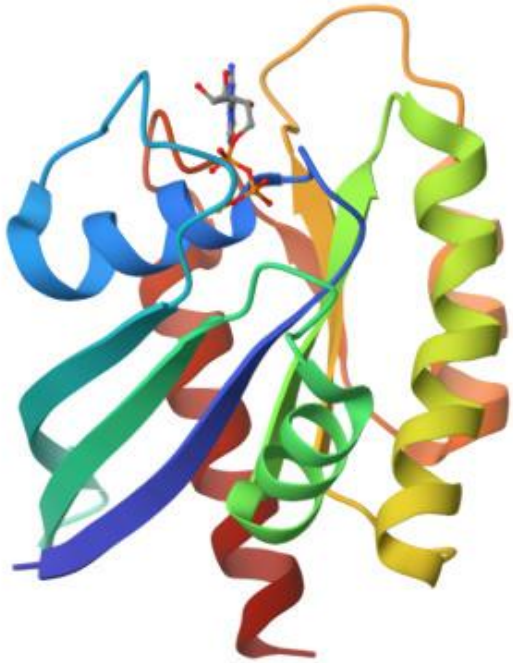
LLGDFFRKSKKEKIGKEFKRI

VORIKDFLRNLVPRTES
PDB 2K6O • α -helical amphipathic peptide

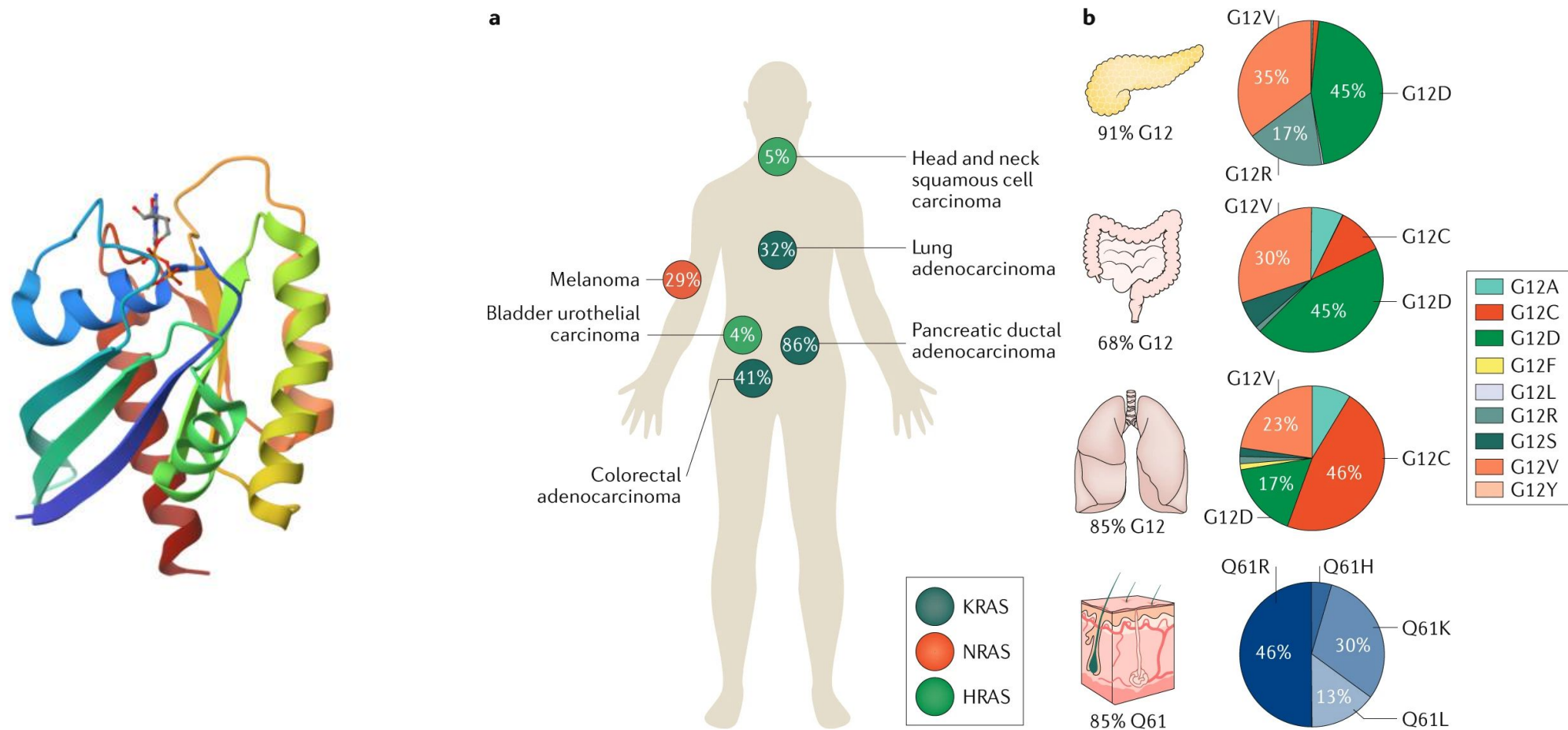


spined soldier bug

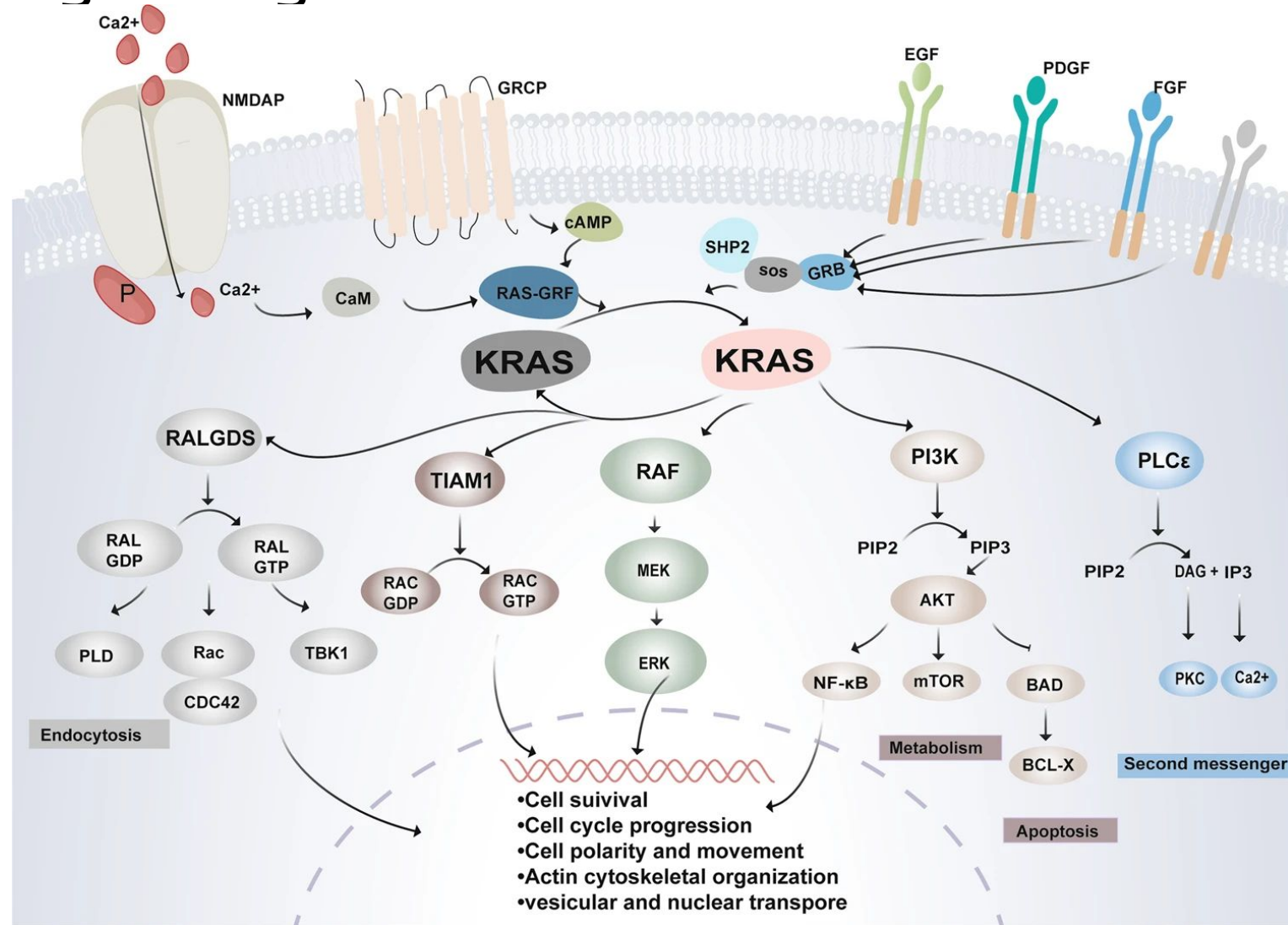
GMTEYKLVVVGAVGVGKSALTIQLIQNHFVDEYDPTIEDSYRKQVVIDGET
CLLDILDTAGQEEYSAMRDQYMRTGEGFLCVFAINNTKSFEDIHHYREQIK
RVKDSEDVPMVLVG NKCDLPSRTVDTKQAQDLARSYGIPFIETSAKTRQG
VDDAFYTLVREIRKHKE



KRAS – most mutated protein in cancer



KRAS signalling

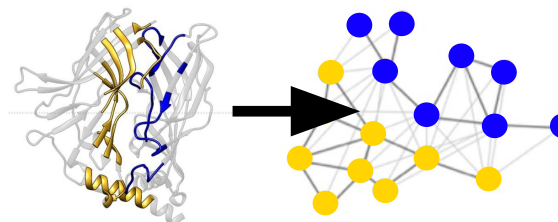
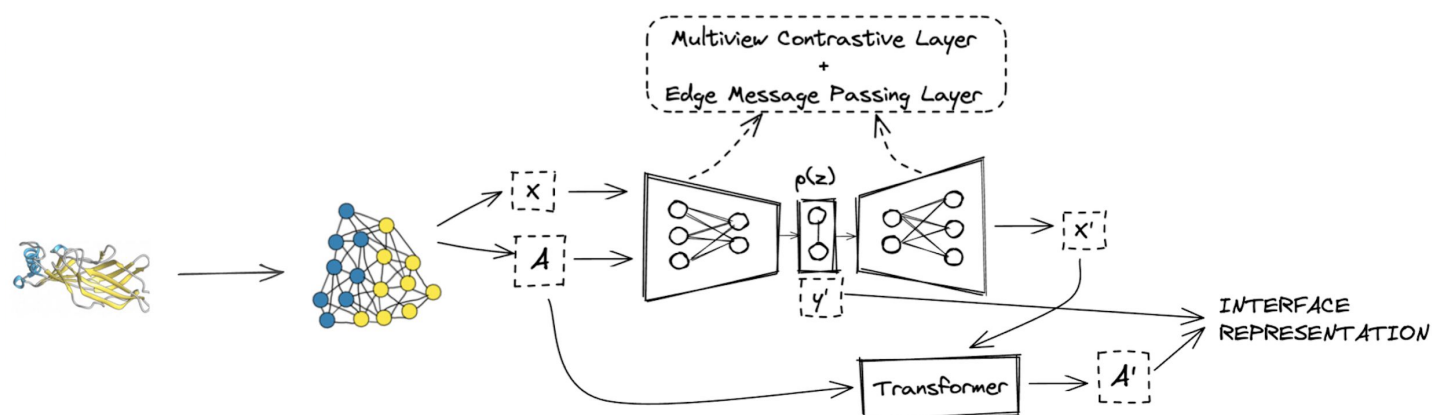




<http://www.cellsignal.com>

Multiview Contrastive Representation Learning and Protein-Protein Interaction Prediction

- *Nodes*: residue type, polarity, residue charge, relative ASA, PP, backbone dihedral angles - Phi (ϕ) and Psi (ψ)
- *Edges*:
 - Sequential edges, Radius edges, K-nearest edges



Journal of Chemical Information and Modeling > Vol 64/Issue 8 > Article

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MACHINE LEARNING AND DEEP LEARNING | March 25, 2024

ProInterVal: Validation of Protein-Protein Interfaces through Learned Interface Representations

Damla Ovek, Ozlem Keskin, and Attila Gursoy*

Can we design target-specific AMPs using Generative AI

- Two AMR-related targets identified
Goal: design **binders that also behave as antimicrobial peptides**
- Challenge:
 - Short peptides
 - Need high activity
 - Low toxicity
 - Good stability

Targets

NDM-5

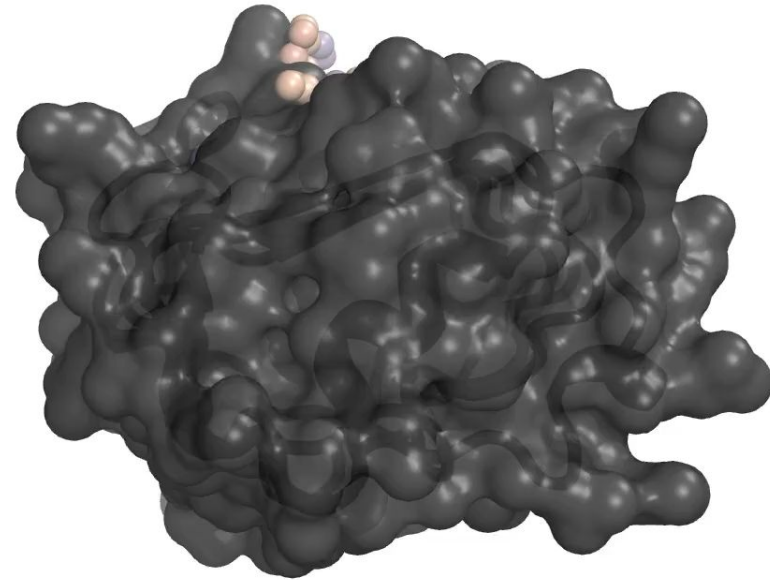
MELPNIMHPVAKLSTALAAALMLSGCMPGEIRPTIGQQMETGDQRFGLVFRQLAPNVWQHTSYLDMPGFGAVASNG
LIVRDGGRVLLVDTAWTDDQTAQILNWIQKQINLPVALAVVTHAHQDKMGGMDALHAAGIATYANALSNQLAPQEGLVA
AQHSLTFAANGWVEPATAPNFGPLKVFPYPGGHTSDNITVGIDGTDAIFGGCLIKDSKAKSLGNLGDADTEHYAASARAF
GAAPKASMIVMSHSAPDSRAAITHTARMADKLR

Close to 4EYL

KPC-3

MSLYRRVLVLLSCLSWPLAGFSATALTNLVAEPFAKLEQDFGGSIGVYAMDTGSGATVSYRAEERFPLCSSFKGFLAAAVLA
RSQQQAGLLDTPIRYGKNALVPWSPISEKYLTGTMTVAELSAAVQYSDNAAANLLLKELGGPAGLTAFMRSIGDTTFR
DRWELELNSAIPGDARDTSSPRAVTESLQKLTLSALAAPQRQQFVDWLKGNNTTGNHRIRAAVPADWAVGDKTGTCGV
YGTANDYAVVWPTGRAPIVLAVYTRAPNKDDKYSEAVIAAAARLALGLGVNGQ

Close to 3DW0

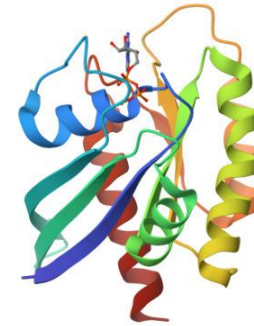
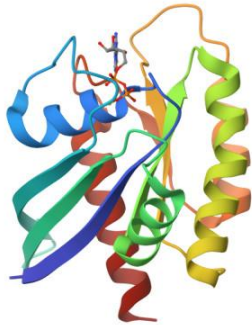


<https://www.bakerlab.org/2023/07/11/diffusion-model-for-protein-design/>

Protein Structure Prediction (Folding)

Protein Design (inverse folding)

GMTEYKLVVVGAVGVGKSALTIQLIQNHFV
DEYDPTIEDSYRKQVVIDGETCLLDILDITAG
QEEYSAMRDQYMRTGEGFLCVFAINNTKS
FEDIHHYREIQIKRVKDSEDVPMVLVGNKC
DLPSRTVDTKQAQDLARSYGIPFIETSAKT
RQGVDDAFYTLVREIRKHKE

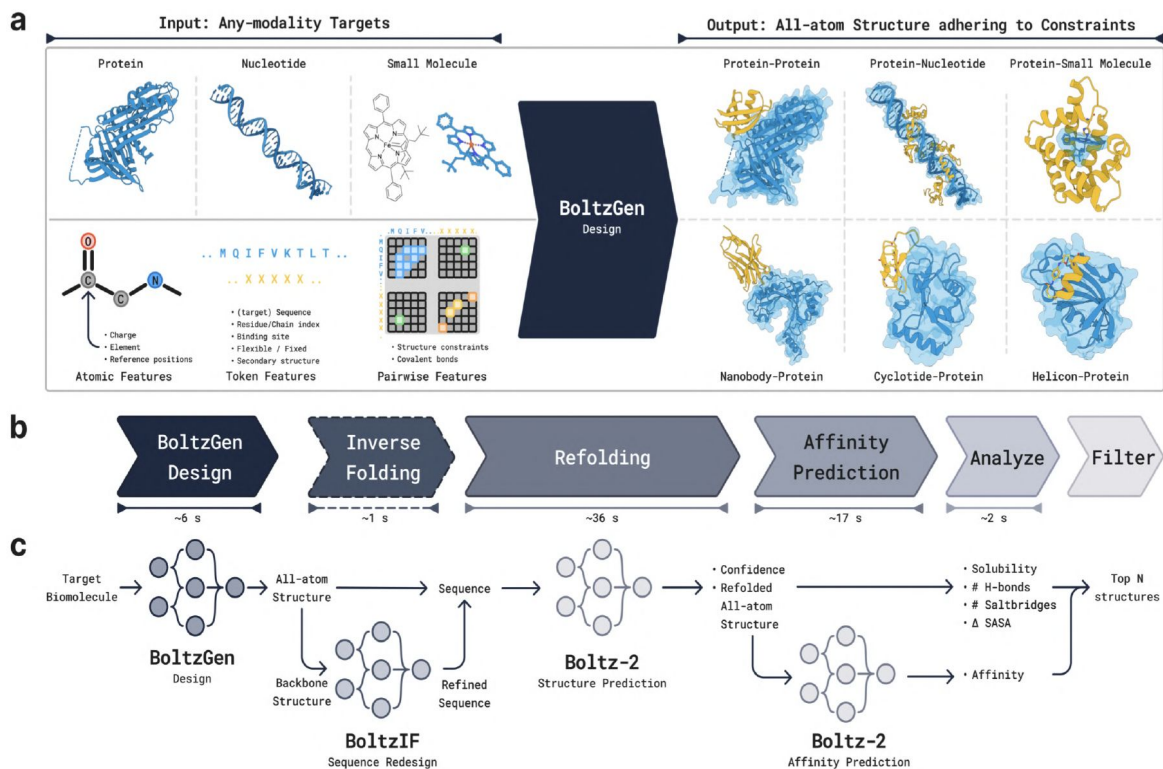


GMTEYKLVVVGAVGVGKSALTIQLIQNHFV
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RQGVDDAFYTLVREIRKHKE

Nobel Prize in Chemistry 2024

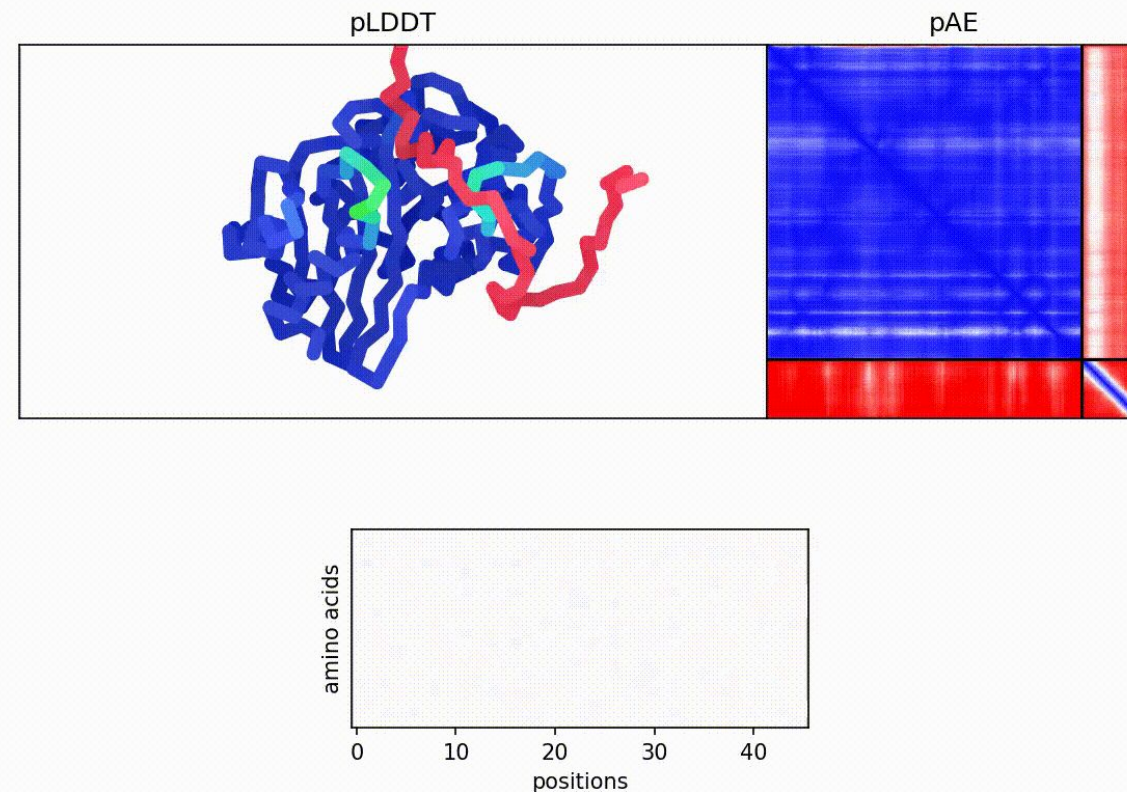
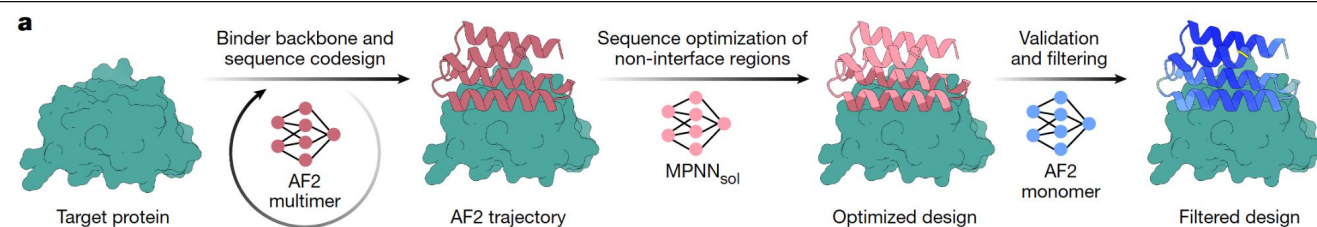
Boltzgen

<https://boltz.bio/boltzgen>

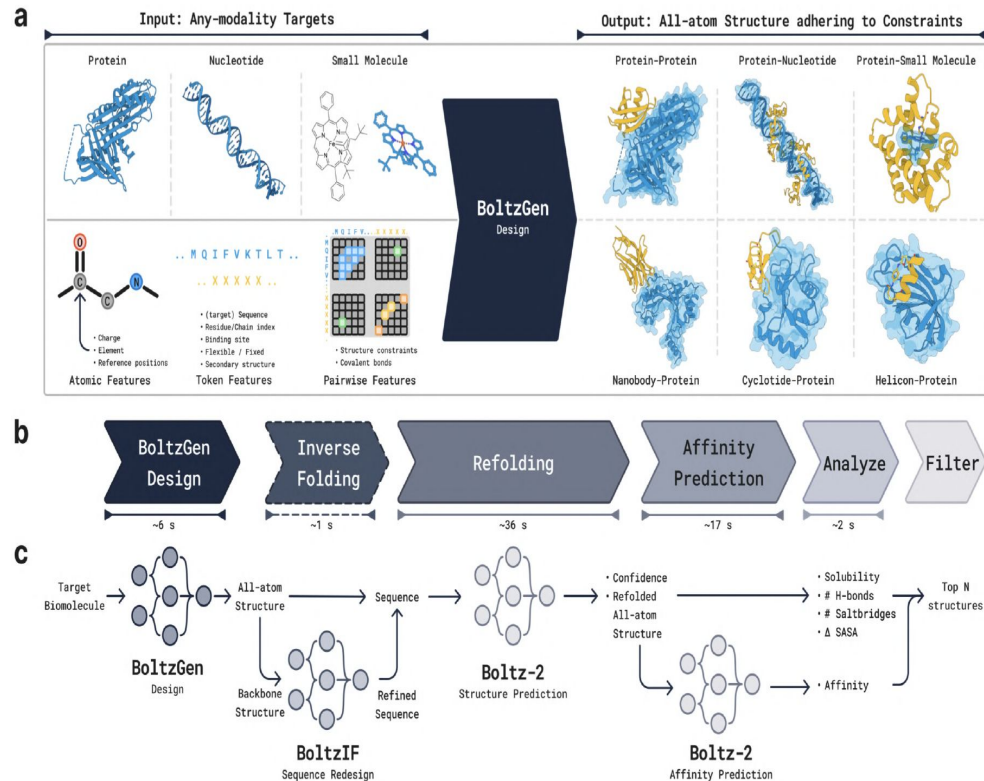


BindCraft

Nature volume 646, pages 483–492 (2025)



Can we use protein design pipelines for AMP design



SoTA Protein Design

Design approach

Use boltzgen to design binders with targets

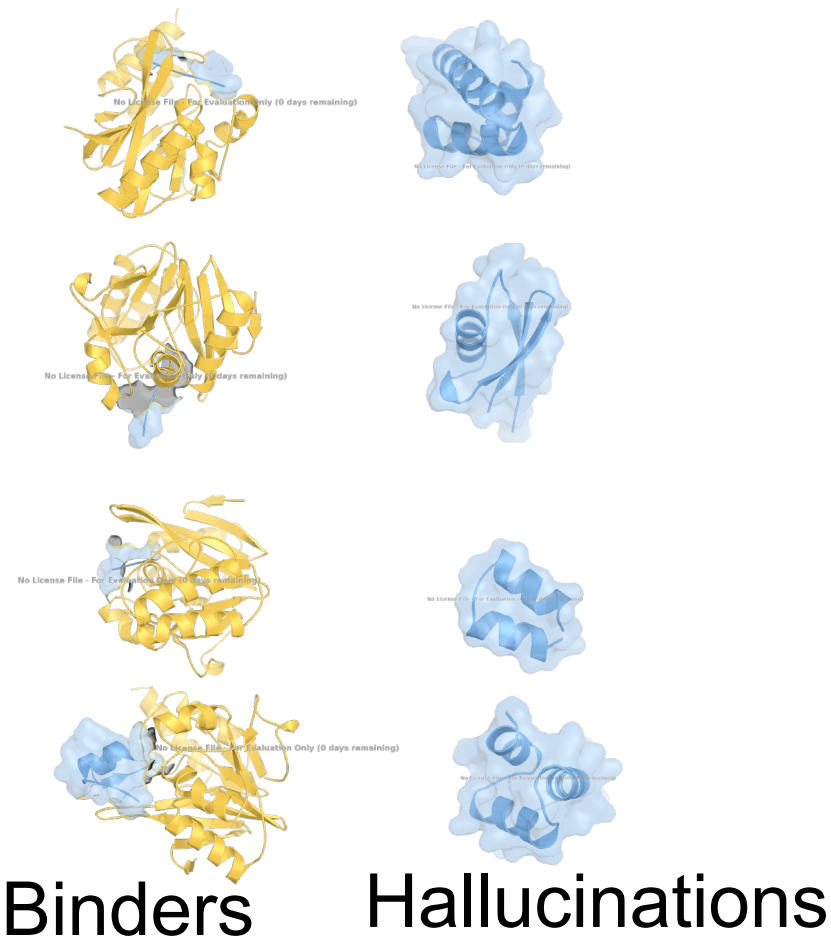
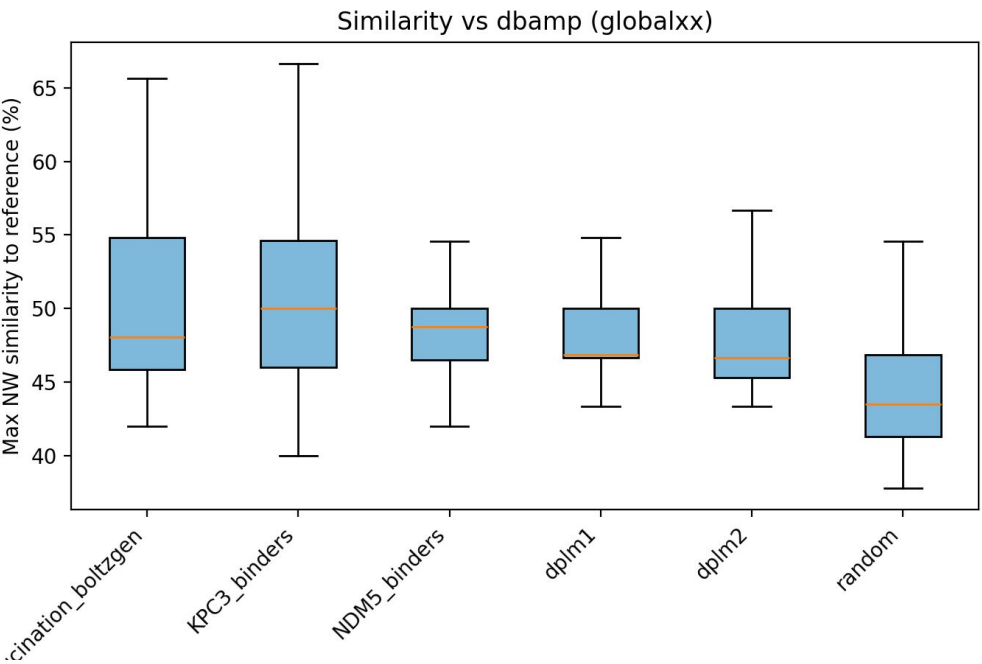
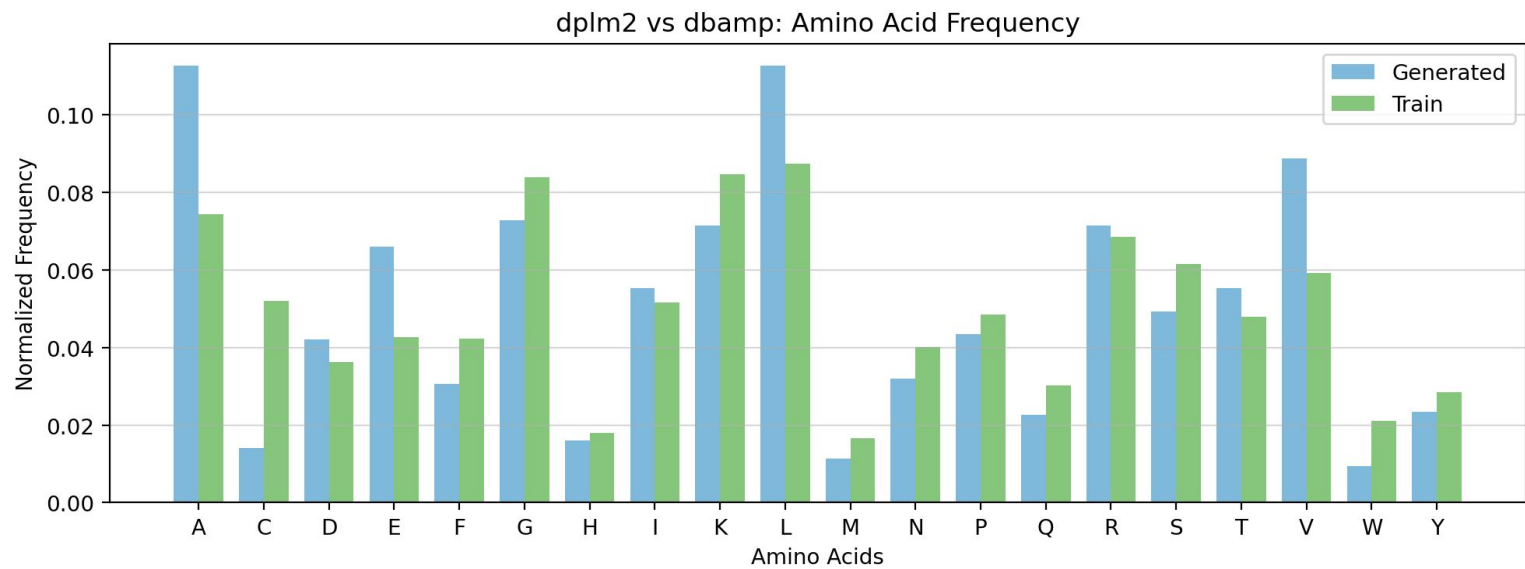
- Filter by Toxin, Macrel, AMPScanner.

Hallucination

Without targets

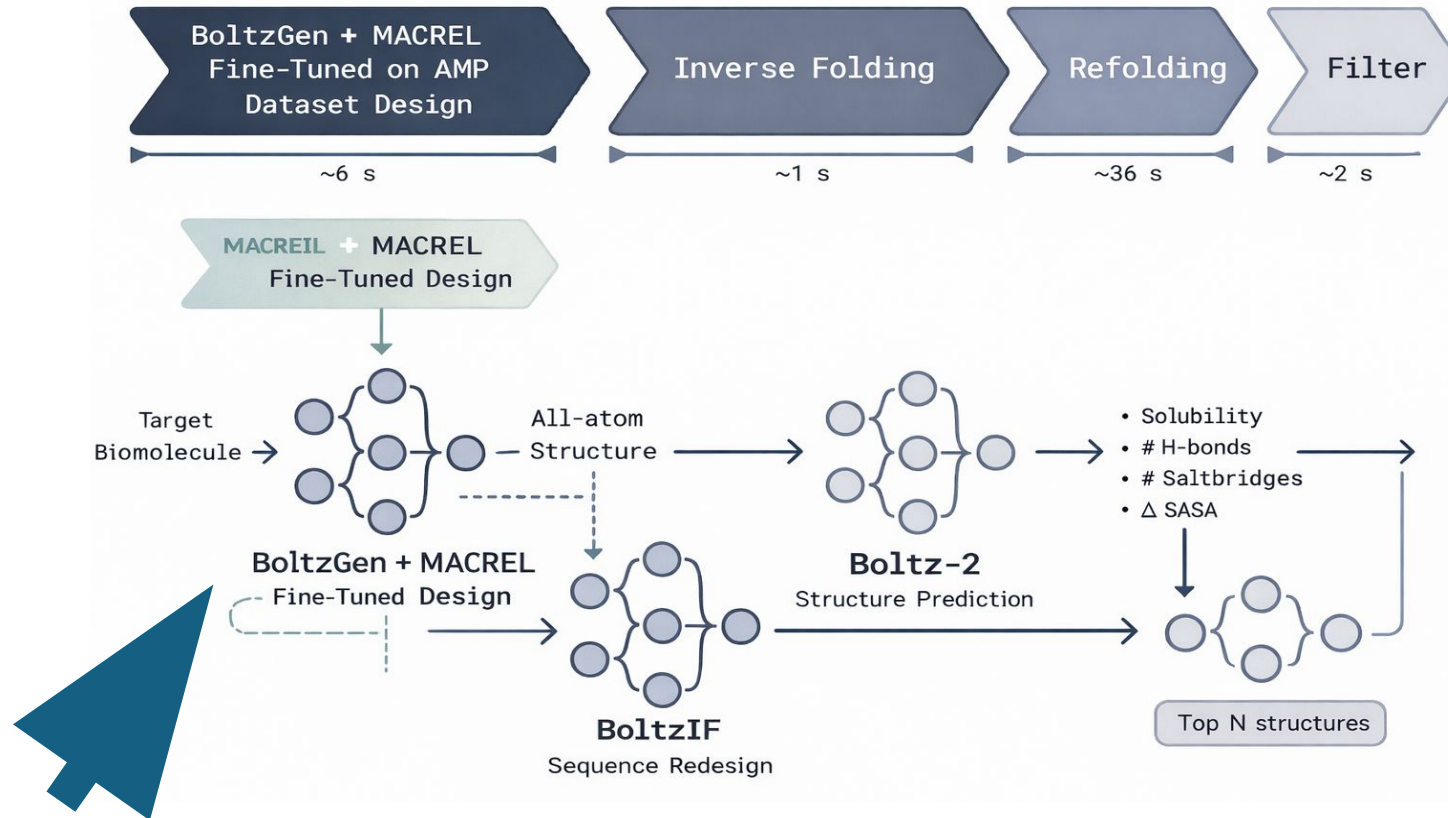
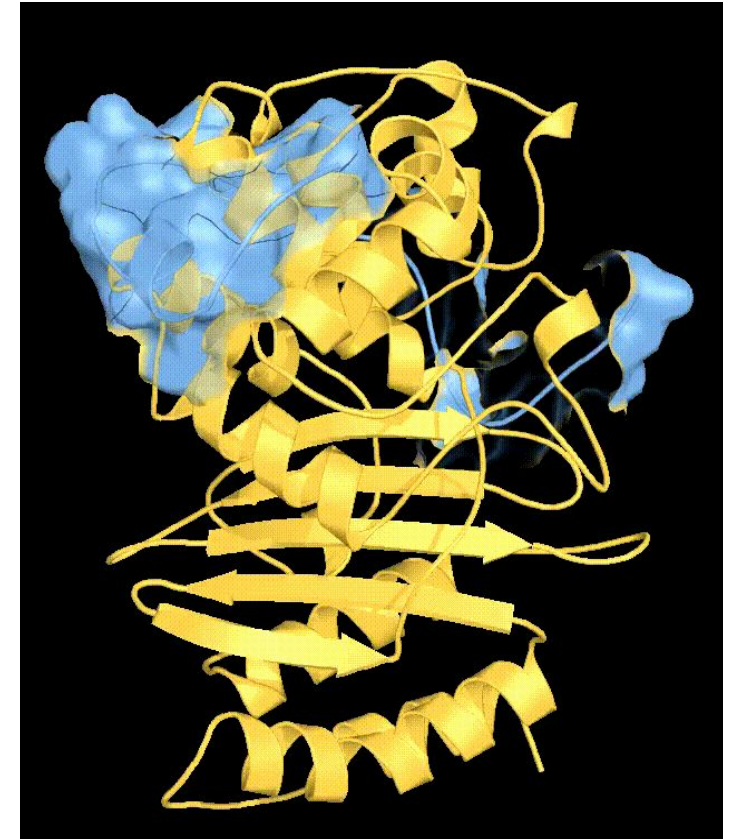
- Input xxxxxxxx to get AMPs.
- Run boltz2, Af2 to get affinity bindings to specific target(NDM).
- Filter by Toxin, Macrel, AMPScanner.

With targets – less AMP like, better binding
Without targets – more AMP like, worse binding



New AMP Design Pipeline:

- Conditioned generation using AMP classifiers (MACREL)
- Generated binders under AMP-activity constraints



Team



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Erkmen Erken MBGE CS DM



Eylül Sevinç MBGE CS DM

Thank you



ID & CM

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Cansel Vatansever
Fatihan Pınarlık
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