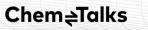


# Is AI in Drug Discovery trapped in the data of the past?

Thras Karydis, Chief Technology Officer





September 25, 2024

#### DEEPCURE

# Leader in AI + robotic chemical synthesis for small molecule drug discovery



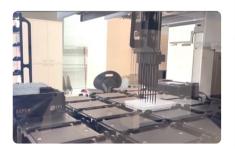
#### **I&I** Therapeutics

DeepCure with Generate Biomedicines, Scorpion Tx, & Valo Health



Leadership in AI

DeepCure with Relay Therapeutics, Exscientia, & Schrödinger



#### World's Most Advanced Chemistry Automation

Fully automated multi-step chemical synthesis

**3** DRUG DISCOVERY PROGRAMS

2025 1<sup>st</sup> CLINICAL TRIAL

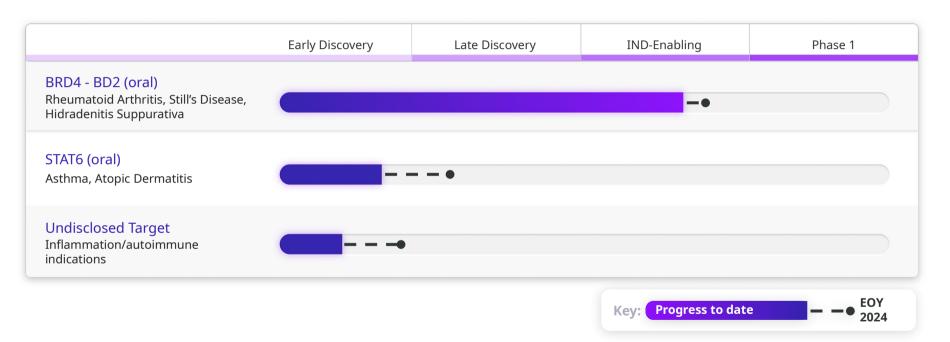


\$71M RAISED

🔷 🏠 DEEPCURE

#### DEEPCURE

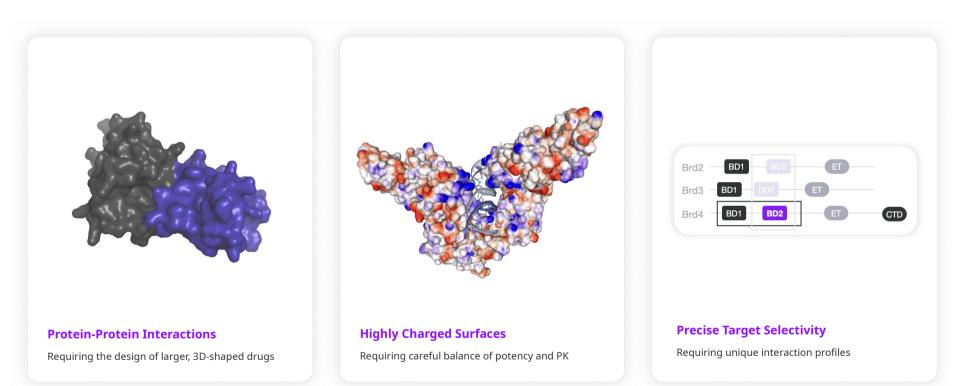
## First- or best-in-class oral small molecule therapies





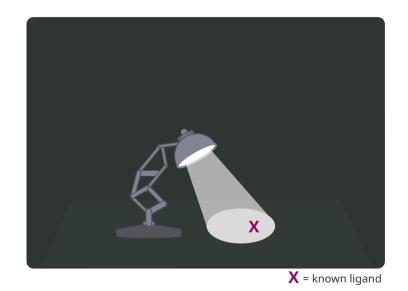
RA – Rheumatoid Arthritis; HS - Hidradenitis Suppurativa; SJIA - Systemic Juvenile Idiopathic Arthritis; AOSD - Adult-Onset Still's Disease; MAS - Macrophage Activation Syndrome; AD - Atopic Dermatitis; IBD - Inflammatory Bowel Disease (Crohn's Disease and Ulcerative Colitis).

## Immune targets pose new challenges for small molecule drug design



### **W DEEPCURE**

# Can AI deliver on it's promise to generate *novel* drugs for intractable targets? So far, no.



# Why? Because it's hard to escape the data trap!

- 1. Scientists and models focus on a known binding mode and existing chemical matter
- 2. Design biases from past data and established processes result in testing similar compounds again and again

### **N** DEEPCURE

How can we develop technology to avoid these innovation pitfalls?

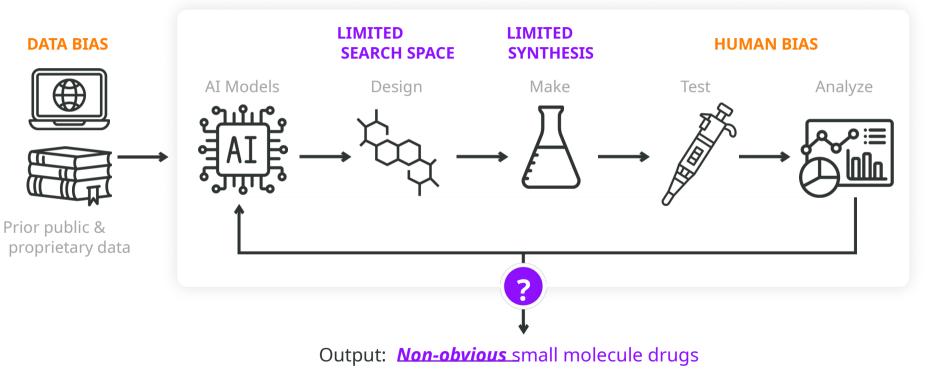


# AI can innovate only if we expand the relevant solution space AND avoid design biases



## Let's take a closer look in the AI-driven drug discovery process

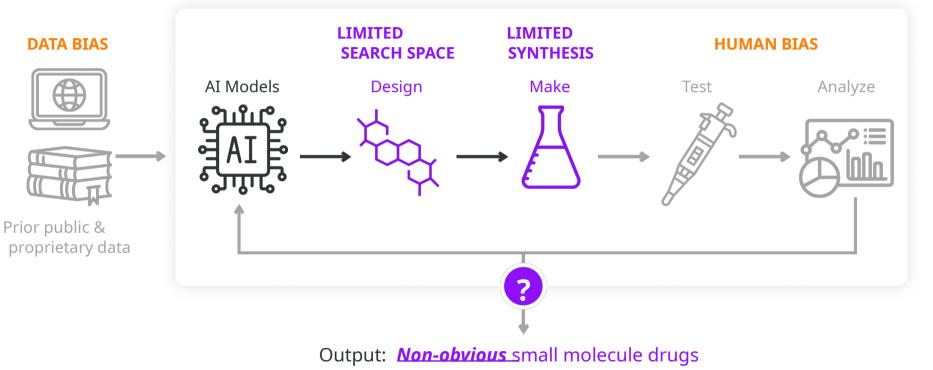
**PROCESS BIAS** 



## **N** DEEPCURE

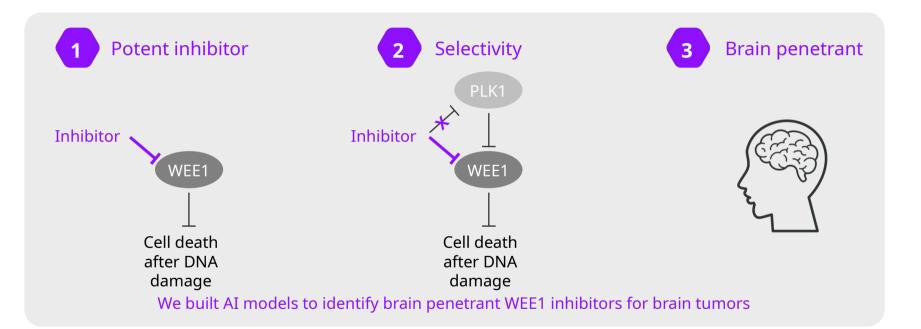
## Let's take a closer look in the AI-driven drug discovery process

**PROCESS BIAS** 



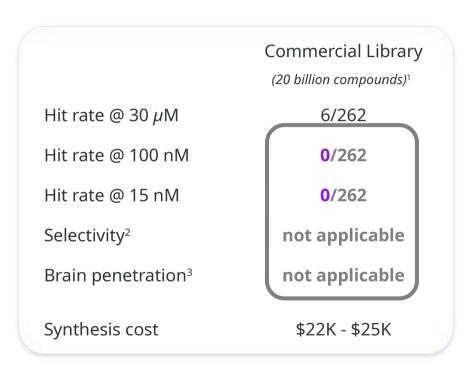
### **W DEEPCURE**

Case study on the importance of expanding the chemical space





## Zero hits in commercial libraries offering limited chemical space





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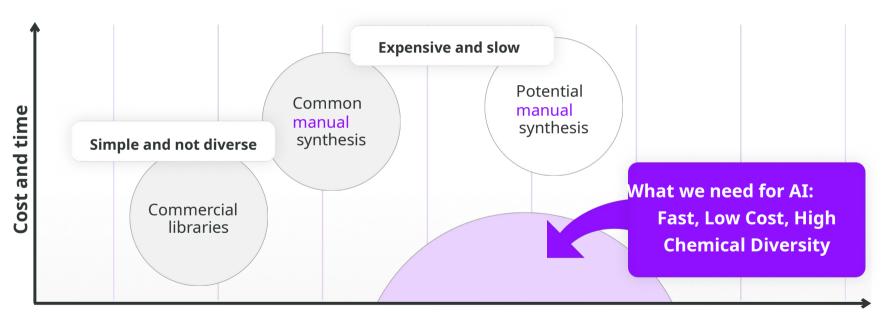
Immediate success when we expanded the chemical space by allowing custom synthesis of compounds top ranked by AI models

	Commercial Library (20 billion compounds)	Custom Synthesis
Hit rate @ 30 $\mu$ M	6/262	7/12
Hit rate @ 100 nM	0/262	7/12
Hit rate @ 15 nM	0/262	Yes (4/12)
Selectivity <sup>1</sup>	not possible	Yes (6/12)
Brain penetration <sup>2</sup>	not possible	Yes (4/12)
Synthesis cost	\$22K - \$25K	\$25K

Lessons:

- 1. Don't assume AI is the problem!
- 2. AI will not help if the search space is limited

We need custom libraries that unlock a larger chemical space and enable more compounds to be synthesized

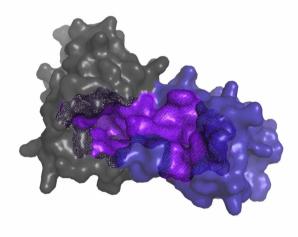


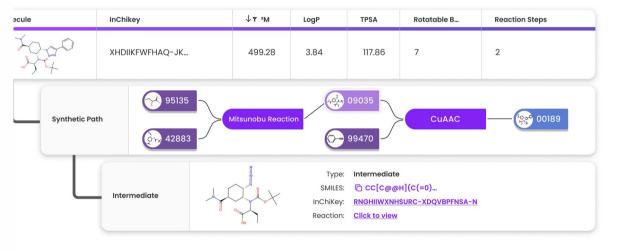
**Chemical diversity and complexity** 



# Using GenAI we can generate custom libraries of fit-for-purpose, synthesizable molecules

#### Unlocking GenAI creativity with physics and organic chemistry

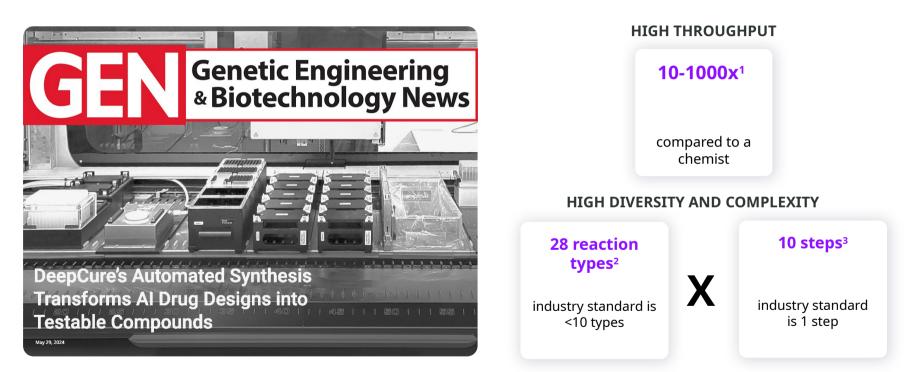




MolGen™



Robotic platform delivers high throughput synthesis **AND** complex compounds so that synthesis is not the bottleneck for AI-guided design



### **W** DEEPCURE

1 Currently at 10x an average chemist (~6 molecules/month) and expect up to 1000x by 2025 | 2 Currently 28 reaction types but expect 100 types by Q1 2026 | 3 Current number of reaction steps is 10 (incl. 5 purifications), but more is feasible.

#### **AVOID DESIGN BIAS**

## Let's take a closer look in the AI-driven drug discovery process

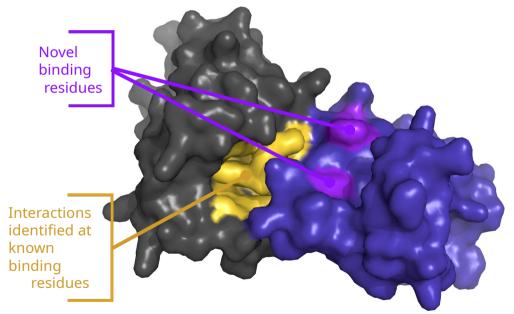
**PROCESS BIAS** LIMITED LIMITED **DATA BIAS HUMAN BIAS SEARCH SPACE SYNTHESIS** AI Models Make Design Test Analyze Prior public & proprietary data

Output: Non-obvious small molecule drugs

### **N** DEEPCURE

#### **AVOID DESIGN BIAS**

# Using first-principles derived hypotheses to eliminate the data bias towards known compounds



#### Exhaustive mapping of protein surface exposes untapped interactions

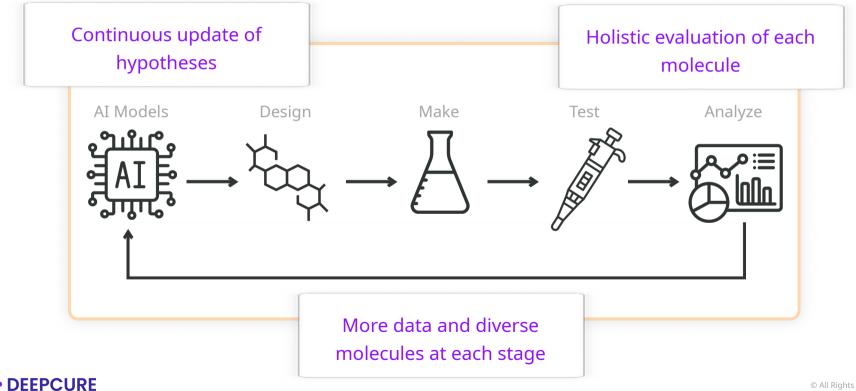
Residue	Interaction Type	Weight
LYS 544	cationpi:ligandpi	0.26
LYS 544	salt-bridge:ligand-protein+	0.1
SER 566	hbond:protein2ligand	0.32
ARG 562	salt-bridge:ligand-protein+	0.1
GLU	salt-bridge:ligand+protein-	0.48
<b>AR</b> G 667	cationpi:ligandpi	0.1
THR 672	hbond:protein2ligand	<del>0</del> .28

### **W DEEPCURE**

#### PocketExpander™

#### **AVOID DESIGN BIAS**

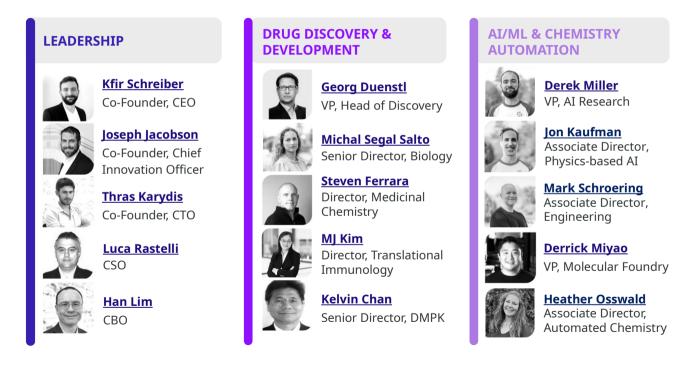
Innovative drug design constantly revisiting hypothesis, data and perspectives at every stage of the discovery process



#### ACKNOWLEDGMENTS

DEEPCURE

Team of drug hunters and innovators collaborating to advance small molecule discovery for challenging targets



## **THANK YOU!**

